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METHODS OF REGULATING METABOLISM AND MITOCHONDRIAL FUNCTION

BACKGROUND OF THE INVENTION

Type 2 diabetes (DM2) affects an estimated 110 million people worldwide and is a major contributor to atherosclerotic vascular disease, blindness, amputation, and kidney failure. Defects in insulin secretion are observed early in patients with MODY, a monogenic form of type 2 diabetes; insulin resistance at tissues such as skeletal muscle is a cardinal feature of patients with fully developed DM2. Many molecular pathways have been implicated in the disease process: beta-cell development, insulin receptor signaling, carbohydrate production and utilization, mitochondrial metabolism, fatty acid oxidation, cytokine signaling, adipogenesis, adrenergic signaling, and others. It remains unclear, however, which of these or other pathways are disturbed in, and might be responsible for, DM2 in its common form.

Therefore, a need remains to identify the molecular pathways implicated in the disease process and to develop new tools and assays to identify therapeutics for the treatment of diabetes.

SUMMARY OF THE INVENTION

One aspect of the invention provides a method of modulating a biological response in a cell, the method comprising contacting the cell with at least one agent that modulates the expression or activity of Errα or Gabp, wherein the biological response is (a) expression of at least one OXPHOS gene; (b) mitochondrial biogenesis; (c) expression of Nuclear Respiratory Factor 1 (NRF-1); (d) β-oxidation of fatty acids; (e) total mitochondrial respiration; (f) uncoupled respiration; (g) mitochondrial DNA replication; (h) expression of mitochondrial enzymes; or (i)skeletal muscle fiber-type switching.

Another aspect of the invention provides a method of determining if an agent is a potential agent for the treatment of a disorder that is characterized by glucose intolerance, insulin resistance or reduced mitochondrial function, the method comprising determining if

the agent increases: (i) the expression or activity of Errα or Gabp in a cell; or (ii) the formation of a complex between a PGC-1 polypeptide and (1) an Errα polypeptide; or (2) a Gabp polypeptide; wherein an agent that increases (i) or (ii) is a potential target for the treatment of the disorder.

The invention also provides a method of identifying an agent that modulates a biological response, the method comprising (a) contacting, in the presence of the agent, a PGC-1 polypeptide and an (i) Errα polypeptide, or (ii) a Gabp polypeptide, under conditions which allow the formation of a complex between the PGC-1 polypeptide and (i) the Errα polypeptide, or (ii) the Gabp polypeptide; and (b) detecting the presence of the complex; wherein an agent that modulates the biological response is identified if the agent increases or decreases the formation of the complex, and wherein the biological response is (a) expression of at least one OXPHOS gene; (b) mitochondrial biogenesis; (c) expression of Nuclear Respiratory Factor 1 (NRF-1); (d) β-oxidation of fatty acids; (e) total mitochondrial respiration; (f) uncoupled respiration; (g) mitochondrial DNA replication; (h) expression of mitochondrial enzymes; or (i) skeletal muscle fiber-type switching.

Additionally, the invention provides a method of treating or preventing a disorder characterized by reduced mitochondrial function, glucose intolerance, or insulin intolerance in a subject, the method comprising administering to the subject a therapeutically effective amount of an agent which (i) increases the expression or activity of Errα or Gabp or both; or (ii) increases the formation of a complex between a PGC-1 polypeptide and (a) an Errα polypeptide; (b) a Gabp polypeptide; or both; or (iii) binds to an (a) Errα binding site, or to a (b) Gabpa binding site, and which increases transcription of at least one gene in the subject, said gene having an Errα binding site, a Gabpa binding site, or both.

Yet another aspect of the invention provides a method of treating or preventing a disorder characterized by reduced mitochondrial function, glucose intolerance, or insulin intolerance in a subject, the method comprising administering to the subject a therapeutically effective amount of an agent which increases the expression or activity of a gene, wherein the gene has an Errα binding site or a Gapba binding site.

The invention also provides a method of reducing the metabolic rate of a subject in

need thereof, the method comprising administering to the subject a therapeutically effective amount of an agent which decreases the expression or activity of at least one of the following: (i) Errα; (ii) Gabpa; (iii) a gene having an Errα binding site, a Gabpa binding site, or both; or (iv) a transcriptional activator which binds to an Errα binding site or to a Gabpa binding site; thereby reducing the metabolic rate of the patient.

The invention further provides a method of identifying a susceptibility locus for a disorder that is characterized by reduced mitochondrial function, glucose intolerance, or insulin intolerance in a subject, the method comprising (i) identifying at least one polymorphisms in a gene, or linked to a gene, wherein the gene (a) has an Errα binding site, a Gabpa binding site, or both; or (b) is Errα, Gabpa, or Gabpb; (ii) determining if at least one polymorphism is associated with the incidence of the disorder, wherein if a polymorphism is associated with the incidence of the disorder then the gene having the polymorphism, or the gene to which the polymorphism is linked, is a susceptibility locus.

A related aspect of the invention provides a method of determining if a subject is at risk of developing a disorder which is characterized by reduced mitochondrial function, the method comprising determining if a gene from the subject contains a mutation which reduces the function of the gene, wherein the gene has an Errα binding site, a Gapba binding site, or both, wherein if a gene from the subject contains a mutation then the subject is at risk of developing the disorder.

Yet another aspect of the invention provides a method of identifying a transcriptional regulator having differential activity between an experimental cell and a control cell, the method comprising (i) determining the level of gene expression of at least two genes in the experimental cell and in the control cell; (ii) ranking genes according to a difference metric of their expression level in the experimental cell compared to the control cell; (iii) identifying a subset of genes, wherein each gene in the subset contains the same DNA sequence motif; (iv) testing using a nonparametric statistic if the subset of genes are enriched at either the top or the bottom of the ranking; (v) optionally reiterating steps (ii)-(iii) for additional motifs; (vi) for a subset of genes that is enriched, identifying a transcriptional regulator which binds to a DNA sequence motif that is contained in the subset of genes; thereby identifying a transcriptional regulator having differential activity between two cells.

An additional aspect of the invention provides a method of treating impaired glucose tolerance in an individual in need thereof, the method comprising administering to the individual a therapeutically effective amount of an agent which increases the expression level of at least two OXPHOS-CR genes, thereby treating impaired glucose tolerance in the individual. A related aspect provides a method of treating obesity in an individual, comprising administering to the individual a therapeutically effective amount of an agent which increases the expression level of at least two OSPHOS-CR genes, thereby treating obesity in the individual.

One aspect of the invention provides a method of detecting statistically-significant differences in the expression level of at least one biomarker belonging to a biomarker set, between the members of a first and of a second experimental group, comprising: (a) obtaining a biomarker sample from members of the first and the second experimental groups; (b) determining, for each biomarker sample, the expression levels of at least one biomarker belonging to the biomarker set and of at least one biomarker not belonging to the set; (c) generating a rank order of each biomarker according to a difference metric of its expression level in the first experimental group compared to the second experimental group; (d) calculating an experimental enrichment score for the biomarker set by applying a non parametric statistic; and (e) comparing the experimental enrichment score with a distribution of randomized enrichment scores to calculate the fraction of randomized enrichment scores greater than the experimental enrichment score, wherein a low fraction indicates a statistically-significant difference in the expression level of the biomarker set, between the members of a first and of a second experimental group. In one embodiment, the distribution of randomized enrichment scores is generated by (i) randomly permutating the assignment of each biomarker sample to the first or to the second experimental group; (ii) generating a rank order of each biomarker according to the absolute value of a difference metric of its expression level in the first experimental group compared to the second experimental group; (iii) calculating an experimental enrichment score for the biomarker set by applying a non parametric statistic to the rank order; and (iv) repeating steps (i), (ii) and (iii) a number of times sufficient to generate the distribution of randomized enrichment scores.

In addition, the invention provides a method of identifying an agent that regulates expression of OXPHOS-CR genes, the method comprising (a) contacting (i) an agent to be

assessed for its ability to regulate expression of OXPHOS-CR genes with (ii) a test cell; and (b) determining whether the expression of at least two OXPHOS-CR gene products show a coordinate change in the test cell compared to an appropriate control, wherein a coordinate change in the expression of the OXPHOS-CR gene products indicates that the agent regulates the expression levels of OXPHOS-CR genes. In one embodiment, the OXPHOS-CR genes are selected from the group consisting of NDUFB3, SDHA, NDUFA8, COX7A1, UQCRC1, NDUFC1, NDUFS2, ATP5O, NDUFS3, SDHB, NDUFS5, NDUFB6, COX5B, CYC1, NDUFA7, UQCRB, COX7B, ATP5L, COX7C, NDUFA5, GRIM19, ATP5J, COX6A2 NDUFB5, CYCS, NDUFA2 and HSPC051.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a schematic overview of an embodiment of gene set enrichment analysis (GSEA). The goal of GSEA is to determine whether any *a priori* defined gene sets (step 1) are enriched at the top of list of genes ordered on the basis of expression difference between two classes (*e.g.*, high in NGT vs. DM2). Genes, $R_1,\ldots R_N$, are rank ordered on the basis of expression difference (step 2) using an appropriate difference measure (*e.g.*, signal to noise ratio (SNR), see Methods). To determine whether the G members of a gene set S are enriched at the top of this list (step 3), a Kolmogorov-Smirnov (K-S) running sum statistic is computed: beginning with the top ranking gene, the running sum increases when a gene annotated to be a member of gene set S is encountered, and decreases otherwise. The enrichment score (*ES*) for a single gene set is defined as the greatest positive deviation of the running sum across all N genes. When many members of S appear at the top of the list, *ES* is high. The enrichment score is computed for every gene set using actual data, and the maximum *ES* (*MES*) achieved is recorded (step 4). To determine whether *one or more* of the gene sets are enriched in one diagnostic class relative to the other (step 5), the entire procedure (steps 2-4) is repeated 1000 times, using permuted diagnostic assignments, and building a histogram of the maximum *ES* achieved by *any* pathway in a given permutation. The *MES* achieved using the actual data is then compared to this histogram (step 6, red arrow), providing us with a global *P*-value for assessing whether *any* gene set is associated with the diagnostic categorization.

Figure 2 shows that OXPHOS gene expression is reduced in diabetic muscle. (a) The mean expression of all genes (gray) and for OXPHOS genes (red) is plotted for DM2 vs.

NGT individuals. (b) Histogram of mean gene expression level differences between NGT and DM2, using the data from (b), for all genes (black) and for OXPHOS genes (red).

Figure 3 shows that OXPHOS-CR represents a co-regulated subset of OXPHOS genes responsive to the transcriptional co-activator PGC-1α. (a) Normalized expression profile of 52 mouse homologs of the human OXPHOS genes across the mouse expression atleas (Su, A.I. et al. *Proc Natl Acad Sci U S A* 99, 4465-70. (2002)). These 52 genes were hierarchically clustered (Eisen et al. *Proc Natl Acad Sci U S A* 95, 14863-8. (1998)). The purple tree corresponds to a sub-cluster with a correlation coefficient of 0.65. Applicants call the human homologs of these mouse genes the OXPHOS-CR set. The human homologs of this tightly coregulated cluster, marked with an * and delimited with a yellow box, are: *ATP5J, ATP5L, ATP5O, COX5B, COX6A2, COX7A1, COX7B, COX7C, CYC1, CYCS, GRIM19, HSPC051, NDUFA2, NDUFA5, NDUFA7, NDUFA8, NDUFB3, NDUFB5, NDUFB6, NDUFC1, NDUFS2, NDUFS3, NDUFS5, SDHA, SDHB, UQCRB, UQCRC1.* (b) Normalized expression profile of OXPHOS mouse homologs in a mouse skeletal muscle cell line during a three-day time course in response to PGC-1α. The expression profile includes infection with control (*GFP*) or with *PGC*-1α, at day 0 (prior to infection) as well as on days 1, 2, and 3 following adenoviral infection, all performed in duplicate.

Figure 4 shows that OXPHOS-CR accounts for the bulk of OXPHOS signal seen in NGT vs. DM2. Histogram of signal:noise ratio for (a) All 10,983 human genes meeting the clipping and filtering criteria in the GSEA enrichment screen between NGT and DM2, (b) 106 OXPHOS genes meeting these clipping and filtering criteria, (c) 47 OXPHOS genes for which reliable mouse homologs are available in the mouse microarray, (d) OXPHOS-CR genes, and (e) OXPHOS genes but not in the OXPHOS-CR set.

Figure 5 shows that OXPHOS-CR predicts total body aerobic capacity (VO2max). (a) Linear regression was used to model VO2max with diabetes status, the mean centroid of OXPHOS-CR gene expression, ubiquinol cytochrome *c* reductase binding protein (*UQCRB*) expression, or in combination as explanatory (predictor) variables. The explanatory power and significance of the model are shown in the table. (b) Linear regression of VO2max against the mean centroid of OXPHOS-CR gene expression.

Figure 6 shows previously known and newly identified mitochondrial proteins (mito-

P). (A) Proteomic survey of mitochondria from mouse brain, heart, kidney, and liver resulted in the identification of 422 proteins, 262 of which were previously annotated as being mitochondrial. The distributions for (B) molecular weight, (C) isoelectric point, (D) mitochondrial compartments are plotted for proteins detected (pink) or not detected (blue) by our proteomic survey. Isolectric point, molecular weight, and subcellular distribution data came from the MITOchondria Project (MITOP, (Scharfe et al., 2000)). (E) Cumulative distribution of mRNA abundance for those genes whose protein product was detected (pink) or not detected (blue) by proteomics. The median expression levels for both groups are indicated. The cumulative distribution function for the proteins detected in proteomics is significantly greater than the cumulative distribution function for proteins not detected (Kolmogorov-Smirnov statistic, D=0.3618, P=9.4x10-18).

Figure 7 shows modules of tightly co-regulated mito-P genes. Pairwise correlation matrix for the 388 mitochondrial genes present in the GNF mouse tissue compendium. Red represents strong positive correlation, blue represents strong negative correlation. Dominant gene modules are labeled 1-7 with functional annotations.

Figure 8 shows the mRNA expression profile for 388 mitochondrial genes (rows) across 47 different mouse tissues (columns) in the GNF mouse expression atlas (Su et al., 2002). These genes and tissues were hierarchically clustered and visualized using DCHIP (Schadt et al., 2001). Key tissues showing high expression levels are labeled at the top of the panel. Evidence for being in mito-P is indicated by the white (previously known but not found in proteomics), gray (previously known and found in proteomics), and black (not previously known but found in proteomics) bars placed to the right of the correlogram.

Figure 9 shows mitochondria neighborhood analysis. The mitochondria neighborhood index (N_{100}) is defined as the number of mito-P genes that occur within the nearest 100 expression neighbors of a given gene. The distribution of N_{100} is plotted for all genes (white), mito-P genes (gray), and for the ancestral mito-P genes (black).

Figure 10 shows a schematic overview of motifADE and application to the PGC-1a timecourse. (A) motifADE identifies <u>motif</u>s <u>a</u>ssociated with <u>d</u>ifferential <u>e</u>xpression. It begins with a list of genes ordered on the basis of differential expression across two conditions. Each gene is then annotated for the presence of a given motif in the promoter region. A

nonparametric statistic is used to assess whether genes with the motif tend to rank high on this list (see Methods). In this example, genes with Motif 1 are randomly distributed on the list, while genes with Motif 2 tend to rank high, suggesting an association between Motif 2 and the differential expression. (B) C2C12 cells were infected with an adenovirus expressing either GFP (control) or with PGC-1α and profiled over a three day period. Experiments were performed in duplicate and relative gene expression measures are shown. Genes are ranked according to the difference in expression between PGC-1a and GFP on day 3. Mouse genes having a perfect Errα motif (5'-TGACCTTG-3'), a perfect Gabpa/b motif (5'-CTTCCG-3'), or both motifs are labeled with a black bar on the right side of the correlogram.

Figure 11 shows a proposed model of mechanism of action of PGC-1a. PGC-1a is a highly regulated gene that responds to external stimuli, e.g., reduced in diabetes and increased following exercise. When PGC-1a levels rise, the expression of Errα and Gabpa are immediately induced via a double positive feedback loop. This results in the strong induction of Errα as well as Gabpa. These levels rise and over the course of 2-3 days, these factors couple with PGC-1a to induce the expression of NRF-1 as well as hundreds of downstream targets, such as OXPHOS and other mitochondrial genes.

Figure 12 shows cooperativity between the Errα and Gabpa binding sites. All 5034 genes from motifADE analysis are rank ordered on the basis of expression difference (signal to noise ratio) on day 3 between cells treated with PGC-1a vs. GFP. The cumulative fraction of genes with a specified motif (Errα, blue; Gabpa, pink; both, black) is plotted as a function of fractional rank ordering of all 5034 genes.

DETAILED DESCRIPTION OF THE INVENTION

I. Overview

The invention broadly relates to novel therapeutics for regulating metabolism, mitochondrial function, and for treating disorders, including obesity and type 2 diabetes, and to related methods. The invention stems, in part, from the discovery by applicants of a new group of coordinately-regulated genes, termed OXPHOS, which are involved in oxidative phosphorylation. OXPHOS-CR genes have the following key characteristics: (a) they are members of oxidative phosphorylation; (b) they are transcriptionally co-regulated and highly expressed at the major sites of insulin mediated glucose uptake (brown fat, heart, skeletal

muscle); (c) they are targets of the transcriptional co-activator PPARGC1 (PGC-1α); (d) they show a subtle but extremely consistent expression decrease in diabetic and pre-diabetic muscle; and (e) their expression predicts total body aerobic capacity in humans.

Applicant have discovered that OXPHOS genes are downregulated in subjects afflicted with type 2 diabetes or with glucose intolerance and that Peroxisome Proliferator-Activated Receptor γ-Coactivator -1α (PGC-1α) transcriptionally regulates the OXPHOS genes. Applicants have also discovered that PGC-1α acts through Errα and Gabp to regulate OXPHOS gene expression. Such discoveries provide the basis for novel assays and methods of treatment relating to the genes and disorders.

The invention provides, in part, methods of modulating mitochondrial function, expression of the OXPHOS genes, mitochondrial biogenesis, expression of Nuclear Respiratory Factor 1 (NRF-1), β-oxidation of fatty acids, total mitochondrial respiration, uncoupled respiration, mitochondrial DNA replication, or expression of mitochondrial enzymes, by modulating the expression or activity of Errα, Gabpa, Gabpb or of genes containing Errα binding sites, Gabpa binding sites, or both. Modulation of these biological activities may be carried out in a cell, such as contacting a cell with an agent, or in a subject in need thereof. The invention further provides agents for treating these disorders and for modulating Errα, Gabp and PGC-1 function.

A related aspect of the invention provides a method of identifying agents useful for treating disorders related to altered glucose homeostasis, insulin resistance or reduced mitochondrial function. Furthermore, the invention provides methods of diagnosing such disorders or of identifying subjects at risk of developing the disorders.

The invention also provides cell-based methods of identifying agents which modulate the expression of OXPHOS genes. Since applicants have discovered that PGC-1α, Errα and Gabp regulate the expression of level of OXPHOS genes, such methods are useful in identifying agents which regulate the expression or activity of PGC-1α, Errα and Gabp. Furthermore, expression of OXPHOS genes may be used to predict total body aerobic capacity in humans and other mammals.

Another aspect of the invention provides a method of detecting statistically-significant

differences in the expression level of at least one biomarker belonging to a biomarker set, between the members of a first and of a second experimental group. Such a method may be applied, for example, to identify biomarker sets which are differentially expressed in an experimental group afflicted with a disorder, even when the changes in expression between the two groups are very subtle. Biomarker sets identified using the methods described herein may be used in the development of diagnostic tools and treatments for the disorder for which they are associated. A related aspect of the invention provides methods of identifying transcriptional regulators which display differential activity between two sets of conditions. Such methods may be applied to the bio markers identified using the related methods provided herein, and may be useful in identifying disease genes and targets for novel therapeutics to treat or prevent disease.

II. Definitions

For convenience, certain terms employed in the specification, examples, and appended claims, are collected here. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

The term “expression vector” and equivalent terms are used herein to mean a vector which is capable of inducing the expression of DNA that has been cloned into it after transformation into a host cell. The cloned DNA is usually placed under the control of (i.e., operably linked to) certain regulatory sequences such a promoters or enhancers. Promoters sequences maybe constitutive, inducible or repressible.

The term "operably linked" is used herein to mean molecular elements that are positioned in such a manner that enables them to carry out their normal functions. For example, a gene is operably linked to a promoter when its transcription is under the control of the promoter and, if the gene encodes a protein, such transcription produces the protein normally encoded by the gene. For example, a binding site for a transcriptional regulator is said to be operably linked to a promoter when transcription from the promoter is regulated by protein(s) binding to the binding site. Likewise, two protein domains are said to be operably linked in a protein when both domains are able to perform their normal functions.

The articles “a” and “an” are used herein to refer to one or to more than one (i.e., to at least one) of the grammatical object of the article. By way of example, “an element” means

one element or more than one element.

The term "including" is used herein to mean, and is used interchangeably with, the phrase "including but not limited to".

The term "or" is used herein to mean, and is used interchangeably with, the term "and/or," unless context clearly indicates otherwise.

The term "such as" is used herein to mean, and is used interchangeably, with the phrase "such as but not limited to".

A "patient" or "subject" to be treated by the method of the invention can mean either a human or non-human animal, preferably a mammal.

The term "encoding" comprises an RNA product resulting from transcription of a DNA molecule, a protein resulting from the translation of an RNA molecule, or a protein resulting from the transcription of a DNA molecule and the subsequent translation of the RNA product.

The term "promoter" is used herein to mean a DNA sequence that initiates the transcription of a gene. Promoters are typically found 5' to the gene and located proximal to the start codon. If a promoter is of the inducible type, then the rate of transcription increases in response to an inducer. Promoters may be operably linked to DNA binding elements that serve as binding sites for transcriptional regulators. The term "mammalian promoter" is used herein to mean promoters that are active in mammalian cells. Similarly, "prokaryotic promoter" refers to promoters active in prokaryotic cells.

The term "expression" is used herein to mean the process by which a polypeptide is produced from DNA. The process involves the transcription of the gene into mRNA and the translation of this mRNA into a polypeptide. Depending on the context in which used, "expression" may refer to the production of RNA, protein or both.

The term "recombinant" is used herein to mean any nucleic acid comprising sequences which are not adjacent in nature. A recombinant nucleic acid may be generated *in*

vitro, for example by using the methods of molecular biology, or *in vivo*, for example by insertion of a nucleic acid at a novel chromosomal location by homologous or non-homologous recombination.

The term "transcriptional regulator" refers to a biochemical element that acts to prevent or inhibit the transcription of a promoter-driven DNA sequence under certain environmental conditions (e.g., a repressor or nuclear inhibitory protein), or to permit or stimulate the transcription of the promoter-driven DNA sequence under certain environmental conditions (e.g., an inducer or an enhancer).

The term "microarray" refers to an array of distinct polynucleotides or oligonucleotides synthesized on a substrate, such as paper, nylon or other type of membrane, filter, chip, glass slide, or any other suitable solid support.

The terms "disorders" and "diseases" are used inclusively and refer to any deviation from the normal structure or function of any part, organ or system of the body (or any combination thereof). A specific disease is manifested by characteristic symptoms and signs, including biological, chemical and physical changes, and is often associated with a variety of other factors including, but not limited to, demographic, environmental, employment, genetic and medically historical factors. Certain characteristic signs, symptoms, and related factors can be quantitated through a variety of methods to yield important diagnostic information.

The terms "level of expression of a gene in a cell" or "gene expression level" refer to the level of mRNA, as well as pre-mRNA nascent transcript(s), transcript processing intermediates, mature mRNA(s) and degradation products, encoded by the gene in the cell.

The term "modulation" refers to upregulation (i.e., activation or stimulation), downregulation (i.e., inhibition or suppression) of a response, or the two in combination or apart. A "modulator" is a compound or molecule that modulates, and may be, e.g., an agonist, antagonist, activator, stimulator, suppressor, or inhibitor.

The term "prophylactic" or "therapeutic" treatment refers to administration to the subject of one or more of the subject compositions. If it is administered prior to clinical manifestation of the unwanted condition (e.g., disease or other unwanted state of the host

animal) then the treatment is prophylactic, i.e., it protects the host against developing the unwanted condition, whereas if administered after manifestation of the unwanted condition, the treatment is therapeutic (i.e., it is intended to diminish, ameliorate or maintain the existing unwanted condition or side effects therefrom).

The term "therapeutic effect" refers to a local or systemic effect in animals, particularly mammals, and more particularly humans caused by a pharmacologically active substance. The term thus means any substance intended for use in the diagnosis, cure, mitigation, treatment or prevention of disease or in the enhancement of desirable physical or mental development and conditions in an animal or human. The phrase "therapeutically-effective amount" means that amount of such a substance that produces some desired local or systemic effect at a reasonable benefit/risk ratio applicable to any treatment. In certain embodiments, a therapeutically-effective amount of a compound will depend on its therapeutic index, solubility, and the like. For example, certain compounds discovered by the methods of the present invention may be administered in a sufficient amount to produce a reasonable benefit/risk ratio applicable to such treatment.

The term "improving mitochondrial function" may refer to (a) substantially (e.g., in a statistically significant manner, and preferably in a manner that promotes a statistically significant improvement of a clinical parameter such as prognosis, clinical score or outcome) restoring to a normal level at least one indicator of glucose responsiveness in cells having reduced glucose responsiveness and reduced mitochondrial mass and/or impaired mitochondrial function; or (b) substantially (e.g., in a statistically significant manner, and preferably in a manner that promotes a statistically significant improvement of a clinical parameter such as prognosis, clinical score or outcome) restoring to a normal level, or increasing to a level above and beyond normal levels, at least one indicator of mitochondrial function in cells having impaired mitochondrial function or in cells having normal mitochondrial function, respectively. Improved or altered mitochondrial function may result from changes in extra-mitochondrial structures or events, as well as from mitochondrial structures or events, in direct interactions between mitochondrial and extra-mitochondrial genes and/or their gene products, or in structural or functional changes that occur as the result of interactions between intermediates that may be formed as the result of such interactions, including metabolites, catabolites, substrates, precursors, cofactors and the like.

The term "effective amount" refers to the amount of a therapeutic reagent that when administered to a subject by an appropriate dose and regime produces the desired result.

The term "subject in need of treatment for a disorder" is a subject diagnosed with that disorder or suspected of having that disorder.

The term "metabolic disorder" refers to a disorder, disease or condition which is caused or characterized by an abnormal metabolism (i.e., the chemical changes in living cells by which energy is provided for vital processes and activities) in a subject. Metabolic disorders include diseases, disorders, or conditions associated with aberrant thermogenesis or aberrant adipose cell (e.g., brown or white adipose cell) content or function. Metabolic disorders can detrimentally affect cellular functions such as cellular proliferation, growth, differentiation, or migration, cellular regulation of homeostasis, inter- or intra-cellular communication; tissue function, such as liver function, muscle function, or adipocyte function; systemic responses in an organism, such as hormonal responses (e.g., insulin response). Examples of metabolic disorders include obesity, diabetes, hyperphagia, hypophagia, endocrine abnormalities, triglyceride storage disease, Bardet-Biedl syndrome, Lawrence-Moon syndrome, Prader-Labhart-Willi syndrome, Kearns-Sayre syndrome, anorexia, medium chain acyl-CoA dehydrogenase deficiency, and cachexia. Obesity is defined as a body mass index (BMI) of 30 $kg/^2m$ or more (National Institute of Health, Clinical Guidelines on the Identification, Evaluation, and Treatment of Overweight and Obesity in Adults (1998)). However, the present invention is also intended to include a disease, disorder, or condition that is characterized by a body mass index (BMI) of 25 $kg/^2m$ or more, 26 $kg/^2m$ or more, 27 $kg/^2m$ or more, 28 $kg/^2m$ or more, 29 $kg/^2m$ or more, 29.5 $kg/^2m$ or more, or 29.9 $kg/^2m$ or more, all of which are typically referred to as overweight (National Institute of Health, Clinical Guidelines on the Identification, Evaluation, and Treatment of Overweight and Obesity in Adults (1998)).

A "susceptibility locus" for a particular disease is a sequence or gene locus implicated in the initiation or progression of the disease. The susceptibility locus can be, for example, a gene or a microsatellite repeat, as identified by a microsatellite marker, or can be identified by a defined single nucleotide polymorphism. Generally, susceptibility genes implicated in specific diseases and their loci can be found in scientific publications, but may also be determined experimentally.

The term "Gabp polypeptide" comprises Gabpa and Gabpb polypeptides. In preferred embodiments of the methods described herein, the Gabpa and Gabpb polypeptides are mammalian polypeptides, preferably human. The amino acid sequences of human Gabpa and Gabpb are deposited as Genbank Accession Nos. NP_002031 and NP_852092, respectively. Gabpa is also known as E4TF1-53 in the art, while Gabpb is also known as E4TF1-60. Additional assays to those described herein for assaying the transcriptional activity of Gabpa and Gabpb, and additional isoforms of these subunits, may be found in the art (Sawa et al., Nucleic Acids Res. 24(24):4954-61 (1996); Watanabe, et al. Mol. Cell. Biol. 13 (3), 1385-1391 (1993), Sawada, J. et al J. Biol. Chem. 274 (50), 35475-35482 (1999); Suzuki,F. et al J. Biol. Chem. 273 (45), 29302-29308 (1998); Sawa, C.,et al. Nucleic Acids Res. 24 (24), 4954-4961 (1996); Gugneja, S.et al Mol. Cell. Biol. 15 (1), 102-111 (1995); de la Brousse, F.C.et al. Genes Dev. 8 (15), 1853-1865 (1994); Virbasius, J.V. et al. Genes Dev. 7 (3), 380-392 (1993)), the teachings of which are incorporated by referenced herein.

The term "PGC-1 polypeptide" comprises PGC-1a and PGC-1b polypeptides. In preferred embodiments of the methods described herein, the PGC-1a and PGC-1b polypeptides are mammalian polypeptides, preferably human. The amino acid sequences of human PGC-1a and PGC-1b are deposited as Genbank Accession Nos. NP_573570 and AF453324, respectively. Additional assays to those described herein for assaying the transcriptional activity of Gabpa and Gabpb, and additional isoforms of these subunits, may be found in the art (Huss, J.M., et al. Biol. Chem. 277 (43), 40265-40274 (2002); Kressler, D., et al. J. Biol. Chem. 277 (16), 13918-13925 (2002); Lin, J., et al. J. Biol. Chem. 277 (3), 1645-1648 (2002); Lin et al. J. Biol. Chem., Vol. 277, Issue 3, 1645-1648, January 18, (2002)), the teachings of which are incorporated by referenced herein.

The term "Errα polypeptide" includes Errα polypeptides from any species. In some preferred embodiments of the methods described herein, an Errα polypeptide is a mammalian polypeptide, preferably a human polypeptide. The sequence of human Errα corresponds to Genbank Accession No. NP_004442. Additional isoforms of Errα and methods for assaying Errα activity are known in the art e.g. Schreiber, S.N., et al. J. Biol. Chem. 278 (11), 9013-9018 (2003); Igarashi, M., et al. J. Gen. Virol. 84 (Pt 2), 319-327 (2003); Kraus, R.J., et al. J. Biol. Chem. 277 (27), 24826-24834 (2002); Vanacker, J.M., Oncogene 17 (19), 2429-2435 (1998); Sladek, R.,et al. Genomics 45 (2), 320-326 (1997); Sladek, R., et al. Mol.

Cell. Biol. 17 (9), 5400-5409 (1997); Shi, H., et al. Genomics 44 (1), 52-60 (1997); Yang, N., et al. J. Biol. Chem. 271 (10), 5795-5804 (1996); Giguere, V et al. Nature 331 (6151), 91-94 (1988); Eiler, S., et al Protein Expr. Purif. 22 (2), 165-173 (2001), the teachings of which are incorporated by referenced herein.

The term "nuclear hormone receptors" comprises comprise a large, well-defined family of ligand-activated transcription factors which modify the expression of target genes by binding to specific cis-acting sequences (Laudet et al., 1992, EMBO J, Vol, 1003-1013; Lopes da Silva et al., 1995, TINS 18, 542-548; Mangelsdorfet al., 1995, Cell 83, 835-839; Mangelsdorf et al., 1995, Cell 83, 841-850). Family members include both orphan receptors and receptors for a wide variety of clinically significant ligands including steroids, vitamin D, thyroid hormones, retinoic acid, etc. Additional receptors may be found in the literature (See for example The Nuclear Receptor FactsBook; Vincent Laudet (Editor); Elsevier Science & Technology, 2001).

The term "antibody" as used herein is intended to include whole antibodies, e.g., of any isotype (IgG, IgA, IgM, IgE, etc), and includes fragments thereof which are also specifically reactive with a vertebrate, e.g., mammalian, protein. Antibodies can be fragmented using conventional techniques and the fragments screened for utility and/or interaction with a specific epitope of interest. Thus, the term includes segments of proteolytically-cleaved or recombinantly-prepared portions of an antibody molecule that are capable of selectively reacting with a certain protein. Non-limiting examples of such proteolytic and/or recombinant fragments include Fab, F(ab')2, Fab', Fv, and single chain antibodies (scFv) containing a V[L] and/or V[H] domain joined by a peptide linker. The scFv's may be covalently or non-covalently linked to form antibodies having two or more binding sites. The term antibody also includes polyclonal, monoclonal, or other purified preparations of antibodies and recombinant antibodies.

The term "recombinant" as used in reference to a nucleic acid indicates any nucleic acid that is positioned adjacent to one or more nucleic acid sequences that it is not found adjacent to in nature. A recombinant nucleic acid may be generated in vitro, for example by using the methods of molecular biology, or in vivo, for example by insertion of a nucleic acid at a novel chromosomal location by homologous or non-homologous recombination. The

term “recombinant” as used in reference to a polypeptide indicates any polypeptide that is produced by expression and translation of a recombinant nucleic acid.

The following terms are used to describe the sequence relationships between two or more polynucleotides: "reference sequence," "comparison window," "sequence identity," "percentage of sequence identity," and "substantial identity." A reference sequence is a defined sequence used as a basis for a sequence comparison; a reference sequence can be a subset of a larger sequence, for example, as a segment of a fall length cDNA or gene sequence given in a sequence listing, or may comprise a complete cDNA or gene sequence. Generally, a reference sequence is at least 20 nucleotides in length, frequently at least 25 nucleotides in length, and often at least 50 nucleotides in length. Since two polynucleotides can each (1) comprise a sequence (for example a portion of the complete polynucleotide sequence) that is similar between the two polynucleotides, and (2) may further comprise a sequence that is divergent between the two polynucleotides, sequence comparisons between two (or more) polynucleotides are typically performed by comparing sequences of the two polynucleotides over a "comparison window" to identify and compare local regions of sequence similarity. A comparison window, as used herein, refers to a conceptual segment of at least 20 contiguous nucleotide positions wherein a polynucleotide sequence may be compared to a reference sequence of at least 20 contiguous nucleotides and wherein the portion of the polynucleotide sequence in the comparison window can comprise additions and deletions (for example, gaps) of 20 percent or less as compared to the reference sequence (which would not comprise additions or deletions) for optimal alignment of the two sequences. Optimal alignment of sequences for aligning a comparison window can be conducted by the local identity algorithm (Smith and Waterman, Adv. Appl. Math., 2:482 (1981)), by the identity alignment algorithm (Needleman and Wunsch, J. Mol. Bio., 48:443 (1970)), by the search for similarity method (Pearson and Lipman, Proc. Natl. Acid. Sci. U.S.A. 85:2444 (1988)), by the computerized implementations of these algorithms such as GAP, BESTFIT, FASTA and TFASTA (Wisconsin Genetics Software Page Release 7.0, Genetics Computer Group, Madison, Wis.), or by inspection. Preferably, the best alignment (for example, the result having the highest percentage of identity over the comparison window) generated by the various methods is selected.

The term "diagnostic" refers to assays that provide results which can be used by one skilled in the art, typically in combination with results from other assays, to determine if an

individual is suffering from a disease or disorder of interest such as diabetes, including type I and type II, whereas the term "prognostic" refers to the use of such assays to evaluate the response of an individual having such a disease or disorder to therapeutic or prophylactic treatment. The term "pharmacogenetic" refers to the use of assays to predict which individual patients in a group will best respond to a particular therapeutic or prophylactic composition or treatment.

Other technical terms used herein have their ordinary meaning in the art that they are used, as exemplified by a variety of technical dictionaries, such as the McGraw-Hill Dictionary of Chemical Terms and the Stedman's Medical Dictionary.

III. Methods of Modulating Biological Responses in a Cell

In one aspect, the invention provides methods of modulating biological responses in a cell. One specific aspect of the invention provides a method of modulating a biological response in a cell, the method comprising contacting the cell with at least one agent that modulates the expression or activity of Errα or Gabp, wherein the biological response is (a) expression of at least one OXPHOS gene; (b) mitochondrial biogenesis; (c) expression of Nuclear Respiratory Factor 1 (NRF-1); (d) β-oxidation of fatty acids; (e) total mitochondrial respiration; (f) uncoupled respiration; (g) mitochondrial DNA replication; (h) expression of mitochondrial enzymes; or (i) skeletal muscle fiber-type switching.

In one embodiment of the methods described herein, the biological response that is modulated is the expression of at least one OXPHOS gene. OXPHOS genes have been described in Mootha et al., Nat Genet. 2003; 34(3):267-73, hereby incorporated by reference in its entirety. In one embodiment, the OXPHOS gene is NDUFB3, SDHA, NDUFA8, COX7A1, UQCRC1, NDUFC1, NDUFS2, ATP5O, NDUFS3, SDHB, NDUFS5, NDUFB6, COX5B, CYC1, NDUFA7, UQCRB, COX7B, ATP5L, COX7C, NDUFA5, GRIM19, ATP5J, COX6A2 NDUFB5, CYCS, NDUFA2 or HSPC051.

In another embodiment of the methods described herein, the biological response that is modulated is mitochondrial biogenesis. U.S. Patent Publication No. 2002/0049176 describes assays for determining mitochondrial mass, volume or number, and is hereby incorporated by reference in its entirety.

In another embodiment of the methods described herein, the biological response that is modulated is expression of Nuclear Respiratory Factor 1 (NRF-1). NRF-1 is a transcription factor occurring as a homodimer of a 54 KDa polypeptide encoded by the nuclear gene nrf-1 (Evans and Scarpulla, Genes & Development 4:1023-1034 (1990), Scarpulla, J. Bioenergetics and Biomembranes 29:109-119 (1997), Moyes et al., J. Exper. Biol. 201:299-307 (1998)). NRF-1 binds to the upstream promoters of nuclear genes that encode respiratory components associated with mitochondrial transcription and replication. NRF-1 can be any NRF-1, such as rat, mouse or human. NRF-1 nucleotide and polypeptide sequences are described in U.S. Patent Publication No. 20020049176, hereby incorporated by reference in its entirety.

In another embodiment of the methods described herein, the biological response that is modulated is β-oxidation of fatty acids. In another embodiment of the methods described herein, the biological response that is modulated is total mitochondrial respiration. In another embodiment of the methods described herein, the biological response that is modulated uncoupled respiration. Uncoupled respiration occurs when electron transport is uncoupled from ATP synthesis

In another embodiment of the methods described herein, the biological response that is modulated is mitochondrial DNA replication. Quantification of mitochondrial DNA (mtDNA) content may be accomplished by one with routine skill in the art using any of a variety of established techniques that are useful for this purpose, including but not limited to, oligonucleotide probe hybridization or polymerase chain reaction (PCR) using oligonucleotide primers specific for mitochondrial DNA sequences (see, e.g., Miller et al., 1996 J. Neurochem. 67:1897; Fahy et al., 1997 Nucl. Ac. Res. 25:3102; U.S. patent application Ser. No. 09/098,079; Lee et al., 1998 Diabetes Res. Clin. Practice 42:161; Lee et al., 1997 Diabetes 46(suppl. 1): 175A). A particularly useful method is the primer extension assay disclosed by Fahy et al. (Nucl. Acids Res. 25:3102, 1997) and by Ghosh et al. (Am. J. Hum. Genet. 58:325, 1996). Suitable hybridization conditions may be found in the cited references or may be varied according to the particular nucleic acid target and oligonucleotide probe selected, using methodologies well known to those having ordinary skill in the art (see, e.g., Ausubel et al., Current Protocols in Molecular Biology, Greene Publishing, 1987; Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring

Harbor Press, 1989).

In another embodiment of the methods described herein, the biological response that is modulated is expression of mitochondrial enzymes. In one embodiment, mitochondrial enzymes are Electron Transport Chain (ETC) enzymes. An ETC enzyme refers to any mitochondrial molecular component that is a mitochondrial enzyme component of the mitochondrial electron transport chain (ETC) complex associated with the inner mitochondrial membrane and mitochondrial matrix. An ETC enzyme may include any of the multiple ETC subunit polypeptides encoded by mitochondrial and nuclear genes. The ETC is typically described as comprising complex I (NADH:ubiquinone reductase), complex II (succinate dehydrogenase), complex III (ubiquinone: cytochrome c oxidoreductase), complex IV (cytochrome c oxidase) and complex V (mitochondrial ATP synthetase), where each complex includes multiple polypeptides and cofactors (for review see, e.g., Walker et al., 1995 *Meths. Enzymol.* 260:14; Ernster et al., 1981 *J. Cell Biol.* 91:227s-255s, and references cited therein). A mitochondrial enzyme of the present invention may also comprise a Krebs cycle enzyme, which includes mitochondrial molecular components that mediate the series of biochemical/bioenergetic reactions also known as the citric acid cycle or the tricarboxylic acid cycle (see, e.g., Lehninger, Biochemistry, 1975 Worth Publishers, NY; Voet and Voet, Biochemistry, 1990 John Wiley & Sons, NY; Mathews and van Holde, Biochemistry, 1990 Benjamin Cummings, Menlo Park, Calif.). Krebs cycle enzymes include subunits and cofactors of citrate synthase, aconitase, isocitrate dehydrogenase, the α-ketoglutarate dehydrogenase complex, succinyl CoA synthetase, succinate dehydrogenase, fumarase and malate dehydrogenase. Krebs cycle enzymes further include enzymes and cofactors that are functionally linked to the reactions of the Krebs cycle, such as, for example, nicotinamide adenine dinucleotide, coenzyme A, thiamine pyrophosphate, lipoamide, guanosine diphosphate, flavin adenine dinucloetide and nucleoside diphosphokinase.

In another embodiment of the methods described herein, the biological response that is modulated is skeletal muscle fiber-type switching, that is, a shift towards type I oxidative skeletal muscle fibers. International PCT Application WO 03/068944 describes skeletal muscle fiber-type switching. In some embodiments, the agent increases at least one of the biological responses. In alternate embodiments, the agent decreases at least one of the biological responses.

The methods described herein for modulating a biological activity in a cell may be applied to any type of cell. In specific embodiments, the cell is a skeletal muscle cell, a smooth muscle cell, a cardiac muscle cell, a hepatocyte, an adipocyte, a neuronal cell, or a pancreatic cell. The cell may be a primary cell, a cell derived from a cell line, or a cell which has differentiated in vitro, such as a differentiated cell obtained through manipulation of a stem cell. In some embodiments, the cell in an organism, while in other embodiments the cell is manipulated ex vivo, such as in cell or tissue culture. The methods described herein also apply to groups of cells, such as to whole tissues or organs. In some embodiments, the organism is a mammal, such as a mouse, rat, an ungulate, a horse, a dog or a human.

In some embodiments, the human is afflicted, at risk of developing, or suspected with being afflicted, with a disorder. In some embodiments, the disorder comprises a metabolic disorder, a disorder characterized by altered mitochondrial activity, a disorder characterized by sugar intolerance, or a combination thereof. In specific embodiments of the methods described herein, the disorder is diabetes, obesity, cardiac myopathy, aging, coronary atherosclerotic heart disease, diabetes mellitus, Alzheimer's Disease, Parkinson's Disease, Huntington's disease, dystonia, Leber's hereditary optic neuropathy (LHON), schizophrenia, myodegenerative disorders such as "mitochondrial encephalopathy, lactic acidosis, and stroke" (MELAS). and "myoclonic epilepsy ragged red fiber syndrome" (MERRF), NARP (Neuropathy; Ataxia; Retinitis Pigmentosa), MNGIE (Myopathy and external ophthalmoplegia, neuropathy; gastro-intestinal encephalopathy, Kearns-Sayre disease, Pearson's Syndrome, PEO (Progressive External Ophthalmoplegia), congenital muscular dystrophy with mitochondrial structural abnormalities, Wolfram syndrome, Diabetes Insipidus, Diabetes Mellitus, Optic Atrophy Deafness, Leigh's Syndrome, fatal infantile myopathy with severe mitochondrial DNA (mtDNA) depletion, benign "later-onset" myopathy with moderate reduction in mtDNA, dystonia, medium chain acyl-CoA dehydrogenase deficiency, arthritis, and mitochondrial diabetes and deafness (MIDD), mitochondrial DNA depletion syndrome.

In one embodiment of the methods for modulating biological responses in a cell described herein, the agent modulates the formation of a complex between a PGC-1 polypeptide and (i) an Errα polypeptide; or (ii) a Gabp polypeptide. The agent may be an agent which increases formation of the complex in the cell, or it may be an agent that reduces

formation of the complex in the cell. In embodiments where the agent increases a biological activity of the cell, the agent increases complex formation, whereas in embodiments where a biological activity is to be decreased, complex formation is decreased. One skilled in the art would recognize that complex formation, as used herein, refers to the normal association between the polypeptides which results in the transcriptional activation of target genes by the complex. Therefore, an agent which resulted in an aberrant aggregation of PGC-1α and Errα polypeptides, wherein the resulting complex has reduced transcriptional activating activity, would not result in increased biological activity but instead in less. Likewise, an agent which increased complexed formation, but the resulting complex was degraded in the cell, would result in less biological activity in the cell. Accordingly, in some specific embodiments for reducing biological activity, the agent results in increase complex formation, wherein the complex has reduced transcriptional activity or stability.

In one embodiment of the methods for modulating biological responses in a cell described herein, the agent modulates the expression level or the transcriptional activity of an Errα polypeptide, a Gabp polypeptide, or of both. The agent may comprise a polypeptide, a nucleic acid, or a chemical compound. In one embodiment of the methods for modulating biological responses in a cell described herein, the agent is itself an Errα polypeptide or fragments thereof, or a Gapb polypeptide or a fragment thereof, or a nucleic acid encoding such polypeptides or fragments thereof.

In some embodiments of the methods for increasing biological responses in a cell described herein, the agent increases complex formation between a PGC-1 polypeptide and an Errα polypeptide. In preferred embodiments, the agent is specific for the complex formation between a PGC-1 polypeptide and an Errα polypeptide. In a preferred embodiment, the agent increases Errα activity by preferentially promoting complex formation between a PGC-1 polypeptide and an Errα polypeptide over complex formation between a PGC-1 polypeptide and at least one other polypeptide to which PGC-1 normally binds in an organism. Polypeptides to which PGC-1 normally binds in an organism include the following: nearly all nuclear receptor (e.g., PPAR-gamma, PPAR-alpha, thyroid hormone receptor, HNF4α, etc.) as well as other transcription factors, such as NRF1, NFAT, etc (see Puigserver and Spiegelman, Endocr Rev. 2003;24(1):78-90).

In another preferred embodiment, the agent increases Erra α activity by preferentially promoting complex formation between a PGC-1 polypeptide and an Errα polypeptide over a PGC-1 polypeptide and another nuclear receptor. In some embodiments, the affinity of an agent which increases complex formation between PGC-1 polypeptide and Errα does so at least 2, 5, 10, 20, 40, 50, 100, 200, 500, 1000, 5000, 10,000, 50,000 or 100,000-fold times more potently than complex formation between the same PGC-1 polypeptide and (i) at least another polypeptide to which PGC-1 normally binds in an organism; or (ii) a nuclear receptor; or (iii) both. The fold-level of potency may be determined by measuring the association constant, the disassociation constant, or more preferably the K_d of the agent for the various complexes.

In parallel embodiments of the methods for inhibiting a biological response in a cell described herein, the agent preferentially inhibits complex formation between a PGC-1 polypeptide and an Errα polypeptide over a PGC-1 polypeptide and another nuclear receptor. In some embodiments, the affinity of an agent which decreases complex formation between PGC-1 polypeptide and an Errα does so at least 2, 5, 10, 20, 40, 50, 100, 200, 500, 1000, 5000, 10,000, 50,000 or 100,000-fold times more potently than complex formation between the same PGC-1 polypeptide and (i) at least another polypeptide to which PGC-1 normally binds in an organism; or (ii) a nuclear receptor; or (iii) both. In other embodiments, the IC50 for disrupting the interaction between a PGC-1 polypeptide and an Errα polypeptide is 2, 5, 10, 20, 40, 50, 100, 200, 500, 1000, 5000, 10,000, 50,000 or 100,000-fold lower than that for disrupting the interaction between a PGC-1 polypeptide and (i) at least one another polypeptide to which PGC-1 normally binds in an organism; or (ii) a nuclear hormone receptor.

In other embodiments of the methods described herein for modulating biological responses in a cell, a Gabp polypeptide may replace the Errα polypeptide. For example, instead of using an agent that modulates the interaction between a PGC-1 polypeptide and an Errα polypeptide, an agent is used that modulates the interaction between a polypeptide PGC-1 polypeptide and an Gabp polypeptide. Thus all variations of the methods described herein for modulating biological responses in a cell using an Errα polypeptide may be applied to an Gabp polypeptide, such as a Gabpa polypeptide.

Another embodiment of the methods described herein for modulating biological responses in a cell, the cell is contacted with two agents, wherein one agent modulates the expression or activity of Errα and the other agent modulates the expression or activity of a Gabp polypeptide, such as a Gabpa polypeptide. In another embodiment, the cell is contacted with one agent which modulates the expression or activity of both Errα and of a Gabp polypeptide.

IV. Methods of Preventing/Treating Disease

Some aspects of the invention provide methods of treating or preventing a disorder. Some aspects provide methods of preventing disorders which are associated with glucose intolerance, excess glucose production, insulin resistance, aberrant metabolism or abnormal mitochondrial function.

The invention further provides agents for the manufacture of medicaments to treat any of the disorders described herein. Any methods disclosed herein for treating or preventing a disorder by administering an agent to a subject may be applied to the use of the agent in the manufacture of a medicament to treat that disorder. For example, in one specific embodiment, an Errα agonist may be used in the manufacture of a medicament for the treatment of a disorder characterized by low mitochondrial function or by sugar intolerance, such as diabetes.

One aspect of the invention provides method of treating or preventing a disorder characterized by reduced mitochondrial function, glucose intolerance, or insulin intolerance in a subject, the method comprising administering to the subject a therapeutically effective amount of an agent which (i) increases the expression or activity of Errα or Gabp or both; or (ii) increases the formation of a complex between a PGC-1 polypeptide and (a) an Errα polypeptide; (b) a Gabp polypeptide; or both; or (iii) binds to an (a) Errα binding site, or to a (b) Gabpa binding site, and which increases transcription of at least one gene in the subject, said gene having an Errα binding site, a Gabpa binding site, or both.

In one embodiment, the agent which binds to an (a) Errα binding site, or to a (b) Gabp binding site, comprises at least one DNA binding domain. In a further embodiment, the DNA binding domain comprises at least one zinc-finger. In some embodiments, such agents

comprise a DNA binding domain and a transactivation domain. Methods are known in the art for designing transcriptional activator or repressors which bind to specific DNA sequences, including those disclosed in U.S. Patent Nos. 6,607,882, 6,453,242 and 6,511,808.

In one embodiment, the disorder is type 2 diabetes mellitus. In one embodiment of any of the methods described herein, a disorder characterized by reduced mitochondrial function, glucose intolerance, or insulin intolerance is diabetes, obesity, cardiac myopathy, aging, coronary atherosclerotic heart disease, diabetes mellitus, Alzheimer's Disease, Parkinson's Disease, Huntington's disease, dystonia, Leber's hereditary optic neuropathy (LHON), schizophrenia, myodegenerative disorders such as "mitochondrial encephalopathy, lactic acidosis, and stroke" (MELAS). and "myoclonic epilepsy ragged red fiber syndrome" (MERRF), NARP (Neuropathy; Ataxia; Retinitis Pigmentosa), MNGIE (Myopathy and external ophthalmoplegia, neuropathy; gastro-intestinal encephalopathy, Kearns-Sayre disease, Pearson's Syndrome, PEO (Progressive External Ophthalmoplegia), congenital muscular dystrophy with mitochondrial structural abnormalities, Wolfram syndrome, Diabetes Insipidus, Diabetes Mellitus, Optic Atrophy Deafness, Leigh's Syndrome, fatal infantile myopathy with severe mitochondrial DNA (mtDNA) depletion, benign "later-onset" myopathy with moderate reduction in mtDNA, dystonia, medium chain acyl-CoA dehydrogenase deficiency, arthritis, and mitochondrial diabetes and deafness (MIDD), mitochondrial DNA depletion syndrome.

The invention further provides a method of treating or preventing a disorder characterized by reduced mitochondrial function, glucose intolerance, or insulin intolerance in a subject, the method comprising administering to the subject a therapeutically effective amount of an agent which increases the expression or activity of a gene, wherein the gene has an Errα binding site or a Gapba binding site.

In one preferred embodiment of this method, the gene has both an Errα binding site and a Gapba binding site. In one embodiment, the Errα binding site comprises the sequence 5'-TGACCTTG-3' or the sequence '5-CAAGGTCA-3'. In one embodiment, the Gapba binding site comprises the sequence '5-CTTCCG-3' or '5-CGGAAG-3'. It is well known by one of routine skill in the art that transcriptional factors may have optimal binding sites to which they may bind in vivo or in vitro with substantially the same binding affinity as their

optimal binding sites. Accordingly, in some embodiments, an Errα binding site comprises any sequence that, when operably bound to a promoter, allows transcriptional control of the promoter by Errα. In another embodiment, an Errα binding site comprises any sequence that may be bound by an Errα polypeptide with high affinity, such as with a K_d that is less than at least about 10^{-5} M, about 10^{-6} M, about 10^{-7} M, about 10^{-8} M, about 10^{-9} M, about 10^{-10} M, about 10^{-11} M, or about 10^{-12} M. Likewise, in some embodiments, an Gabpa binding site comprises any sequence that, when operably bound to a promoter, allows transcriptional control of the promoter by Gabpa. In another embodiment, an Errα binding site comprises any sequence that may be bound by an Gabpa polypeptide with high affinity, such as with a K_d that is less than at least about 10^{-5} M, about 10^{-6} M, about 10^{-7} M, about 10^{-8} M, about 10^{-9} M, about 10^{-10} M, about 10^{-11} M, or about 10^{-12} M. In some embodiments, an Errα binding site comprises a sequence which is about 50%, 62.5%, 75%, or 87.5% identical to either 5'-TGACCTTG-3' or to '5-CAAGGTCA-3'. In some embodiments, a Gabpa binding site comprises a sequence which is about 50%, 66.6%, or 83.3%, identical to either '5-CTTCCG-3' or '5-CGGAAG-3'.

In another embodiment of any of the methods described herein, a gene which has an Errα binding site is any one of the genes listed on Table 10, a gene which has a Gabpa binding site is any one of the genes on Table 11, and a gene having both an Errα and a Gabpa binding site is any one of the genes listed on Table 12.

In yet another embodiment of this method, the binding sites are located within the promoter region of the gene. In one embodiment, the promoter region comprises from at least 0.5, 1, 1.5, 2, 2.5, 3, 4, 5 or 10 kb upstream of the transcriptional start site of the gene to at least either (i) 0.5, 1, 1.5, 2, 2.5, 3, 4, 5 or 10 kb downstream of the transcriptional start site of the gene; or (ii) 0.5, 1, 1.5, 2, 2.5, 3, 4, 5 or 10 kb downstream of the stop codon of the gene. In yet another embodiment of this methods, the promoter region comprises a masked promoter region. A masked promoter region comprises the regions of promoters that are conserved between two organisms. For example, a masked promoter region may comprise the promoter sequences which are conserved between human and another mammal, such as a mouse. By sequences that are conserved, it is meant sequences which share at least 70% sequence identity between the two species across a window size of at least 8, 9, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, or 50 nucleotides, or more preferably a window of 10

nucleotides.

In another embodiment, the binding sites are located within the promoter region, the coding region, the exons, the introns, or the untranslated region of the gene, or a combination thereof.

In yet another specific embodiment of the method, the gene having an Errα binding site or a Gapba binding site is not Errα, while in another embodiment, the gene is not Gabpa. The agent which increases the activity or expression of a specific gene may be selected by one skilled in the art according to the type of protein that is encoded. For example, if the gene encodes an enzyme, then enzyme activators are expected to increase the activity of the enzyme. Likewise, if the gene is a receptor, a receptor agonist may be administered. Such agonist may comprise small organic molecules, such as those having less than 1 kDa in mass, or may comprise an antibody that binds to the gene product and increases its activity. For any gene, an agent which increases the activity of the gene may comprise a polypeptide of the gene itself, or a nucleic acid containing the gene or an active fragment thereof.

In one embodiments of the methods described herein, reduced mitochondrial function comprises reduced total mitochondrial respiration, reduced uncoupled respiration, reduced expression of mitochondrial enzymes, reduced mitochondrial biogenesis or a combination thereof. In some embodiments of the methods for preventing or treating a disorder in a subject, at least one of the agents increases the expression or activity of Errα, of a Gabp polypeptide, or of both. In another embodiment, the agent promotes the expression or activity of a binding partner of PGC-1α or of PGC-1β. In yet another embodiment, the agent promotes the binding of PGC-1α to a transcriptional regulator. In some embodiments, the transcriptional regulator is Errα or Gabpa. In one preferred embodiment, the agent induces mitochondrial activity in skeletal muscle.

Another aspect of the invention provides a method of treating impaired glucose tolerance in an individual, comprising administering to the individual a therapeutically effective amount of an agent which increases the expression level of at least two OXPHOS-CR genes, thereby treating impaired glucose tolerance in the individual. Another aspect of the invention provides a method of treating obesity in an individual, comprising

administering to the individual a therapeutically effective amount of an agent which increases the expression level of at least two OSPHOS-CR genes, thereby treating obesity in the individual. In preferred embodiments, the expression level of the OXPHOS-CR genes is increased in the skeletal muscle cells of the subject by at least 10%, 20%, 30%, 40%, 50% or 75%.

Another aspect of the invention provides methods of treating or preventing disorders characterized by an elevated metabolic rate in a subject and methods of lowering a metabolic rate in a subject. The invention provides a method of reducing the metabolic rate of a subject in need thereof, the method comprising administering to the subject a therapeutically effective amount of an agent which decreases the expression or activity of at least one of the following: (i) Errα; (ii) Gabpa; (iii) a gene having an Errα binding site, a Gabpa binding site, or both; or (iv) a transcriptional activator which binds to an Errα binding site or to a Gabpa binding site; thereby reducing the metabolic rate of the patient.

In some embodiments of the methods provided for reducing the metabolic rate of a subject in need thereof, the subject is afflicted with an infection, such as a viral infection. In one specific embodiment, the viral infection is a human immunodeficiency virus infection.

In another embodiment of methods for reducing metabolic rates, the subject is afflicted with cancer or with cachexia. Cachexia is a metabolic condition characterized by weight loss and muscle wasting. It is associated with a wide range of conditions including inflammation, heart failure and malignancies, and is well known and described in the clinical literature e.g., J. Natl. Cancer Inst. 89(23): 1763-1773 (1997) 1. The mechanistic derangements underlying cachexia are not known, but it is clear that a negative energy balance obtains in the face of severe weight loss. In specific embodiments, the subject is afflicted with cancer cachexia, pulmonary cachexia, Russell's Diencephalic Cachexia, cardiac cachexia or chronic renal insufficiency.

In some embodiments of the methods provided for reducing the metabolic rate of a subject in need thereof, the agent decreases the formation of a complex between a PGC-1 polypeptide and (i) an Errα polypeptide; or (ii) a Gabp polypeptide. In preferred embodiments, the PGC-1 polypeptide is a PGC-1α polypeptide. In another embodiment, the

agent decreases the expression level or the transcriptional activity of an Errα polypeptide, a Gabp polypeptide, or of both, while in additional embodiments the agent inhibits the expression or activity of a gene which has an Errα binding site, a Gabpa binding site, or both. In some embodiments, the agents comprise double stranded RNA reagents, dominant negative polypeptides or nucleic acids encoding them, or antibodies directed to Errα, Gabpa, Gabpb, or to genes (or their gene products) which have an Errα binding site, a Gabpa binding site, or both, such as binding sites in their promoter regions.

U.S. Patent Application No. 5,602,009 describes a method of generating inhibitory nuclear hormone receptors. Such methods may be applied to Errα or to Gabp to generate polypeptides or nucleic acids which encode them, which may be used as agents in the methods described herein for reducing the metabolic rate of a subject.

V. Methods of Diagnosing/Identifying Disease Genes

One aspect of the invention provides methods of identifying a susceptibility loci for a disorder characterized by reduced mitochondrial function or reduced metabolism. The identification of these loci allows for the diagnosis of the disorders and for the design or screening of agents for the treatment of these disorders.

The invention provides a method of identifying a susceptibility locus for a disorder that is characterized by reduced mitochondrial function, glucose intolerance, or insulin intolerance in a subject, the method comprising (i) identifying at least one polymorphisms in a gene, or linked to a gene, wherein the gene (a) has an Errα binding site, a Gabpa binding site, or both; or (b) is Errα, Gabpa, or Gabpb; (ii) determining if at least one polymorphism is associated with the incidence of the disorder, wherein if a polymorphism is associated with the incidence of the disorder then the gene having the polymorphism, or the gene to which the polymorphism is linked, is a susceptibility locus.

In one embodiment of the methods described herein for identifying a susceptibility locus for a disorder, the gene is any one of the gene listed on Tables 10-12.

As used herein, the term "polymorphism" refers to the co-existence, within a population, of more than one form of a gene or portion thereof (e.g. allelic variant), at a

frequency too high to be explained by recurrent mutation alone. A portion of a gene of which there are at least two different forms, i.e. two different nucleotide sequences, is referred to as a polymorphic region of a gene". A specific genetic sequence at a polymorphic region of a gene is an allele.

A polymorphic region can be a single nucleotide or more than one nucleotide, the identity of which differs in different alleles. A polymorphic region can be a restriction fragment length polymorphism (RFLP). A RFLP refers to a variation in DNA sequence that alters the length of a restriction fragment as described in Botstein et al., Am. J. Hum. Genet. 32. 3 14-33 1 (1980). The RFLP may create or delete a restriction site, thus changing the length of the restriction fragment. RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, Cell 5 1, 3) 19-33)7 (1987); Lander et al. Genetics 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the individual will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri-and tetranucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (U.S. Pat. No. 5,075,217; Armour et al., FEBS Lett. 307, 1 3- 1 15 (1992); Horn et al. WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such single nucleotide variations may arise due to substitution of one nucleotide for another at the polymorphic site or from a deletion of a nucleotide or an insertion of a nucleotide relative to a referenced allele. These single nucleotide variations are referred to herein as single nucleotide polymorphism (SNPs). Such SNPs are far more frequent than RFLPS, STRs and VNTRs. Some SNPs may occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective protein and, potentially, a genetic disease. Other SNPs may occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g. as a result of defective splicing). Other SNPs may have no phenotypic effects.

Techniques for determining the presence of particular alleles would be those known to persons skilled in the art and include, but are not limited to, nucleic acid techniques based on size or sequence, such as restriction fragment length polymorphism (RFLP), nucleic acid sequencing, or nucleic acid hybridization. The nucleic acid tested may be RNA or DNA. These techniques may also comprise the step of amplifying the nucleic acid before analysis. Amplification techniques are known to those of skill in the art and include, but are not limited to, cloning, polymerase chain reaction (PCR), polymerase chain reaction of specific alleles (PASA), polymerase chain ligation, nested polymerase chain reaction, and the like. Amplification products may be assayed in a variety of ways, including size analysis, restriction digestion followed by size analysis, detecting specific tagged oligonucleotide primers in the reaction products, allele-specific oligonucleotide (ASO) hybridization, allele specific exonuclease detection, sequencing, hybridization and the like. Polymorphic variations leading to altered protein sequences or structures may also be detected by analysis of the protein itself. Additional methods for the detection of polymorphisms are described in U.S. Patent No. 6,453,244 and in International PCT publications No. WO 04/011668, WO 03/048384, WO 01/20031 and WO 03/038125, the teachings of which are hereby incorporated by reference.

General methods are available to one skilled in the art for determining if a particular allele is associated with the incidence of the disorder, such as those described in Analysis of Human Genetic Linkage, by Jurg Ott: Johns Hopkins University Press, 1999; and Statistical Genomics: Linkage, Mapping, and QTL Analysis by Ben Hui Liu: CRC Press, 1997.

The invention also provides a related method for determining if a subject is at risk of developing a disorder which is characterized by reduced mitochondrial function, the method comprising determining if a gene from the subject contains a mutation which reduces the function of the gene, wherein the gene has an Errα binding site, a Gapba binding site, or both, wherein if a gene from the subject contains a mutation then the subject is at risk of developing the disorder.

In one embodiment of this method, the mutation reduces the function of the gene. In another embodiment, the disorder is diabetes, obesity, premature aging, cardiomyopathy, a

neurodegenerative disease, or retinal degeneration. In further embodiments, the gene is any one of the genes on Tables 10-12.

The proposed role of the candidate genes proteins can be validated by traditional overexpression or knockout approaches to ascertain the effects of such manipulations on mitochondrial biogenesis in the engineered cell lines. This approach ultimately identifies additional molecules whose expression or activity can be modulated to enhance mitochondrial function. For example, cultured skeletal muscle cells may be used with electrical stimulation or thyroid hormone as the stimulus for mitochondrial biogenesis. Alternatively, a fat cell culture such as 3T3-L1 cells may be used, with norepinephrine providing the stimulus for mitochondrial biogenesis. Alternatively, cultured cells such as HeLa or HEK293 that express PGC-l and/or NRF-1 under a tetracycline inducible system may be used, wherein induced expression of PGC-1 and/or NRF-1 stimulates mitochondrial biogenesis. After sufficient time with the appropriate stimulus to allow induction (1-2 days), the cells are incubated with P^{32} orthophosphate for 4 hrs. Cells are then harvested and subjected to SDS-PAGE to resolve the labeled proteins. Using these systems, the function of a candidate disease gene may be altered, such as through overexpression, expression of dominant negative forms of the proteins, inhibitory RNAi reagents, antibodies, and the like, and the effects on mitochondrial biogenesis or function determined.

VI. Methods of Identifying Therapeutic agents

One aspect of the invention provides methods of identifying agents which modulate biological responses in a cell, which modulate expression of the OXPHOS-CR genes or which prevent or treat a disorder.

One aspect of the invention provides a method of determining if an agent is a potential agent for the treatment of a disorder that is characterized by glucose intolerance, insulin resistance or reduced mitochondrial function, the method comprising determining if the agent increases: (i) the expression or activity of Errα or Gabp in a cell; or (ii) the formation of a complex between a PGC-1 polypeptide and (i) an Errα polypeptide; or (ii) a Gabp polypeptide; wherein an agent that increases (i) or (ii) is a potential target for the treatment of the disorder.

In some embodiments of the methods described herein for determining if an agent is a

potential agent for the treatment of a disorder, the disorder is diabetes, obesity, cardiac myopathy, aging, coronary atherosclerotic heart disease, diabetes mellitus, Alzheimer's Disease, Parkinson's Disease, Huntington's disease, dystonia, Leber's hereditary optic neuropathy (LHON), schizophrenia, myodegenerative disorders such as "mitochondrial encephalopathy, lactic acidosis, and stroke" (MELAS). and "myoclonic epilepsy ragged red fiber syndrome" (MERRF), NARP (Neuropathy; Ataxia; Retinitis Pigmentosa), MNGIE (Myopathy and external ophthalmoplegia, neuropathy; gastro-intestinal encephalopathy, Kearns-Sayre disease, Pearson's Syndrome, PEO (Progressive External Ophthalmoplegia), congenital muscular dystrophy with mitochondrial structural abnormalities, Wolfram syndrome, Diabetes Insipidus, Diabetes Mellitus, Optic Atrophy Deafness; Leigh's Syndrome, fatal infantile myopathy with severe mitochondrial DNA (mtDNA) depletion, benign "later-onset" myopathy with moderate reduction in mtDNA, medium chain acyl-CoA dehydrogenase deficiency, dystonia, arthritis, and mitochondrial diabetes and deafness (MIDD), or mitochondrial DNA depletion.

Any general method known to one skilled in the art may be applied to determine if an agent increases the expression or activity of Errα or Gabp. In one specific embodiment for determining if an agent increases the expression of Errα or Gabp, a cell is contacted with an agent, and an indicator of gene expression, such as mRNA level or protein level, is determined. Levels of mRNA may be determined, for example, using such techniques as Northern Blots, reverse-transcriptase polymerase chain reaction (RT-PCR), RNA protection assays or a DNA microarray comprising probes capable of detecting Errα or Gabp mRNA or cDNA molecules. Likewise, protein levels may be quantitated using techniques well-known in the art, such as western blotting, immuno-sandwich assays, ELISA assays, or any other immunological technique. Techniques for quantitating nucleic acids and proteins may be found, for example, in Molecular Cloning: A Laboratory Manual, 3rd Ed., ed. by Sambrook and Russell (Cold Spring Harbor Laboratory Press: 2001); and in Current Protocols in Cell Biology, ed. by Bonifacino, Dasso, Lippincott-Schwartz, Harford, and Yamada, John Wiley and Sons, Inc., New York, 1999, hereby incorporated by reference in their entirety.

In one example, an RC cell culture system can be used to identify compounds which activate production of ERRα or, once ERRα production has been activated in the cells, can be used to identify compounds which lead to suppression or switching off of ERRα,

production. Alternatively, such a cell culture system can be used to identify compounds or binding partners of ERRα which increase its expression. Compounds thus identified are useful as therapeutics in conditions where ERRα production is deficient or excessive. Similar experiments may be carried out with Gabpa or Gabpb or both.

Likewise, any general method known to one skilled in the art may be applied to determining if an agent increases the activity of Errα or Gabp. Activities of Errα or Gabp include their ability to bind to DNA, their ability to bind to other transcriptional regulators or their ability to promote transcription of target genes. In one embodiment, candidate agents are tested for their ability to modulate ERRα activity by (a) providing a system for measuring a biological activity of ERRα; and (b) measuring the biological activity of ERRα in the presence or absence of the candidate compound, wherein a change in ERRα activity in the presence of the compound relative to ERRα activity in the absence of the compound indicates an ability to modulate ERRα activity. In specific embodiments, the biological activity is the ability of Errα to bind the promoter of a target gene, such as the promoter or medium chain acyl-CoA dehydrogenase (MCAD), which may be determined using chromatin immunoprecipitation and analysis of the DNA bound to the Errα polypeptide. In another embodiment, the biological activity is the ability of Errα to complex with PGC-1a or PGC-1b, which may be measured by immunoprecipitation of either Errα or a PGC-1 polypeptide and determining the presence of the other protein by western blotting. In another embodiment, the biological activity is promoting transcription of a target gene. An indicator of gene expression for a target gene whose transcription is regulated by Errα or by Gabp can be compared between cells which have or have not been contacted with the agent. In specific embodiments, PGC-1α or PGC-1β is also present when testing of an agent modulates the transcriptional activating activity of Errα or Gabp polypeptides. Target genes which may be used include those which contain either an Errα or a Gabp binding site, such as OXPHOS genes or those provided by the invention. Because Gabpa and Gabpb form a complex, in some preferred embodiments both proteins, or nucleic acids encoding them, are present in the assay systems described herein.

One particular embodiment for identifying agents which modulate activity of Errα employs two genetic constructs. One is typically a plasmid that continuously expresses the

transcriptional regulator of interest when transfected into an appropriate cell line. The second is a plasmid which expresses a reporter, e.g., luciferase under control of the transcriptional regulator. For example, if a compound which acts as a ligand for Errα is to be evaluated, one of the plasmids would be a construct that results in expression of the Errα in the cell line. The second would possess a promoter linked to the luciferase gene in which an Errα response element is inserted. If the compound to be tested is an agonist for the Errα receptor, the ligand will complex with the receptor and the resulting complex binds the response element and initiates transcription of the luciferase gene. In time the cells are lysed and a substrate for luciferase added. The resulting chemiluminescence is measured photometrically. Dose response curves are obtained and can be compared to the activity of known ligands. Other reporters than luciferase can be used including CAT and other enzymes. In one specific embodiments of this approach, the cells further express PGC-1α or PGC-1β, either endogenously or by introduction of a third plasmid encoding said polypeptides. The presence of PGC-1 polypeptides in the cell further allows for the identification of agents which increase or decrease the binding interaction between a PGC-1 polypeptide and Errα. This approach may also be modified to express both Gabpa and Gabpb to identify agents which modulate their transcriptional activity. Alternatively, a cell may be used which endogenously expresses any combination of polypeptides, such that only a plasmid encoding a reporter gene is introduced into the cell.

Viral constructs can be used to introduce the gene for Errα Gabp or PGC-1 and the reporter into a cell. An usual viral vector is an adenovirus. For further details concerning this preferred assay, see U.S. Pat. No. 4,981,784 issued Jan. 1, 1991 hereby incorporated by reference, and Evans et al., WO88/03168 published on 5 May 1988, also incorporated by reference.

Errα antagonists can be identified using this same basic "agonist" assay. A fixed amount of an antagonist is added to the cells with varying amounts of test compound to generate a dose response curve. If the compound is an antagonist, expression of luciferase is suppressed.

Additional methods for the isolation of agonists and antagonist of transcriptional regulators are described in U.S. Patent Nos. 6,187,533, 5,620,887, 5,804,374, and 5,298,429,

and U.S. Patent Publication Nos. 2004/003394, 2003/0077664, 2003/0215829 and 2003/0039980. Any of the methods described herein may be easily adapted to identify agonists or antagonists of any one Errα or Gabp polypeptides.

U.S. Patent No. 6,555,326 (PCT Pub No. WO 99/27365) describes a fluorescent polarization assay for identifying agents which regulate the activity of nuclear hormone receptors, by using a nuclear hormone receptor, a peptide sensor and a candidate agent. Table 1 of this patent also lists exemplary nuclear hormone receptors. Such a method may easily be modified by one skilled in the art to identify agents which regulate the activity of Errα or Gabp.

The invention also provides a method for screening a candidate compound for its ability to modulate ERRα activity in a suitable system, in the presence or absence of the candidate compound. A change in ERRα activity the presence of the compound relative to ERRα activity in the absence of the compound indicates that the compound modulates ERRα activity. ERRα activity is increased relative to the control in the presence of the compound, the compound is an ERRα agonist. Conversely, if ERRα activity is decreased in the presence of the compound, the compound is an ERRα antagonist.

Another way of determining if an agent increases the activity of Errα or Gabp may also be based on binding of the agent to an ERRα or to a Gabp polypeptide or fragment thereof. Such competitive binding assays are well known to those skilled in the art.

For example, the invention provides screening methods for compounds able to bind to ERRα which are therefore candidates for modifying the activity of ERRα. Various suitable screening methods are known to those in the art, including immobilization of ERRα on a substrate and exposure of the bound ERRα to candidate compounds, followed by elution of compounds which have bound to the ERRα. Additional methods and assays for identifying agents which modulate Errα activity, for generating Errα knock out animals and cells, and for generating ERRα reagents, such as anti-Errα antibodies are described in International PCT publication No. WO 00/122988, hereby incorporated by reference in its entirety.

Another aspect of the invention provides a method of identifying an agent that

modulates a biological response, the method comprising (a) contacting, in the presence of the agent, a PGC-1 polypeptide and an (i) Errα polypeptide, or (ii) a Gabp polypeptide, under conditions which allow the formation of a complex between the PGC-1 polypeptide and (i) the Errα polypeptide, or (ii) the Gabp polypeptide; and (b) detecting the presence of the complex; wherein an agent that modulates the biological response is identified if the agent increases or decreases the formation of the complex, and wherein the biological response is (a) expression of the OXPHOS genes; (b) mitochondrial biogenesis; (c) expression of Nuclear Respiratory Factor 1 (NRF-1); (d) β-oxidation of fatty acids; (e) total mitochondrial respiration; (f) uncoupled respiration; (g) mitochondrial DNA replication; or (h) expression of mitochondrial enzymes.

In some embodiments of the methods for identifying an agent that modulates a biological response, the method comprises an agent that increases the formation of the complex and that increases the biological response. In alternate embodiments, the agent decreases the formation of the complex and decreases the biological response. In some embodiments, the conditions which allow the formation of a complex between the PGC-1 polypeptide and an Errα polypeptide or a Gabpa polypeptide comprise in vitro conditions, while in other embodiments they comprise in vivo conditions such as expression in a cell or in an organism.

The following embodiments of methods for identifying a compound that modulates a biological response, although directed at Errα and PGC-1α, are equally applicable to Gabp polypeptides, such as Gabpa polypeptides, or to PGC-1β polypeptides.

One embodiment for the of the methods for identifying a compound that modulates a biological response comprises: 1) combining: a Errα polypeptide or fragment thereof, a PGC-1α polypeptide or fragment thereof, and an agent, under conditions wherein the Err alpha and PGC-1α polypeptides physically interact in the absence of the agent, 2) determining if the agent interferes with the interaction, and 3) for an agent that interferes with the interaction, further assessing its ability to promote the any of the biological responses of the cell, such as (a) expression of the OXPHOS genes, mitochondrial biogenesis, expression of Nuclear Respiratory Factor 1 (NRF-1), β-oxidation of fatty acids, total mitochondrial respiration,

uncoupled respiration, mitochondrial DNA replication or expression of mitochondrial enzymes.

A variety of assay formats will suffice and, in light of the present disclosure; those not expressly described herein will nevertheless be comprehended by one of ordinary skill in the art. Assay formats which approximate such conditions as formation of protein complexes, enzymatic activity, may be generated in many different forms, and include assays based on cell-free systems, e.g. purified proteins or cell lysates, as well as cell-based assays which utilize intact cells. Simple binding assays can also be used to detect agents which bind to Errα or PGC-1α. Such binding assays may also identify agents that act by disrupting the interaction between a Errα polypeptide and PGC-1α. Agents to be tested can be produced, for example, by bacteria, yeast or other organisms (e.g. natural products), produced chemically (e.g. small molecules, including peptidomimetics), or produced recombinantly. Because Errα and PGC-1a polypeptides contain multiple domains, specific embodiments of the assays and methods described to identify agents which modulate complex formation between Errα and PGC-1a employ fragments of Errα rather than full-length polypeptides, such as those lacking the DNA binding domains. Fragments of PGC-1α may also be used in some embodiments, in particular fragments which retain the ability to complex with Errα.

In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays of the present invention which are performed in cell-free systems, which may be developed with purified or semi-purified proteins or with lysates, are often preferred as "primary" screens in that they can be generated to permit rapid development and relatively easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test agent can be generally ignored in the in vitro system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an alteration of binding affinity with other proteins or changes in enzymatic properties of the molecular target.

In preferred in vitro embodiments of the present assay, a reconstituted Errα/PGC-1α complex comprises a reconstituted mixture of at least semi-purified proteins. By semi-

purified, it is meant that the proteins utilized in the reconstituted mixture have been previously separated from other cellular or viral proteins. For instance, in contrast to cell lysates, the proteins involved in Errα /PGC-1α complex formation are present in the mixture to at least 50% purity relative to all other proteins in the mixture, and more preferably are present at 90-95% purity. In certain embodiments of the subject method, the reconstituted protein mixture is derived by mixing highly purified proteins such that the reconstituted mixture substantially lacks other proteins (such as of cellular or viral origin) which might interfere with or otherwise alter the ability to measure Errα/PGC-1α complex assembly and/or disassembly.

Assaying Errα/PGC-1α complexes, in the presence and absence of a candidate agent, can be accomplished in any vessel suitable for containing the reactants. Examples include microtiter plates, test tubes, and micro-centrifuge tubes. In a screening assay, the effect of a test agent may be assessed by, for example, determining the effect of the test agent on kinetics, steady-state and/or endpoint of the reaction.

In one embodiment of the present invention, drug screening assays can be generated which detect inhibitory agents on the basis of their ability to interfere with assembly or stability of the Errα/PGC-1a complex. In an exemplary binding assay, the compound of interest is contacted with a mixture comprising a Errα/PGC-1a complex. Detection and quantification of Errα/PGC-1α complexes provides a means for determining the compound's efficacy at inhibiting (or potentiating) interaction between the two polypeptides. The efficacy of the compound can be assessed by generating dose response curves from data obtained using various concentrations of the test compound. Moreover, a control assay can also be performed to provide a baseline for comparison. In the control assay, the formation of complexes is quantitated in the absence of the test compound.

Complex formation may be detected by a variety of techniques. For instance, modulation in the formation of complexes can be quantitated using, for example, detectably labeled proteins (e.g. radiolabeled, fluorescently labeled, or enzymatically labeled), by immunoassay, or by chromatographic detection. Surface plasmon resonance systems, such as those available from Biacore © International AB (Uppsala, Sweden), may also be used to detect protein-protein interaction.

The proteins and peptides described herein may be immobilized. Often, it will be desirable to immobilize the peptides and polypeptides to facilitate separation of complexes from uncomplexed forms of one of the proteins, as well as to accommodate automation of the assay. The peptides and polypeptides can be immobilized on any solid matrix, such as a plate, a bead or a filter. The peptide or polypeptide can be immobilized on a matrix which contains reactive groups that bind to the polypeptide. Alternatively or in combination, reactive groups such as cysteines in the protein can react and bind to the matrix. In another embodiment, the polypeptide may be expressed as a fusion protein with another polypeptide which has a high binding affinity to the matrix, such as a fusion protein to streptavidin which binds biotin with high affinity.

In an illustrative embodiment, a fusion protein can be provided which adds a domain that permits the protein to be bound to an insoluble matrix. For example, a GST-ERRα fusion protein can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtitre plates, which are then combined with a PGC-1a polypeptide, e.g. an ^{35}S-labeled polypeptide, and the test compound and incubated under conditions conducive to complex formation. Following incubation, the beads are washed to remove any unbound interacting protein, and the matrix bead-bound radiolabel determined directly (e.g. beads placed in scintillant), or in the supernatant after the complexes are dissociated, e.g. when microtitre plate is used. Alternatively, after washing away unbound protein, the complexes can be dissociated from the matrix, separated by SDS-PAGE gel, and the level of interacting polypeptide found in the matrix-bound fraction quantitated from the gel using standard electrophoretic techniques.

In yet another embodiment, the Errα and PGC-1α polypeptides can be used to generate an interaction trap assay (see also, U.S. Patent No: 5,283,317; Zervos et al. (1993) Cell 72:223-232; Madura et al. (1993) J Biol Chem 268:12046-12054; Bartel et al. (1993) Biotechniques 14: 920-924; and Iwabuchi et al. (1993) Oncogene 8:1693-1696), for subsequently detecting agents which disrupt binding of the proteins to one and other.

In still further embodiments of the present assay, the Errα/PGC-1αcomplex is generated in whole cells, taking advantage of cell culture techniques to support the subject

assay. For example, as described below, the Errα/PGC-1α complex can be constituted in a eukaryotic cell culture system, such as a mammalian cell and a yeast cell. Other cells know to one skilled in the art may be used. Advantages to generating the subject assay in a whole cell include the ability to detect inhibitors which are functional in an environment more closely approximating that which therapeutic use of the inhibitor would require, including the ability of the agent to gain entry into the cell. Furthermore, certain of the in vivo embodiments of the assay, such as examples given below, are amenable to high through-put analysis of candidate agents.

The components of the Errα/PGC-1a complex can be endogenous to the cell selected to support the assay. Alternatively, some or all of the components can be derived from exogenous sources. For instance, fusion proteins can be introduced into the cell by recombinant techniques (such as through the use of an expression vector), as well as by microinjecting the fusion protein itself or mRNA encoding the fusion protein.

In still further embodiments of the present assay, the Errα/PGC-1a complex is generated in whole cells and the level of interaction is determined by measuring the level of gene expression of an (i) endogenous gene or of a transgene, whose expression is dependent on the formation of a complex. Genes which are responsive to Errα/PGC-1a complex are provided by the invention and some may be found in the literature.

In specific embodiments, the cells used in the methods described herein for identifying agents are cells in culture or from a subject, such as a tissue, fluid or organ or a portion of any of the foregoing. For example, cells can preferably be from tissues that are involved in glucose metabolism, such as pancreatic cells, islates of Langerhans, pancreatic beta cells, muscle cells, liver cells or other appropriate cells. Preferably, cells are provided in culture and can be a primary cell line or a continuous cell line and can be provided as a clonal population of cells or a mixed population of cells.

VII. Methods of Identifying Agents which Modulate OXPHOS-CR Expression

Applicants have identified a core set of genes (OXPHOS-CR) that help unify previous observations from clinical investigation, exercise physiology, pharmacology, and genetics. Drugs that modulate OXPHOS-CR activity may be promising candidates for the prevention

and/or treatment of type 2 diabetes. Applicants discovery of OXPHOS-CR properties and previous observations support the hypothesis that drugs that increase OXPHOS-CR activity in muscle and fat will improve insulin resistance, while agents that reduce it will worsen insulin resistance. These drugs may have benefit in other processes characterized by aberrant oxidative capacity in these tissues, including obesity and aging.

The methods described in this section for identifying agents which regulate the expression level of one or more OXPHOS-CR genes may also identify agents which modulate PGC-1α, Gabp or Errα expression or activity, or agents which mimic or functionally substitute for these genes, since applicants have demonstrated that these three transcriptional regulators regulate the expression of OXPHOS-CR genes. Likewise, these methods also identify therapeutic agents which modulate metabolism or mitochondrial function in a subject in need thereof, such as a subject afflicted with diabetes.

Accordingly, the invention further provides cell based methods for identifying agents which regulate the expression of OXPHOS-CR genes. On aspect provides a method of identifying an agent that regulates expression of OXPHOS-CR genes, the method comprising (a) contacting (i) an agent to be assessed for its ability to regulate expression of OXPHOS-CR genes with (ii) a test cell; and (b) determining whether the expression level of at least two OXPHOS-CR gene products show a coordinate change in the test cell compared to an appropriate control, wherein a coordinate change in the expression of the OXPHOS-CR gene products relative to the appropriate control indicates that the agent regulates the expression of OXPHOS-CR genes.

A related aspect of the invention provides method of identifying an agent that regulates expression of a gene, wherein the gene is an OXPHOS-CR gene, the method comprising (a) contacting (i) an agent to be assessed for its ability to regulate expression of the gene with (ii) a test cell; and (b) determining whether the expression level of two or more OXPHOS-CR gene products show a coordinate change in the test cell compared to an appropriate control, wherein the gene does not encode the two or more OXPHOS-CR gene products, and wherein a coordinate change in the expression of the OXPHOS-CR gene products relative to the appropriate control indicates that the agent regulates the expression level of the gene.

In some embodiments, the OXPHOS-CR gene products comprise an mRNA or a polypeptide. The gene products of the two genes need not be of the same type. For instance, in one specific embodiment, the mRNA levels of a first OXPHOS-CR gene, the polypeptide levels of a second OXPHOS-CR gene, and the enzymatic activity of a third OXPHOS-CR genes are determined. In a preferred embodiment, all the gene products comprises mRNAs.

In additional embodiments, determining whether the expression of at least two OXPHOS-CR gene products show a coordinate change in the test cell comprises detecting, either qualitatively, semiquantitatively, or more preferably quantitatively, the levels of the OXPHOS-CR gene products. In one embodiment, the coordinate change comprises an increase or a decrease in expression in all the genes tested. In another embodiment, a coordinate change comprises an increase or a decrease in at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 95%, 97%, 98% or 99% of the genes tested.

In a variation of this method, more than one cell is contacted with the agent. In yet another variation, multiple cells or cell populations are contacted with the agent, such that each cell or cell population provides a measure of expression for each of the OXPHOS-CR gene products. For example, if the expression level of four OXPHOS-CR genes is to be determined, then four cell populations, such as one on each well of a 96-well plate, is contacted with the agent, and from each well the expression level of one of the OXPHOS genes is determined. Alternatively, two cell populations could be used and the expression level of two gene products could be determined from each of the two cell populations. In another embodiment, the cell or cell population is contacted with more than one agent.

The expression level of the OXPHOS-CR gene products may be determined using techniques known in the art. Gene products which comprise an mRNA may be detected, for example, using reverse transcriptase mediated polymerase chain reaction (RT-PCR), Northern blot analysis, in situ hybridization, microarray analysis, etc. (Schena et al., Science 270:467-470 (1995); Lockhart et al., Nature Biotech. 14: 1675-1680 (1996), and U.S. Patent Nos. 5,770,151, 5,807,522, 5,837,832, 5,952,180, 6,040,138 and 6,045,996). Polypeptide products may be detected using, for example, standard immunoassay methods known in the art. Such immunoassays include but are not limited to, competitive and non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme-linked

immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitin reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzymatic, or radioisotope labels, for example), Western blots, 2-dimensional gel analysis, precipitation reactions, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays.

When the gene product comprises an enzyme, the level of gene product may be determined using a measure of enzymatic activity. Products of enzyme catalytic activity may be detected by suitable methods that will depend on the quantity and physicochemical properties of the particular product. Thus, detection may be, for example by way of illustration and not limitation, by radiometric, calorimetric, spectrophotometric, fluorimetric, immunometric or mass spectrometric procedures, or by other suitable means that will be readily apparent to a person having ordinary skill in the art. In certain embodiments of the invention, detection of a product of enzyme catalytic activity may be accomplished directly, and in certain other embodiments detection of a product may be accomplished by introduction of a detectable reporter moiety or label into a substrate or reactant such as a marker enzyme, dye, radionuclide, luminescent group, fluorescent group or biotin, or the like. The amount of such a label that is present as unreacted substrate and/or as reaction product, following a reaction to assay enzyme catalytic activity, is then determined using a method appropriate for the specific detectable reporter moiety or label. For radioactive groups, radionuclide decay monitoring, scintillation counting, scintillation proximity assays (SPA) or autoradiographic methods are generally appropriate. For immunometric measurements, suitably labeled antibodies may be prepared including, for example, those labeled with radionuclides, with fluorophores, with affinity tags, with biotin or biotin mimetic sequences or those prepared as antibody-enzyme conjugates (see, e.g., Weir, D. M., Handbook of Experimental Immunology, 1986, Blackwell Scientific, Boston; Scouten, W. H., Methods in Enzymology 135:30-65, 1987; Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, 1988; Haugland, 1996 Handbook of Fluorescent Probes and Research Chemicals--Sixth Ed., Molecular Probes, Eugene, Oreg.; Scopes, R. K., Protein Purification: Principles and Practice, 1987, Springer-Verlag, NY; Hermanson, G. T. et al., Immobilized Affinity Ligand Techniques, 1992, Academic Press, Inc., NY; Luo et al., 1998 J. Biotechnol. 65:225 and references cited therein). Spectroscopic methods may be used to detect dyes (including, for example, colorimetric products of enzyme reactions), luminescent groups and fluorescent groups. Biotin may be detected using avidin or streptavidin, coupled

to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic, spectrophotometric or other analysis of the reaction products. Standards and standard additions may be used to determine the level of enzyme catalytic activity in a sample, using well known techniques.

In one embodiment, the promoter regions for two or more OXPHOS-CR genes (or larger portions of such genes) may be operatively linked to a reporter gene and used in a reporter gene-based assay to detect agents that enhance or diminish OXPHOS-CR gene expression. In such embodiments, the OXPHOS gene product is the mRNA or polypeptide encoded by the reporter gene. In a specific embodiment, the recombinant fluorescent polypeptide comprises a polypeptide selected from the group consisting of the green fluorescent protein (GFP), DsRed, zFP538, mRFP1, BFP, CFP, YFP, mutants thereof, or functionally-active fragments thereof. GFP is described in U.S. Pat. No. 5,491,084, while zFP538 is described in Zagranichny et al. Biochemistry. 2004;43(16):4764-72.

In another specific embodiment, the appropriate control comprises the expression level of the two or more OXPHOS-CR gene products in cells that (a) have not been contacted with the agent; (b) have been contacted with a different dosage of the agent; (c) have been contacted with a second agent; or (d) a combination thereof. Alternatively, an appropriate control may be a measure of the gene product in the cell prior to contacting with the agent. In another embodiment, the level of gene expression of the OXPHOS-CR gene product in the cell can be compared with a standard (e.g., presence or absence of an OXPHOS-CR gene product) or numerical value determined (e.g. from analysis of other samples) to correlate with a normal or expected level of expression.

In some embodiments, the identification of agents which regulate the expression of OXPHOS-CR genes is carried out in a high-throughput fashion. When screening agents in a high-throughput manner, such as when test compounds are screened for their effects on the cellular phenotype, arrays of cells may be prepared for parallel handling of cells and reagents. Standard 96 well microtiter plates which are 86 mm by 129 mm, with 6 mm diameter wells on a 9 mm pitch, may be used for compatibility with current automated loading and robotic handling systems. The microplate is typically 20 mm by 30 mm, with cell locations that are 100-200 microns in dimension on a pitch of about 500 microns. Methods for making

microplates are described in U.S. Patent No. 6,103,479, incorporated by reference herein in its entirety. Microplates may consist of coplanar layers of materials to which cells adhere, patterned with materials to which cells will not adhere, or etched 3-dimensional surfaces of similarly pattered materials. For the purpose of the following discussion, the terms `well` and `microwell` refer to a location in an array of any construction to which cells adhere and within which the cells are imaged. Microplates may also include fluid delivery channels in the spaces between the wells. The smaller format of a microplate increases the overall efficiency of the system by minimizing the quantities of the reagents, storage and handling during preparation and the overall movement required for the scanning operation. In addition, the whole area of the microplate can be imaged more efficiently.

In specific embodiments, the test cell that is contacted with the agent may be a primary cell, a cell within a tissue, or a cell line. In a preferred embodiment, the test cell is a liver cell, a skeletal muscle cell, such as a C2C12 myoblast or a fat cell, such as 3T3-L1 preadipocyte.

In one embodiment, the method for identifying an agent that regulates expression of OXPHOS-CR genes comprises determining whether the expression of at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26 or 27 OXPHOS-CR gene products. In a preferred embodiment, the expression level of five or less OXPHOS-CR gene products is determined. In a specific embodiment, the OXPHOS-CR gene products are selected from the group consisting of NDUFB3, SDHA, NDUFA8, COX7A1, UQCRC1, NDUFC1, NDUFS2, ATP5O, NDUFS3, SDHB, NDUFS5, NDUFB6, COX5B, CYC1, NDUFA7, UQCRB, COX7B, ATP5L, COX7C, NDUFA5, GRIM19, ATP5J, COX6A2 NDUFB5, CYCS, NDUFA2 and HSPC051. In a specific embodiment, one of the OXPHOS-CR genes is ubiquinol cytochrome *c* reductase binding protein (*UQCRB*). In a preferred embodiment, the OXPHOS-CR gene products are human OXPHOS-CR products. The OXPHOS-CR genes whose expression level is determined may be encoded by (i) mitochondrial DNA (mtDNA); (ii) nuclear DNA; or (iii) a combination thereof.

In one embodiment of the methods described herein for identifying agents which regulate the expression of OXPHOS-CR genes, the method further comprises determining if the agent regulates the expression of at least one gene which is not an OXPHOS-CR gene. In some embodiments, the method further comprises determining if the agent regulates the

expression of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or 50 genes which are not an OXPHOS-CR genes. Such genes may be mitochondrial genes or, in preferred embodiments, not mitochondrial genes, such as actin genes. The expression level of another gene which is not an OXPHOS-CR gene may serve as an internal control, such that agents which specifically modulate the expression of an OXPHOS-CR gene may be identified.

In other embodiments, a secondary screening step is performed on the agent. In a specific embodiment, the agent is tested in additional assays for its effects on mitochondrial cell number or a mitochondrial function, such as coupled oxygen consumption. Such assays may comprise contacting a cell with the agent, measuring mitochondrial cell number or function, and comparing it to an appropriate control. U.S. Patent Publication No. 20020049176 describes assays for determining mitochondrial mass, volume or number, and U.S. Patent Publication No. 2002/0127536 describes assays for determining coupled oxygen consumption. Accordingly, in one embodiment, the agent being tested in the assays described herein additionally (a) increases the number of mitochondria in the test cell; (b) increases coupled oxygen consumption in the cell; (c) increases mtDNA copy number in the test cell; or (d) a combination thereof.

Agents identified using the methods of the present invention may also be tested in model systems for their efficacy in inducing the desired biological response or in treating disorders. One example is high-fat diet induced obesity and insulin resistance. In another example, agents may also be tested for their efficacy in treating diabetes by using a non-obese diabetic (NOD) mouse. The successful use of this animal model in diabetic drug discovery is reported in the literature (Yang et al., J. Autoimmun. 10:257-260 (1997), Akashi et al., Int. Immunol. 9:1159-1164 (1997), Suri and Katz, Immunol. Rev. 169:55-65 (1999), Pak et al., Autoimmunity 20:19-24 (1995), Toyoda and Formby, Bioessays 20:750-757 (1998), Cohen, Res. Immunol. 148:286-291 (1997), Baxter and Cooke, Diabetes Metal. Rev. 11:315-335 (1995), McDuffie, Curr. Opin. Immunol. 10:704-709 (1998), Shieh et al. Autoimmunity 15:123-135 (1993), Anderson et al., Autoimmunity 15:113-122 (1993)).

It is well understood by one skilled in the art that many of the methods described herein may be carried out using variants of the polypeptides described. Variants include truncated polypeptides, mutant polypeptides, such as those carrying point mutations, and fusions between domains of the subject polypeptides and other polypeptides. In some

embodiments, the subject polypeptides, or their domains, may be fused to reporter proteins, such as to GFP or to enzymes. In some embodiments of any of the methods described herein, the polypeptides used are 50, 60, 70, 80, 90, 95, 98 or 99% identical to the sequences referenced to in the various Genbank Accession numbers.

In the methods described herein for identifying an agent, the agent may comprise a recombinant polypeptide, a synthetic molecule, or a purified or partially purified naturally occurring molecule. In a specific embodiment, the agent comprises a virus or a phage. In another embodiment, the agent is a nuclear hormone, such as estrogen, thyroid hormone, cortisol, testosterone, and others. Additional agents include nucleic acids encoding nuclear hormone receptors.

In another embodiment, the agent comprises a set of environmental conditions. The condition may be a physical condition of the environment in which the cell resides, a chemical condition of the environment, and/or a biological condition of the site. Exposure may be for any suitable time. The exposure may be continuous, transient, periodic, sporadic, etc. Physical conditions include any physical state of the examination site. The physical state may be the temperature or pressure of the sample, or an amount or quality of light (electromagnetic radiation) at the site. Alternatively, or in addition, the physical state may relate to an electric field, magnetic field, and/or particle radiation at the site, among others. Chemical conditions include any chemical aspect of the fluid in which the sample populations are disposed. The chemical aspect may relate to presence or concentration of a test compound or material, pH, ionic strength, and/or fluid composition, among others.

Biological conditions include any biological aspect of the shared fluid volume in which cell populations are disposed. The biological aspects may include the presence, absence, concentration, activity, or type of cells, viruses, vesicles, organelles, biological extracts, and/or biological mixtures, among others. The assays described herein may screen a library of conditions to test the activity of each library member on a set of cell populations. A library generally comprises a collection of two or more different members. These members may be chemical modulators (or candidate modulators) in the form of molecules, ligands, compounds, transfection materials, receptors, antibodies, and/or cells (phages, viruses, whole cells, tissues, and/or cell extracts), among others, related by any suitable or desired common characteristic. This common characteristic may be "type." Thus, the library may comprise a

collection of two or more compounds, two or more different cells, two or more different antibodies, two or more different nucleic acids, two or more different ligands, two or more different receptors, or two or more different phages or whole cell populations distinguished by expressing different proteins, among others. This common characteristic also may be "function." Thus, the library may comprise a collection of two or more binding partners (e.g., ligands and/or receptors), agonists, or antagonists, among others, independent of type.

Library members may be produced and/or otherwise generated or collected by any suitable mechanism, including chemical synthesis in vitro, enzymatic synthesis in vitro, and/or biosynthesis in a cell or organism. Chemically and/or enzymatically synthesized libraries may include libraries of compounds, such as synthetic oligonucleotides (DNA, RNA, peptide nucleic acids, and/or mixtures or modified derivatives thereof), small molecules (about 100 Da to 10 KDa), peptides, carbohydrates, lipids, and/or so on. Such chemically and/or enzymatically synthesized libraries may be formed by directed synthesis of individual library members, combinatorial synthesis of sets of library members, and/or random synthetic approaches. Library members produced by biosynthesis may include libraries of plasmids, complementary DNAs, genomic DNAs, RNAs, viruses, phages, cells, proteins, peptides, carbohydrates, lipids, extracellular matrices, cell lysates, cell mixtures, and/or materials secreted from cells, among others. Library members may be contact arrays of cell populations singly or as groups/pools of two or more members.

VIII. Methods of Identifying Transcriptional Regulators

Another aspect of the invention provides methods of identifying transcriptional regulators. In some aspects, the invention provides methods of identifying transcriptional regulators which display differential activity between two cells.

The invention provides a method of identifying a transcriptional regulator having differential activity between an experimental cell and a control cell, the method comprising (i) determining the level of gene expression of at least two genes in the experimental cell and in the control cell; (ii) ranking genes according to a difference metric of their expression level in the experimental cell compared to the control cell; (iii) identifying a subset of genes, wherein each gene in the subset contains the same DNA sequence motif; (iv) testing via a nonparametric statistic if the subset of genes are enriched at either the top or the bottom of the ranking; (v) optionally reiterating steps (ii)-(iii) for additional motifs;

(vi) for a subset of genes that is enriched, identifying a transcriptional regulator which binds to a DNA sequence motif that is contained in the subset of genes; thereby identifying a transcriptional regulator having differential activity between two cells.

The methods provided by the invention for identifying transcriptional regulators with differential activity are not limited to any type of cell or to any type of difference between the two cell. The cells may be eukaryotic, prokaryotic, yeast, nematode, insect, mammalian or human cells. The cells may be primary cells, or cell lines. The cells may be in an organism. In one specific embodiment, the cells are isolated from a subject.

The control and the experimental cell may be the same type of cell or they may be different types of cells. In one embodiment, the experimental cell and the control cell are both cells derived from the same cell line or from the same tissue types. In some embodiments, the experimental cell and the control cell are from different organisms, such as from two different subjects. In some specific embodiments in which the cells are derived from the same organism, one cell is a normal cell and another cell is a diseased cell. For instance, one cell may be a cancer cell and one may be a non-cancer cell, or one cell may be a virus infected cell and one may be a non-infected cell. In some embodiments, both cells may be diseased cells, but differ in their disease states. For instance, the two cells may be hyperplastic cells but at different stages of cancer progression e.g. one cell may be a tumor cell and the other a metastatic cell derived from that tumor. Furthermore, the two cells may differ genetically or they may be clonal cells with essentially identical genotypes. One or both of the cells may be experimentally manipulated, such as by contacting one of the cells with an agent, or contacting both cells with an agent but at different concentrations.

In some embodiments of the method, the subject from which one or both of the cells are derived in is afflicted with a disorder. The method is not limited by any particular disorder. In some specific embodiments, the disorder is a metabolic disorder or a hyperplastic condition. Hyperplastic conditions include renal cell cancer, Kaposi's sarcoma, chronic leukemia, prostate cancer, breast cancer, sarcoma, pancreatic cancer, leukemia, ovarian carcinoma, rectal cancer, throat cancer, melanoma, colon cancer, bladder cancer, lymphoma, mastocytoma, lung cancer, mammary adenocarcinoma, pharyngeal squamous cell carcinoma, testicular cancer, gastrointestinal cancer, or stomach cancer, or a combination thereof. Additional disorders to which this method may be applied may be

found, for example, in Braunwald, E. et al. eds. Harrison's Principles of Internal Medicine, 15th Edition (McGraw-Hill Book Company, New York, 2001).

In some embodiments, a transgene is introduced into the experimental cell. The transgene may encode any protein, such as transcriptional regulators or proteins that regulate the activity of transcriptional regulators, such as kinase and phosphatases. The transgene may also encode an inhibitory RNA, such as a hairpin RNA, so that the function of the gene to which the hairpin RNA is directed may be knocked down, allowing a comparison of gene expression in between the two cells. In some embodiments, the transgenes is a transgene associated with a disease state. For example, a gene whose overexpressing leads to cancer may be overexpressed to identify transcriptional regulators expressing differential activity between the two cells. These transcriptional regulators may then be used as therapeutic targets for the treatment of cancer. In some embodiments, the transgene is a mutant transgene, such as a mutant transgene associated with a disease state.

In some embodiments, the DNA sequence motif comprises at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 nucleotides in length, preferably at least 5. The DNA sequence motif may be any combination of nucleotides, and it may represent a known binding site or a novel binding site. In some embodiments, the DNA sequence motif comprises undefined nucleotide positions which may contain more than one base. For instance, a DNA sequence motif may comprise the sequence GATNNATC, wherein the 3rd and 4th positions would include any of the four bases. Similarly, a DNA sequence motif comprising the sequence GAT(G/T)ATC would have a G or a T in the fourth position. In some embodiments, DNA sequence motif comprises at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 defined positions.

The method can be applied to any number of motifs. In one embodiment, all permutations of DNA sequence motifs of at least 6, 7, 8 and 9 bases in length are tested. The number selected may depend on the number of genes in the subset, the computational capabilities available, and the size of the window in each gene in which the DNA sequence motif is search.

The method is not limited to any particular method of measuring gene expression. In some embodiments, determining the level of expression of a gene in a cell comprises

determining the levels of mRNA for the gene in the cell. Any method known in the art may be used to determine mRNA levels. In one embodiment, mRNA is isolated from the cell, and the levels of mRNA for each gene in the subset is determined by hybridizing the mRNA, or cDNA derived from the mRNA, to a DNA microarray.

In some embodiments of the methods described herein, identifying the transcriptional regulator which binds to a DNA sequence motif comprises searching a database comprising transcriptional regulators and DNA sequence motifs to which they bind. For example, the TRANSFAC transcription factor database, maintained at the GBF Braunschweig, Germany, defines sequence specific binding site patterns, or motifs, for transcription factors. In another embodiment, the transcriptional regulator is identified by comparing the sequences identified to those found in the literature. It is understood by one skilled in the art that more than one transcriptional regulator may bind to a given DNA sequence motif, and therefore multiple transcriptional regulators may be identified.

In some embodiments of the method described herein, identifying a transcriptional regulator which binds to a DNA sequence motif comprises experimentally identifying a transcriptional regulator which binds to the DNA sequence motif. In one embodiment, this is achieved by These may be achieved by (i) identifying, from a library of genes, a transcriptional regulator capable of driving the expression of a selectable marker, wherein the expression of the selectable marker is dependent on binding of the transcriptional regulator to the DNA sequence motif. In a specific embodiment, a reporter gene is introduced into a cell, such as a mammalian cell or a yeast cell, wherein the promoter of the reporter gene is operably linked to the DNA sequence motif. A plasmid library which comprises candidate transcriptional regulator genes is introduced into the cells such that the transcriptional regulators are expressed in the cell. If a transcriptional regulator is able to bind to the DNA sequence motif, it will increase or decrease expression of the reporter gene, allowing identification of the cell expressing said regulator and thus allowing its identification. In a specific embodiment, a yeast one-hybrid approach, or other approaches well known to one skilled in the art, is used to identify a transcriptional regulator which binds to the DNA sequence motif (Vidal M et al. Nucleic Acids Res. 1999;27(4):919-29, Kadonaga et al., (1986) Proc. Natl Acad. Sci. USA, 83, 5889-5893.. Singh et el.. (1988) Cell, 52, 415-423; Chong, J.A. et al.(1997) In Bartel, P.L. and Fields, S. (eds), The Yeast Two-Hybrid System. Oxford University Press, New York, NY, pp. 289-297). Transcriptional regulators may also

be identified based on its binding affinity for the DNA sequence motif, such by standard affinity chromatography.

In some embodiments, the non-parametric statistic is a nonparametric, rank sum statistic. In specific embodiments, the non-parametric statistic is selected from the group consisting of a Kolmogorov-Smirnov, Mann-Whitney or Wald-Wolfowitz. Non-parametric statistics are well-known in the art (David J. Sheskin,, Handbook of Parametric and Nonparametric Statistical Procedures, CRC Press, 2003; Myles Hollander, Douglas A. Wolfe, Nonparametric Statistical Methods, Wiley, John & Sons, Inc., 1998; Larry Wasserman , All of Statistics, Springer-Verlag New York, Incorporated, 2003). In some embodiments, the difference metric is a difference in arithmetic means, t-test scores, or signal to noise ratios. In some embodiments, a gene set is said to be enriched if the probability that the gene set would be enriched by chance, or when compared to an appropriate null hypothesis, is less than 0.05, 0.04, 0,03, 0.02, 0.01, 0.005, 0.0001, 0.00005 or 0.00001.

In some embodiments where the experimental cell expresses a recombinant transgene, such as a recombinant transcriptional regulator, the recombinant transcriptional regulator may itself be found to have differential activity. In other embodiments where the experimental cell expresses a recombinant transgene, the method may yield transcriptional regulators whose activity or expression is itself regulated by the recombinant transcriptional regulator, and if a recombinant transcriptional regulator is used whose activity is related to a disease state is used, identification of transcriptional regulators having differential activity between the two cells may yield therapeutic targets to treat the disorder.

IX. Biomarker Set Enrichment Analysis (BSEA)

One aspect of the invention provides methods of detecting statistically-significant differences in the expression level of at least one biomarker belonging to a biomarker set, between the members of a first and of a second experimental group. Applicants have named this new analytical technique Biomarker Set Enrichment Analysis (BSEA), or Gene Set Enrichment Analysis (GSEA) when the biomarker is a gene or a gene product.

GSEA may be valuable in efforts to relate genomic variation to disease and measures of total body physiology. Single-gene methods are powerful only where the individual gene effect is dramatic and the variance small, which may not be the case in many disease states.

Methods like GSEA are complementary, and provide a framework with which to examine changes operating at a higher level of biological organization. This may be needed if common, complex disorders typically result from modest variation in the expression or activity of multiple members of a pathway e.g. gene (biomarker) sets. As gene sets are systematically assembled using functional and genomic approaches, methods such as GSEA will likely be valuable in detecting coordinated but subtle variation in gene function that contribute to common human diseases. Accordingly, in a preferred embodiment, the methods detect statistically-significant differences in the expression level in more than one biomarker.

One aspect of the invention provides a method of detecting statistically-significant differences in the expression level of at least one biomarker belonging to a biomarker set, between the members of a first and of a second experimental group, comprising: (a) obtaining a biomarker sample from members of the first and the second experimental groups; (b) determining, for each biomarker sample, the expression levels of at least one biomarker belonging to the biomarker set and of at least one biomarker not belonging to the set; (c) generating a rank order of each biomarker according to a difference metric of its expression level in the first experimental group compared to the second experimental group; (d) calculating an experimental enrichment score for the biomarker set by applying a non parametric statistic; and (e) comparing the experimental enrichment score with a distribution of randomized enrichment scores to calculate the fraction of randomized enrichment scores greater than the experimental enrichment score, wherein a low fraction indicates a statistically-significant difference in the expression level of the biomarker set between the members of the first and of the second experimental group.

In one embodiment of the foregoing methods, the distribution of randomized enrichment scores is generated by randomly permutating the assignment of each biomarker sample to the first or to the second experimental group; (ii) generating a rank order of each biomarker according to the absolute value of a difference metric of its expression level in the first experimental group compared to the second experimental group; (iii) calculating an experimental enrichment score for the biomarker set by applying a non parametric statistic to the rank order; and (iv) repeating steps (i), (ii) and (iii) a number of times sufficient to generate the distribution of randomized enrichment scores. In a specific embodiment, the number of times sufficient to generate a distribution is at least 20, 30, 40, 50, 60, 70, 80, 90,

100, 150, 200 or 500 times. In another specific embodiment, the low fraction is less than 0.05, while in other embodiments it is less than 0.04, 0.03, 0.02, 0.01, 0.005 or 0.001.

In one embodiment of the foregoing methods, the distribution of randomized enrichment scores is a normal distribution. The difference metric may be any difference metric, such as a difference in arithmetic means, a difference in t-test scores, or a difference in signal-to-noise ratio. Similarly, the non-parametric statistic may be any non-parametric statistic, such Mann-Whitney, Wald-Wolfowitz or more preferably Kolmogorov-Smirnov.

The biomarker set typically comprises elements of a pathway, such as a metabolic pathway, a biochemical pathway, a signaling pathway, or any set of genes which share a common biological function or which are coordinately regulated. In a preferred embodiment, the biomarker is selected from the group consisting of a nucleic acid, a polypeptide, a metabolite and a genotype. For example, when the biomarker set comprises genes encoding enzymes of a metabolic pathway, such as glycolytic enzymes, the biomarkers may comprise the genotype of the glycolytic genes. In the embodiment where the biomarker is a genotype, the genotype of all or a subset of the glycolytic genes may be determined by DNA sequencing, and the expression level of the genotype would correspond to the amount of polymorphic DNA *i.e.* 0, 1 or 2 copies of a wild-type copy of the gene for a diploid cell or organism. Alternatively, the number of mutant copies, or of a specific mutation, can be used in determining the expression level of the genotype.

In other embodiments where the biomarker is the mRNA of each of, or of a subset of, the glycolytic enzymes, the expression level of the mRNA may be determined, or the expression level of a particular splice isoform, using methods well known in the art, such as by northern blots or microarray analysis. In other embodiments where the biomarker is the protein of each of, or of a subset of, the glycolytic enzymes, the level of expression may comprise total protein levels or levels of a particular modified form of the protein, such as the level of phosphorylated or glycosylated protein, both of which may be determined using immunological techniques. Finally, when the biomarker is a metabolite, such as the product whose formation is catalyzed by the glycolytic enzyme, the expression level of the metabolite is its concentration in the biomarker sample, such as its cellular concentration. Metabolite levels may be determined using chromatographic means or other means well known in the

art. The reference to the glycolitic pathway in the examples above is meant to be illustrative and non-limiting, or the same principles may apply to any other pathway or biomarker set.

In one embodiment, experimental groups comprise organisms, such as mammals, or more preferably humans. In such embodiments, the sample from the biomarker sample comprises a sample of cells from the organism, or a sample of bodily fluid, such as serum, saliva, tears, sweat or semen. The difference between the first and second experimental groups may be a disease state. For example, the first experimental group may be afflicted with a disease or disorder, while the second group is not. In a specific embodiment, the disorder is characterized by defective glucose metabolism, such as type II diabetes. In another embodiment where the experimental groups comprise organisms, the first and second experimental groups may differ by any measurable characteristic. For example, the groups may differ by a physical characteristic, such as weight, age, sex, sexual preference, eyesight, percent body fat, percent lean muscle mass, height, right vs. left handedness or race. The groups may also differ by a psychological characteristic, such as intelligence, verbal skills, emotional intelligence and even personality types, such those determined by the Myers-Briggs Type Indicator. The groups may also differ by emotional state, such as relaxed vs. emotionally stressed subjects, or cheerful vs. gloomy subjects. The subjects may also differ by the presence or absence of one or more mutations, such as subjects having mutations in an oncogene. In another embodiment, the two experimental groups differ in that one group has been treated with at least one agent, such as a drug.

In another embodiment, experimental groups comprise cells. The cells may comprise primary cells, cell lines, or come in the form of tissue samples. As described above for organisms, the cells in the two experimental groups may differ by a physical characteristic or differ genetically. In a preferred embodiment, the two experimental groups differ in that the cells in one of the experimental groups have been treated with an agent, such as with a compound or drug. In such embodiments, the methods described herein may be used to detect subtle changes that the agent may have on the biomarker set, such as a biochemical or signaling pathway.

X. Nucleic acid and Polypeptide Agents

In some of embodiments of methods described herein, an agent which reduces the

expression of Errα, Gabpa, Gabpb, or any other gene, or an genet used in any of the methods of screening agents described herein, comprises a double stranded RNAi molecule, a ribozyme, or an antisense nucleic acid directed at said gene.

Certain embodiments of the invention make use of materials and methods for effecting knockdown of one form of a gene, by means of RNA interference (RNAi). RNAi is a process of sequence-specific post-transcriptional gene repression which can occur in eukaryotic cells. In general, this process involves degradation of an mRNA of a particular sequence induced by double-stranded RNA (dsRNA) that is homologous to that sequence. For example, the expression of a long dsRNA corresponding to the sequence of a particular single-stranded mRNA (ss mRNA) will labilize that message, thereby "interfering" with expression of the corresponding gene. Accordingly, any selected gene may be repressed by introducing a dsRNA which corresponds to all or a substantial part of the mRNA for that gene. It appears that when a long dsRNA is expressed, it is initially processed by a ribonuclease III into shorter dsRNA oligonucleotides of in some instances as few as 21 to 22 base pairs in length. Furthermore, RNAi may be effected by introduction or expression of relatively short homologous dsRNAs. Indeed the use of relatively short homologous dsRNAs may have certain advantages as discussed below.

Mammalian cells have at least two pathways that are affected by double-stranded RNA (dsRNA). In the RNAi (sequence-specific) pathway, the initiating dsRNA is first broken into short interfering (si) RNAs, as described above. The siRNAs have sense and antisense strands of about 21 nucleotides that form approximately 19 nucleotide si RNAs with overhangs of two nucleotides at each 3' end. Short interfering RNAs are thought to provide the sequence information that allows a specific messenger RNA to be targeted for degradation. In contrast, the nonspecific pathway is triggered by dsRNA of any sequence, as long as it is at least about 30 base pairs in length. The nonspecific effects occur because dsRNA activates two enzymes: PKR, which in its active form phosphorylates the translation initiation factor eIF2 to shut down all protein synthesis, and 2', 5' oligoadenylate synthetase (2', 5'-AS), which synthesizes a molecule that activates RNAse L, a nonspecific enzyme that targets all mRNAs. The nonspecific pathway may represents a host response to stress or viral infection, and, in general, the effects of the nonspecific pathway are preferably minimized under preferred methods of the present invention. Significantly, longer dsRNAs appear to be required to induce the nonspecific pathway and, accordingly, dsRNAs shorter than about 30

bases pairs are preferred to effect gene repression by RNAi (see Hunter et al. (1975) J Biol Chem 250: 409-17; Manche et al. (1992) Mol Cell Biol 12: 5239-48; Minks et al. (1979) J Biol Chem 254: 10180-3; and Elbashir et al. (2001) Nature 411: 494-8).

RNAi has been shown to be effective in reducing or eliminating the expression of a gene in a number of different organisms including Caenorhabditis elegans (see e.g. Fire et al. (1998) Nature 391: 806-11), mouse eggs and embryos (Wianny et al. (2000) Nature Cell Biol 2: 70-5; Svoboda et al. (2000) Development 127: 4147-56), and cultured RAT-1 fibroblasts (Bahramina et al. (1999) Mol Cell Biol 19: 274-83), and appears to be an anciently evolved pathway available in eukaryotic plants and animals (Sharp (2001) Genes Dev. 15: 485-90). RNAi has proven to be an effective means of decreasing gene expression in a variety of cell types including HeLa cells, NIH/3T3 cells, COS cells, 293 cells and BHK-21 cells, and typically decreases expression of a gene to lower levels than that achieved using antisense techniques and, indeed, frequently eliminates expression entirely (see Bass (2001) Nature 411: 428-9). In mammalian cells, siRNAs are effective at concentrations that are several orders of magnitude below the concentrations typically used in antisense experiments (Elbashir et al. (2001) Nature 411: 494-8).

The double stranded oligonucleotides used to effect RNAi are preferably less than 30 base pairs in length and, more preferably, comprise about 25, 24, 23, 22, 21, 20, 19, 18 or 17 base pairs of ribonucleic acid. Optionally the dsRNA oligonucleotides of the invention may include 3' overhang ends. Exemplary 2-nucleotide 3' overhangs may be composed of ribonucleotide residues of any type and may even be composed of 2'-deoxythymidine resides, which lowers the cost of RNA synthesis and may enhance nuclease resistance of siRNAs in the cell culture medium and within transfected cells (see Elbashi et al. (2001) Nature 411: 494-8). Longer dsRNAs of 50, 75, 100 or even 500 base pairs or more may also be utilized in certain embodiments of the invention. Exemplary concentrations of dsRNAs for effecting RNAi are about 0.05 nM, 0.1 nM, 0.5 nM, 1.0 nM, 1.5 nM, 25 nM or 100 nM, although other concentrations may be utilized depending upon the nature of the cells treated, the gene target and other factors readily discernable to the skilled artisan. Exemplary dsRNAs may be synthesized chemically or produced in vitro or in vivo using appropriate expression vectors. Exemplary synthetic RNAs include 21 nucleotide RNAs chemically synthesized using methods known in the art (e.g. Expedite RNA phophoramidites and thymidine phosphoramidite (Proligo, Germany). Synthetic oligonucleotides are preferably

deprotected and gel-purified using methods known in the art (see e.g. Elbashir et al. (2001) Genes Dev. 15: 188-200). Longer RNAs may be transcribed from promoters, such as T7 RNA polymerase promoters, known in the art. A single RNA target, placed in both possible orientations downstream of an in vitro promoter, will transcribe both strands of the target to create a dsRNA oligonucleotide of the desired target sequence. For example, if Errα is the target of the double stranded RNA, any of the above RNA species will be designed to include a portion of nucleic acid sequence of the Errα gene.

The specific sequence utilized in design of the oligonucleotides may be any contiguous sequence of nucleotides contained within the expressed gene message of the target. Programs and algorithms, known in the art, may be used to select appropriate target sequences. In addition, optimal sequences may be selected utilizing programs designed to predict the secondary structure of a specified single stranded nucleic acid sequence and allowing selection of those sequences likely to occur in exposed single stranded regions of a folded mRNA. Methods and compositions for designing appropriate oligonucleotides may be found, for example, in U.S. Patent Nos. 6,251,588, the contents of which are incorporated herein by reference. Messenger RNA (mRNA) is generally thought of as a linear molecule which contains the information for directing protein synthesis within the sequence of ribonucleotides, however studies have revealed a number of secondary and tertiary structures that exist in most mRNAs. Secondary structure elements in RNA are formed largely by Watson-Crick type interactions between different regions of the same RNA molecule. Important secondary structural elements include intramolecular double stranded regions, hairpin loops, bulges in duplex RNA and internal loops. Tertiary structural elements are formed when secondary structural elements come in contact with each other or with single stranded regions to produce a more complex three dimensional structure. A number of researchers have measured the binding energies of a large number of RNA duplex structures and have derived a set of rules which can be used to predict the secondary structure of RNA (see e.g. Jaeger et al. (1989) Proc. Natl. Acad. Sci. USA 86:7706 (1989); and Turner et al. (1988) Annu. Rev. Biophys. Biophys. Chem. 17:167). The rules are useful in identification of RNA structural elements and, in particular, for identifying single stranded RNA regions which may represent preferred segments of the mRNA to target for silencing RNAi, ribozyme or antisense technologies. Accordingly, preferred segments of the mRNA target can be identified for design of the RNAi mediating dsRNA oligonucleotides as well as for design of appropriate ribozyme and hammerhead ribozyme compositions of the invention.

The dsRNA oligonucleotides may be introduced into the cell by transfection with an heterologous target gene using carrier compositions such as liposomes, which are known in the art- e.g. Lipofectamine 2000 (Life Technologies) as described by the manufacturer for adherent cell lines. Transfection of dsRNA oligonucleotides for targeting endogenous genes may be carried out using Oligofectamine (Life Technologies). Transfection efficiency may be checked using fluorescence microscopy for mammalian cell lines after co-transfection of hGFP-encoding pAD3 (Kehlenback et al. (1998) J Cell Biol 141: 863-74). The effectiveness of the RNAi may be assessed by any of a number of assays following introduction of the dsRNAs. Further compositions, methods and applications of RNAi technology are provided in U.S. Patent Nos. 6,278,039, 5,723,750 and 5,244,805, which are incorporated herein by reference.

Ribozyme molecules designed to catalytically cleave Errα or Gabpa mRNA transcripts can also be used to prevent translation of Errα or Gabpa (see, e.g., PCT International Publication WO90/11364, published October 4, 1990; Sarver et al. (1990) Science 247:1222-1225 and U.S. Patent No. 5,093,246). Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. (For a review, see Rossi (1994) Current Biology 4: 469-471). The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme molecule to complementary target RNA, followed by an endonucleolytic cleavage event. The composition of ribozyme molecules preferably includes one or more sequences complementary to the gene whose activity is to be reduced.

While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy target mRNAs, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. Preferably, the target mRNA has the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Haseloff and Gerlach (1988) Nature 334:585-591; and see PCT Appln. No. WO89/05852, the contents of which are incorporated herein by reference). Hammerhead ribozyme sequences can be embedded in a stable RNA such as a transfer RNA (tRNA) to increase cleavage efficiency in vivo (Perriman et al. (1995) Proc. Natl. Acad. Sci. USA, 92: 6175-79; de Feyter, and Gaudron, Methods in Molecular Biology, Vol. 74, Chapter 43, "Expressing Ribozymes in Plants", Edited by Turner, P. C, Humana Press Inc., Totowa, N.J). In particular, RNA polymerase III-mediated expression of tRNA

fusion ribozymes are well known in the art (see Kawasaki et al. (1998) Nature 393: 284-9; Kuwabara et al. (1998) Nature Biotechnol. 16: 961-5; and Kuwabara et al. (1998) Mol. Cell 2: 617-27; Koseki et al. (1999) J Virol 73: 1868-77; Kuwabara et al. (1999) Proc Natl Acad Sci USA 96: 1886-91; Tanabe et al. (2000) Nature 406: 473-4). There are typically a number of potential hammerhead ribozyme cleavage sites within a given target cDNA sequence. Preferably the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the target mRNA- to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts. Furthermore, the use of any cleavage recognition site located in the target sequence encoding different portions of the C-terminal amino acid domains of, for example, long and short forms of target would allow the selective targeting of one or the other form of the target, and thus, have a selective effect on one form of the target gene product.

In addition, ribozymes possess highly specific endoribonuclease activity, which autocatalytically cleaves the target sense mRNA. The present invention extends to ribozymes which hybridize to a sense mRNA encoding a Errα or Gabpa or any other genes of interest described herein, thereby hybridizing to the sense mRNA and cleaving it, such that it is no longer capable of being translated to synthesize a functional polypeptide product.

The ribozymes of the present invention also include RNA endoribonucleases (hereinafter "Cech-type ribozymes") such as the one which occurs naturally in Tetrahymena thermophila (known as the IVS, or L-19 IVS RNA) and which has been extensively described by Thomas Cech and collaborators (Zaug, et al. (1984) Science 224:574-578; Zaug, et al. (1986) Science 231:470-475; Zaug, et al. (1986) Nature 324:429-433; published International patent application No. WO88/04300 by University Patents Inc.; Been, et al. (1986) Cell 47:207-216). The Cech-type ribozymes have an eight base pair active site which hybridizes to a target RNA sequence whereafter cleavage of the target RNA takes place. The invention encompasses those Cech-type ribozymes which target eight base-pair active site sequences that are present in a target gene or nucleic acid sequence.

Ribozymes can be composed of modified oligonucleotides (e.g., for improved stability, targeting, etc.) and should be delivered to cells which express the target gene in vivo. A preferred method of delivery involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy endogenous

target messages and inhibit translation. Because ribozymes, unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

In a long target RNA chain, significant numbers of target sites are not accessible to the ribozyme because they are hidden within secondary or tertiary structures (Birikh et al. (1997) Eur J Biochem 245: 1-16). To overcome the problem of target RNA accessibility, computer generated predictions of secondary structure are typically used to identify targets that are most likely to be single-stranded or have an "open" configuration (see Jaeger et al. (1989) Methods Enzymol 183: 281-306). Other approaches utilize a systematic approach to predicting secondary structure which involves assessing a huge number of candidate hybridizing oligonucleotides molecules (see Milner et al. (1997) Nat Biotechnol 15: 537-41; and Patzel and Sczakiel (1998) Nat Biotechnol 16: 64-8). Additionally, U.S. Patent No. 6,251,588, the contents of which are hereby incorporated herein, describes methods for evaluating oligonucleotide probe sequences so as to predict the potential for hybridization to a target nucleic acid sequence. The method of the invention provides for the use of such methods to select preferred segments of a target mRNA sequence that are predicted to be single-stranded and, further, for the opportunistic utilization of the same or substantially identical target mRNA sequence, preferably comprising about 10-20 consecutive nucleotides of the target mRNA, in the design of both the RNAi oligonucleotides and ribozymes of the invention.

In other embodiments of methods described herein, an agent which modulates the activity of Errα, Gabpa, Gabpb, or any other gene, comprises an antibody or fragment thereof. An antibody may increase or decrease the activity of any of the subject polypeptides, and it may increase or decrease the binding of two proteins into a complex, such as an Errα/PCG-1a complex.

Chickens, mammals, such as a mouse, a hamster, a goat, a guinea pig or a rabbit, can be immunized with an immunogenic form of the Errα, Gabpa, Gabpb, or any polypeptide provided by the invention, or with peptide variants thereof (*e.g.*, an antigenic fragment which is capable of eliciting an antibody response). Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. For instance, a peptidyl portion of one of the subject proteins can be administered in the presence of adjuvant. The progress of immunization can be monitored by detection of

antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as antigen to assess the levels of antibodies.

Following immunization, antisera can be obtained and, if desired, polyclonal antibodies against the target protein can be further isolated from the serum. To produce monoclonal antibodies, antibody producing cells (lymphocytes) can be harvested from an immunized animal and fused by standard somatic cell fusion procedures with immortalizing cells such as myeloma cells to yield hybridoma cells. Such techniques are well known in the art, and include, for example, the hybridoma technique (originally developed by Kohler and Milstein, Nature, 256: 495-497, 1975), as well as the human B cell hybridoma technique (Kozbar *et al.*, Immunology Today, 4: 72, 1983), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole *et al.*, Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. pp. 77-96, 1985). Hybridoma cells can be screened immunochemically for production of antibodies specifically reactive to the peptide immunogen and the monoclonal antibodies isolated. Accordingly, another aspect of the invention provides hybridoma cell lines which produce the antibodies described herein. The antibodies can then be tested for their effects on the activity and expression of the protein to which they are directed.

The term antibody as used herein is intended to include fragments which are also specifically reactive with a protein described herein or a complex comprising such protein. Antibodies can be fragmented using conventional techniques and the fragments screened in the same manner as described above for whole antibodies. For example, $F(ab')_2$ fragments can be generated by treating antibody with pepsin. The resulting $F(ab')_2$ fragment can be treated to reduce disulfide bridges to produce Fab' fragments. The antibody of the present invention is further intended to include bispecific and chimeric molecules, as well as single chain (scFv) antibodies.

The subject antibodies include trimeric antibodies and humanized antibodies, which can be prepared as described, *e.g.*, in U.S. Patent No: 5,585,089. Also within the scope of the invention are single chain antibodies. All of these modified forms of antibodies as well as fragments of antibodies are intended to be included in the term "antibody".

In yet another embodiment of the methods described herein, the agent is a polypeptide, such as an Errα polypeptide or a Gabp polypeptide, or a fragment thereof which

retains a biological activity or which antagonizes a biological activity of the wild-type polypeptide. For example, an Errα stimulatory agent comprises an active Errα protein, a nucleic acid molecule encoding Errα that has been introduced into the cell. In another embodiment, the agent is a mutant polypeptide which inhibits Errα protein activity. Examples of such inhibitory agents include a nucleic acid molecule encoding a dominant negative Errα a protein, such a fragment of Errα which may compete with wildtype Errα protein for DNA binding or complex formation with PGC-1α.

XI. Therapeutics

In one aspect, the invention provides methods of treating disorders in a subject comprising the administration of a agent or of a composition comprising an agent, such as a therapeutic agent. "Therapeutic agent" or "therapeutic" refers to an agent capable of having a desired biological effect on a host. Chemotherapeutic and genotoxic agents are examples of therapeutic agents that are generally known to be chemical in origin, as opposed to biological, or cause a therapeutic effect by a particular mechanism of action, respectively. Examples of therapeutic agents of biological origin include growth factors, hormones, and cytokines. A variety of therapeutic agents are known in the art and may be identified by their effects. Certain therapeutic agents are capable of regulating cell proliferation and differentiation. Examples include chemotherapeutic nucleotides, drugs, hormones, non-specific (non-antibody) proteins, oligonucleotides (e.g., antisense oligonucleotides that bind to a target nucleic acid sequence (e.g., mRNA sequence)), peptides, and peptidomimetics.

In one embodiment, the compositions are pharmaceutical compositions. Pharmaceutical compositions for use in accordance with the present invention may be formulated in conventional manner using one or more physiologically acceptable carriers or excipients. Thus, the compounds and their physiologically acceptable salts and solvates may be formulated for administration by, for example, by aerosol, intravenous, oral or topical route. The administration may comprise intralesional, intraperitoneal, subcutaneous, intramuscular or intravenous injection; infusion; liposome-mediated delivery; topical, intrathecal, gingival pocket, per rectum, intrabronchial, nasal, transmucosal, intestinal, oral, ocular or otic delivery.

An exemplary composition of the invention comprises an compound capable of modulating the expression or activity of a transcriptional regulator, such as a PGC-1, Gabp or

Errα polypeptide, with a delivery system, such as a liposome system, and optionally including an acceptable excipient. In a preferred embodiment, the composition is formulated for injection.

Techniques and formulations generally may be found in Remmington's Pharmaceutical Sciences, Meade Publishing Co., Easton, PA. For systemic administration, injection is preferred, including intramuscular, intravenous, intraperitoneal, and subcutaneous. For injection, the compounds of the invention can be formulated in liquid solutions, preferably in physiologically compatible buffers such as Hank's solution or Ringer's solution. In addition, the compounds may be formulated in solid form and redissolved or suspended immediately prior to use. Lyophilized forms are also included.

For oral administration, the pharmaceutical compositions may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (e.g., pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (e.g., lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (e.g., magnesium stearate, talc or silica); disintegrants (e.g., potato starch or sodium starch glycolate); or wetting agents (e.g., sodium lauryl sulphate). The tablets may be coated by methods well known in the art. Liquid preparations for oral administration may take the form of, for example, solutions, syrups or suspensions, or they may be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (e.g., sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (e.g., lecithin or acacia); non-aqueous vehicles (e.g., ationd oil, oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (e.g., methyl or propyl-p-hydroxybenzoates or sorbic acid). The preparations may also contain buffer salts, flavoring, coloring and sweetening agents as appropriate.

Preparations for oral administration may be suitably formulated to give controlled release of the active compound. For buccal administration the compositions may take the form of tablets or lozenges formulated in conventional manner. For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane,

dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampoules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides.

In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration bile salts and fusidic acid derivatives. in addition, detergents may be used to facilitate permeation. Transmucosal administration may be through nasal sprays or using suppositories. For topical administration, the oligomers of the invention are formulated into ointments, salves, gels, or creams as generally known in the art. A wash solution can be used locally to treat an injury or inflammation to accelerate healing.

The compositions may, if desired, be presented in a pack or dispenser device which

may contain one or more unit dosage forms containing the active ingredient. The pack may for example comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

For therapies involving the administration of nucleic acids, the oligomers of the invention can be formulated for a variety of modes of administration, including systemic and topical or localized administration. Techniques and formulations generally may be found in Remmington's Pharmaceutical Sciences, Meade Publishing Co., Easton, PA. For systemic administration, injection is preferred, including intramuscular, intravenous, intraperitoneal, intranodal, and subcutaneous for injection, the oligomers of the invention can be formulated in liquid solutions, preferably in physiologically compatible buffers such as Hank's solution or Ringer's solution. In addition, the oligomers may be formulated in solid form and redissolved or suspended immediately prior to use. Lyophilized forms are also included.

Systemic administration can also be by transmucosal or transdermal means, or the compounds can be administered orally. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration bile salts and fusidic acid derivatives. In addition, detergents may be used to facilitate permeation. Transmucosal administration may be through nasal sprays or using suppositories. For oral administration, the oligomers are formulated into conventional oral administration forms such as capsules, tablets, and tonics. For topical administration, oligomers may be formulated into ointments, salves, gels, or creams as generally known in the art.

Toxicity and therapeutic efficacy of the agents and compositions of the present invention can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD50 (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD50/ED50. Compounds which exhibit large therapeutic induces are preferred. While compounds that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC50 (i.e., the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

In one embodiment of the methods described herein, the effective amount of the agent is between about 1mg and about 50mg per kg body weight of the subject. In one embodiment, the effective amount of the agent is between about 2mg and about 40mg per kg body weight of the subject. In one embodiment, the effective amount of the agent is between about 3mg and about 30mg per kg body weight of the subject. In one embodiment, the effective amount of the agent is between about 4mg and about 20mg per kg body weight of the subject. In one embodiment, the effective amount of the agent is between about 5mg and about 10mg per kg body weight of the subject.

In one embodiment of the methods described herein, the agent is administered at least once per day. In one embodiment, the agent is administered daily. In one embodiment, the agent is administered every other day. In one embodiment, the agent is administered every 6 to 8 days. In one embodiment, the agent is administered weekly.

As for the amount of the compound and/or agent for administration to the subject, one skilled in the art would know how to determine the appropriate amount. As used herein, a dose or amount would be one in sufficient quantities to either inhibit the disorder, treat the disorder, treat the subject or prevent the subject from becoming afflicted with the disorder. This amount may be considered an effective amount. A person of ordinary skill in the art can perform simple titration experiments to determine what amount is required to treat the

subject. The dose of the composition of the invention will vary depending on the subject and upon the particular route of administration used. In one embodiment, the dosage can range from about 0.1 to about 100,000 ug/kg body weight of the subject. Based upon the composition, the dose can be delivered continuously, such as by continuous pump, or at periodic intervals. For example, on one or more separate occasions. Desired time intervals of multiple doses of a particular composition can be determined without undue experimentation by one skilled in the art.

The effective amount may be based upon, among other things, the size of the compound, the biodegradability of the compound, the bioactivity of the compound and the bioavailability of the compound. If the compound does not degrade quickly, is bioavailable and highly active, a smaller amount will be required to be effective. The effective amount will be known to one of skill in the art; it will also be dependent upon the form of the compound, the size of the compound and the bioactivity of the compound. One of skill in the art could routinely perform empirical activity tests for a compound to determine the bioactivity in bioassays and thus determine the effective amount. In one embodiment of the above methods, the effective amount of the compound comprises from about 1.0 ng/kg to about 100 mg/kg body weight of the subject. In another embodiment of the above methods, the effective amount of the compound comprises from about 100 ng/kg to about 50 mg/kg body weight of the subject. In another embodiment of the above methods, the effective amount of the compound comprises from about 1 ug/kg to about 10 mg/kg body weight of the subject. In another embodiment of the above methods, the effective amount of the compound comprises from about 100 ug/kg to about 1 mg/kg body weight of the subject.

As for when the compound, compositions and/or agent is to be administered, one skilled in the art can determine when to administer such compound and/or agent. The administration may be constant for a certain period of time or periodic and at specific intervals. The compound may be delivered hourly, daily, weekly, monthly, yearly (e.g. in a time release form) or as a one time delivery. The delivery may be continuous delivery for a period of time, e.g. intravenous delivery. In one embodiment of the methods described herein, the agent is administered at least once per day. In one embodiment of the methods described herein, the agent is administered daily. In one embodiment of the methods described herein, the agent is administered every other day. In one embodiment of the methods described

herein, the agent is administered every 6 to 8 days. In one embodiment of the methods described herein, the agent is administered weekly.

EXEMPLIFICATION

The invention now being generally described, it will be more readily understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention, and are not intended to limit the invention, as one skilled in the art would recognize from the teachings hereinabove and the following examples, that other DNA microarrays, cell types, agents, constructs, or data analysis methods, all without limitation, can be employed, without departing from the scope of the invention as claimed.

The contents of any patents, patent applications, patent publications, or scientific articles referenced anywhere in this application are herein incorporated in their entirety.

The practice of the present invention will employ, where appropriate and unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, virology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are described in the literature. See, for example, Molecular Cloning: A Laboratory Manual, 3rd Ed., ed. by Sambrook and Russell (Cold Spring Harbor Laboratory Press: 2001); the treatise, Methods In Enzymology (Academic Press, Inc., N.Y.); Using Antibodies, Second Edition by Harlow and Lane, Cold Spring Harbor Press, New York, 1999; Current Protocols in Cell Biology, ed. by Bonifacino, Dasso, Lippincott-Schwartz, Harford, and Yamada, John Wiley and Sons, Inc., New York, 1999; and PCR Protocols, ed. by Bartlett et al., Humana Press, 2003.

The tables for all the Experimental genes are listed at the end of the third experimental series.

First Experimental Series

Described herein are results of RNA expression profiling of 43 individuals with varying levels of insulin resistance, carried out to systematically identify pathways and processes operative in diabetes. The 43 individuals were: 17 with normal glucose tolerance

(NGT), 8 with impaired glucose tolerance (IGT), and 18 with type 2 diabetes (DM2). No single gene showed statistically significant expression differences between the diagnostic classes. Therefore, they developed a new analytical technique, called Gene Set Enrichment Analysis (GSEA), that seeks to determine whether members of gene sets (*e.g.*, pathways) are consistently different, even though modestly or slightly, in one diagnostic class versus another. Application of GSEA to the microarray data, demonstrated that the oxidative phosphorylation pathway (OXPHOS) was significantly different. Of the approximately 106 members in this pathway, 94 are diminished in DM2 versus NGT. The effect is subtle – with each gene only showing a 15-20% decrease.

Also described herein are results of work carried out to define mechanisms underlying this coordinated decrease in expression of OXPHOS genes. Analysis of the expression of these OXPHOS genes in a public atlas of mouse gene expression, showed that 2/3 of all OXPHOS genes are tightly co-regulated across all 47 tissues examined, and that they are highly expressed at the major sites of insulin mediated glucose uptake (brown fat, heart, and skeletal muscle). This group of genes is referred to herein as "OXPHOS-CR," for "<u>OXPHOS</u> <u>C</u>o-<u>R</u>egulated." Applicants hypothesized that the transcriptional co-activator PPARGC1 (also known as PGC-1α was responsible for this transcriptional co-regulation. To prove this, Applicants infected mouse muscle cell lines with PPARGC1 and demonstrated that the OXPHOS-CR genes are specifically induced in a time-dependent manner over a three day period. As described in detail below, GSEA was re-applied to the diabetes data, this time testing whether OXPHOS-CR is specifically differentially expressed between the patient classes. Results showed that this accounts for the bulk of the signal detected in the comparison between NGT and DM2, and moreover, appears to be very different between NGT and IGT, as well, suggesting derangements in this group of genes is an early event. Previous studies have suggested that total body aerobic capacity (VO_2max) is predictive of future insulin resistance and diabetes. Interestingly, Applicants found a striking relationship between the mean expression of the OXPHOS-CR genes and total body oxygen consumption.

The following experimental procedures were followed in the first experimental series:

Methods

Human Subjects and Clinical Measurements. Applicants selected 54 men of similar age but with varying degree of glucose tolerance who had been participating in The Malmö

Prevention Study in southern Sweden for more than 12 years (Eriksson et al. Diabetologia 33, 526-31. (1990)). The investigation was approved by the Ethics Committée at Lund University, and informed consent was obtained from each of the volunteers. All subjects were Northern Europeans, and their glucose tolerance status was assessed using standardized 75-gram OGTT and by applying WHO85 criteria (Eriksson et al. Diabetologia 33, 526-31. (1990)). At the initial OGTT performed 10 years earlier, none of the men had DM2 (Eriksson et al. Diabetologia 33, 526-31. (1990)). An OGTT performed at the time the biopsy showed that 20 of the subjects had developed manifest type 2 diabetes (DM2), 8 fulfilled the criteria for IGT and 26 had normal glucose tolerance (NGT). As diabetes was diagnosed at the time of the repeat OGTT, none of the subjects were on medication for hyperglycemia or diabetes-related conditions.

Anthropometric and insulin sensitivity measures were performed as previously described (Groop, L. et al. Diabetes 45, 1585-93. (1996)). Height, weight, waist to hip ratio (WHR) and fat free mass were measured on the day of the euglycemic clamp. Maximal oxygen uptake (VO2max) was measured using an incremental work-conducted upright exercise test with a bicycle ergometer (Monark Varberg, Sweden) combined with continuous analysis of expiratory gases and minute ventilation. Exercise was started at a workload varying between 30-100W depending on the previous history of endurance training or exercise habits and then increased by 20-50W every 3 min, until a perceived exhaustion or a respiratory quotient of 1.0 was reached. Maximal aerobic capacity was defined as the VO2 during the last 30s of exercise and is expressed per lean body mass. Insulin sensitivity was determined with a standard 2 hour-euglycemic hyperinsulinemic clamp combined with infusion of tritiated glucose to estimate endogenous glucose production and indirect calorimetry (Deltatrac, Datex Instrumentarium, Finland) to estimate substrate oxidation (Groop, L. et al. Diabetes 45, 1585-93. (1996)). The rate of glucose uptake (also referred to as the M-value) was calculated from the infusion rate of glucose and the residual rate of endogenous glucose production measured by the tritiated glucose tracer during the clamp.

Percutaneous muscle biopsies (20-50mg) were taken from the *vastus lateralis* muscle under local anesthesia (1% lidocaine) after the 2-h euglycemic hyperinsulinemic clamp using a Bergström needle (Eriksson et al. Diabetes 43, 805-8. (1994)). Fiber-type composition and glycogen concentration were determined as previously described (Schalin et al.Eur J Clin

Invest 25, 693-8. (1995)). Quantification and calculation of the fibers was performed using the COMFAS image analysis system (Scan Beam, Hadsun, Denmark).

Cell Culture and Adenoviral Infection. Mouse myoblasts (C2C12 cells) were cultured and differentiated into myotubes as previously described (Wu, Z. et al. Cell 98, 115-24. (1999)). After 3 days of differentiation, they were infected with an adenovirus containing either green fluorescent protein (*GFP*) or *PGC*-1α as previously described (Lin, J. et al. Nature 418, 797-801. (2002)).

mRNA Isolation, Target Preparation, and Hybridization. Targets were prepared from human biopsy or mouse cell lines as previously described (Golub, T.R. et al. Science 286, 531-7. (1999)) and hybridized to the Affymetrix HG-U133A or MG-U74Av2 chip, respectively. Only scans with 10% Present calls and a GAPDH 3'/GAPDH 5' expression ratio < 1.33 were selected. Applicants obtained gene expression data for 54 human samples, but only 43 met these selection criteria; the analysis in this paper is limited to these 43 individuals.

Data Scaling and Filtering. Human microarray data were subjected to global scaling to correct for intensity related biases. For each scan applicants binned all genes according to their expression intensity in a designated reference scan, and recorded the median intensity of that bin to serve as a calibration curve for that scan. Applicants then scaled the expression to the calibration curve of one NGT scan (patient mm12) which applicants visually inspected and deemed high quality using a linear interpolation between the calibration points. Applicants then filtered the 22,283 genes on the HG-U133A chip to eliminate genes that had extremely low expression. A previous study suggested that an Affymetrix average difference level of 100 corresponds to an extremely low level ("not expressed") (Su, A.I. et al. Proc Natl Acad Sci U S A 99, 4465-70. (2002)). Therefore, applicants only considered genes for which there was at least a single measure (average difference) greater than 100. Of the 22,283 genes on the HG-U133A chip, 10,983 genes met this filtering criterion.

Single Gene Microarray Analysis. Microarray analysis to identify individual genes that are significantly different between diagnostic classes was performed using two software packages. First, marker analysis was performed as previously described using GeneCluster. Significance of individual genes was testing by permutation of class labels (5000 iterations),

as previously described (Golub, T.R. et al. Science 286, 531-7. (1999)). Applicants used both the t-test and signal to noise difference metrics in these analysis, both yielding comparable results. Second, applicants used the software package SAM, using a Δ=0.5, to search for gene expression values significantly different between classes (Tusher et al. Proc Natl Acad Sci U S A 98, 5116-21. (2001)).

Compilation of Gene Sets. Applicants analyzed 149 gene sets consisting of manually curated pathways and clusters defined by public expression compendia. First, applicants used two different sets of metabolic pathway annotations. Applicants manually curated genes belonging to the following pathways: free fatty acid metabolism, gluconeogenesis, glycolysis, glycogen metabolism, insulin signaling, ketogenesis, pyruvate metabolism, reactive oxygen species (ROS) homeostasis, Kreb's cycle, oxidative phosphorylation (OXPHOS), and mitochondria, using standard textbooks, literature reviews, and LocusLink. Applicants also downloaded NetAFFX (Liu, G. et al et al.Nucleic Acids Res 31, 82-6. (2003)) annotations (October 2002) corresponding to GenMAPP metabolic pathways. To identify sets of co-regulated genes, applicants used self-organizing maps to group the GNF mouse expression atlas into 36 clusters (Su, A.I. et al. Proc Natl Acad Sci U S A 99, 4465-70. (2002), Tamayo et al. Proc Natl Acad Sci U S A 96, 2907-12. (1999). Genes in these 36 groups were converted to Affymetrix HG-U133A probe sets using the ortholog tables available at the NetAFFX website (October 2002).

Rationale for Grouped Gene Analysis. Consider a microarray dataset with the samples in two categories, A, B. For the sake of simplicity, let the size of A and B each be n. Consider a gene set S for which the expression levels differ between samples of A and B. Model the dataset so that the entry D_{ij} for gene i and sample j is normally distributed with mean μ_{ij} and standard deviation σ, where

$$\mu_{ij} = \begin{cases} 0, & i \notin S \\ +\alpha, & i \in S, j \in A \\ -\alpha, & i \in S, j \in B \end{cases} .$$

Then the signal to noise for an individual gene in S is proportionate to

$$\frac{\alpha\sqrt{n}}{\sigma}.$$

Suppose on the other hand applicants know S and add the expression levels for all genes in S. Then the signal to noise is proportionate to

$$\frac{\alpha\sqrt{nM}}{\sigma},$$

where M is the number of genes in S. This increases the mean of our statistic (which is standard normal for the null hypothesis of no gene set association) by a factor of $\sqrt{M}$. If the noise is in fact correlated for genes of S, this reduces the benefit, but applicants can still expect a large gain. In practice applicants will not be able to select a gene set containing fully concordant expression levels, but as long as an appreciable fraction of our gene set exhibits this property, applicants can expect a benefit from the grouped gene approach.

Gene Set Enrichment Analysis (GSEA). GSEA determines if the members of a given gene set are enriched amongst the most differentially expressed genes between two classes. First, the genes are rank ordered on the basis of a difference metric. The results presented in the current experimental series use the signal to noise (SNR) difference metric, which is simply the difference in means of the two classes divided by the sum of the standard deviations of the two diagnostic classes. In general other difference metrics can also be used.

For each gene set, applicants then make an enrichment measure, called the enrichment score (*ES*), which is a normalized Kolmogorov-Smirnov statistic. Consider the genes R_1,.., R_N that are rank ordered on the basis of the difference metric between the two classes, and a gene set S containing G members. Applicants define $X_i = -\sqrt{\frac{G}{N-G}}$ if R_i is not a member of S, $X_i = \sqrt{\frac{N-G}{G}}$, if R_i is a member of S. Applicants then compute a running sum across all N genes. The enrichment score (*ES*) is defined as $\max_{1 \le j \le N} \sum_{i=1}^{j} X_i$, or the maximum observed positive deviation of the running sum. *ES* is measured for every gene set considered. To determine whether *any* of the given gene sets shows association with the class phenotype distinction, applicants permute the class labels 1000 times, each time recording the maximum *ES* over all gene sets. Note that in this regard, applicants are testing a single hypothesis. The null hypothesis is that no gene set is associated with the class distinction.

In this experimental series, after identifying OXPHOS-CR as a subset of co-regulated OXPHOS genes, applicants tested it (a single gene set) for association with clinical status using GSEA. Because OXPHOS-CR is not independent of the OXPHOS set interrogated in the initial analysis, this cannot be viewed as an independent hypothesis. For this reason, these *P*-values are explicitly marked as nominal *P*-values.

Gene set enrichment analysis (GSEA) has been implemented as a software tool for use with microarray data and will be presented in fuller detail, including a discussion of different varieties of multiple hypothesis testing and applications to other biomedical problems, in a companion paper (Subramanian *et. al.*, in preparation).

Evaluating OXPHOS Coregulation in Mouse Expression Datasets. Applicants used the NetAFFX to identify probe sets on the mouse expression chips corresponding to human OXPHOS probe sets. Applicants identified a total of 114 (106 of which passed our filtering criterion) probe-sets corresponding to the human oxidative phosphorylation genes. Using the October 2002 ortholog tables at NetAFFX, applicants were able to identify 61 mouse orthologs on the Affymetrix MG-U74Av2 chip. Of these 61 probe-sets, 52 were represented in the GNF mouse expression atlas (Su, A.I. et al. Proc Natl Acad Sci U S A 99, 4465-70. (2002)). These expression data were normalized to a mean of 0 and a variance of 1. Data were hierarchically clustered and visualized using the Cluster and TreeView software packages (Eisen et al. Proc Natl Acad Sci U S A 95, 14863-8. (1998)).

Applicants parsed these 52 genes into 32 co-regulated probe-sets and 20 probe-sets that are not co-regulated, based on the dendrogram in Figures 7 and 8. 40 distinct HG-HG-U133A probe-sets mapped to the 32 co-regulated mouse probe-sets, and 19 distinct HG-U133A probe-sets mapped to the 20 mouse probe-sets that are not co-regulated. Five HG-U133A probe-sets are shared between these two groups, representing ambiguous cases (*i.e.*, these human probe-sets that map to two mouse probe-sets, one of which is co-regulated and the other of which is not co-regulated). Applicants discarded these five ambiguous human probe-sets from our analysis. This left a total of 35 HG-U133A probe-sets which applicants call OXPHOS-CR genes, and a total of 14 HG-U133A probe-sets which applicants call OXPHOS not CR. Note that 34 and 13 of these genes, respectively, passed our filtering criteria, and these were the genes used in Figure 9 as well as in the OXPHOS-CR analysis described in the paper.

Linear Regression Analysis. Applicants generated linear regression models using SAS (SAS Institute, USA). Clinical variables were used as dependent variables, and OXPHOS-CR gene expression levels or other clinical/biochemical measures used as the independent (explanatory or predictor) variables. To compute the mean centroid of OXPHOS-CR, the 34 genes OXPHOS-CR gene expression levels were normalized to a mean 0 and a variance 1 across all 43 patients. The OXPHOS-CR mean centroid vector is simply the mean of these 34 expression vectors. In some regression analyses, applicants introduced dummy variables to represent diabetes status. For the regressions applicants have performed, applicants have reported the adjusted squared correlation coefficient (R^2_{adj}), which corrects for the degrees of freedom.

Example 1: Comparison of Gene Expression in between Experimental Groups

DNA microarrays were used to profile expression of over 22,000 genes in skeletal muscle biopsies from 43 age-matched males (Table 1): 17 with Normal Glucose Tolerance (NGT), 8 with Impaired Glucose Tolerance (IGT), and 18 with Type 2 Diabetes Mellitus (DM2). Biopsies were obtained at the time of diagnosis (before treatment with hypoglycemic medication) and under the controlled conditions of a hyperinsulinemic euglycemic clamp (see Methods). When assessed with either of two different analytical techniques (Golub, T.R. et al. Science 286, 531-7. (1999), Tusher et al. Proc Natl Acad Sci U S A 98, 5116-21. (2001)) that take into account the multiple comparisons implicit in microarray analysis, no single gene exhibited a significant difference in expression between the diagnostic categories. This result is consistent with smaller studies (Sreekumar et al. Diabetes 51, 1913-20. (2002), Yang et al. Diabetologia 45, 1584-93. (2002)) which failed to identify any individual gene whose expression difference was significant when corrected for the large number of hypotheses tested (Kropf et al. Biometrical J. 44, 789-800 (2002), Storey et al. J. R. Statist. Soc. B 64, 479-498 (2002)).

Example 2: Gene Set Enrichment Analysis

To test for sets of related genes that might be systematically altered in diabetic muscle, Applicants devised a simple approach called Gene Set Enrichment Analysis (GSEA), which is introduced here (see Figure 1 and Methods). The method combines information from the members of previously defined sets of genes (*e.g.*, biological pathways) to increase signal relative to noise (see Methods) and improve statistical power.

For a given pairwise comparison (*e.g.*, high in NGT vs DM2), all genes are ranked based on the difference in expression (using an appropriate metric such as signal to noise). The null hypothesis of GSEA is that the rank ordering of the genes in a given comparison is *random* with regard to the diagnostic categorization of the samples. The alternative hypothesis is the rank ordering of the pathway members is associated with the specific diagnostic criteria used to categorize the patient groups.

The extent of association is then measured by a non-parametric, running sum statistic termed the enrichment score (*ES*), and record the Maximum *ES* (*MES*) over all gene sets in the actual patient data (Figure 1). To assess the statistical significance of the *MES*, applicants

use permutation testing of the patient diagnostic labels (for example, whether a patient is NGT or DM2, see Figure 1). Specifically, applicants compare the *MES* achieved in the actual data to that seen in each of 1,000 permutations that shuffled the diagnostic labels among the samples. The significance of the *MES* score is calculated as the fraction of the 1,000 random permutations in which the top pathway gave a stronger result than that observed in the actual data. Because the permutation test involves randomization of the patient labels, it is a test for the dependence on the actual diagnostic status of the patients. Moreover, because the actual *MES* is compared to the distribution of maximal *ES* values over all pathways examined in each of the randomized datasets, it accounts for multiple pathways tested, and no further correction is required (Kropf et al. Biometrical J. 44, 789-800 (2002), Storey et al. J. R. Statist. Soc. B 64, 479-498 (2002).

Example 3: Decreased Expression of Genes Involved in Oxidative Phosphorylation

Applicants applied GSEA to the microarray data described above, using 149 gene sets that applicants compiled (Table 2). Of these gene sets, 113 are based on involvement in metabolic pathways (based on public or local curation (Liu, G. et al et al.Nucleic Acids Res 31, 82-6. (2003)) and 36 consist of gene clusters that exhibit co-regulation in a mouse expression atlas of 46 tissues (Su, A.I. et al. Proc Natl Acad Sci U S A 99, 4465-70. (2002)) (see Methods). The gene sets were selected without regard to the results of the microarray data from our patients. The top gene set in GSEA analysis yielded a Maximal Enrichment Score (*MES*=346) that was significant at *P*=0.029 over the 1,000 permutations of the 149 pathways. That is, in only 29 or 1,000 permutations did the top pathway (of the 149) exceed the score achieved by the top pathway achieved using the actual diagnostic labels.

The maximal *ES* score was obtained for an internally curated set consisting of genes involved in oxidative phosphorylation (applicants refer to this gene set as OXPHOS). Interestingly, the four gene sets with the next highest *ES* scores overlap with this OXPHOS gene set, and their enrichment is almost entirely explained by the overlap: a locally curated set of genes involved in mitochondrial function, a set of genes identified with the keyword 'mitochondria,' a cluster (referred to here as *c*20) of co-regulated genes derived from the comparison of publicly available mouse data, and a set of genes related to oxidative phosphorylation defined at the Affymetrix website (Liu, G. et al et al.Nucleic Acids Res 31, 82-6. (2003)).

Examination of the individual expression values for the 106 OXPHOS genes reveals the source of this signal (Fig. 2). Although the typical decrease in expression for individual OXPHOS genes is very modest (~20%), the decrease is remarkably consistent across the set: 89% (94 of 106) of the genes showing decreased expression in DM2 relative to NGT (Fig. 2). As controls, applicants confirmed that the result is independent of specific aspects of data processing (such as scaling, thresholding, filtering) or of selection of difference metrics. Moreover, the result identified by GSEA is supported by previous observations: others have shown that oxidative capacities are altered in insulin resistant muscle (Bjorntorp, et al. Diabetologia 3, 346-52. (1967), Simoneau et al. Faseb J 9, 273-8. (1995), and recent microarray analyses of human diabetic muscle have identified genes in oxidative phosphorylation among their top-ranked genes (Sreekumar et al. Diabetes 51, 1913-20. (2002)).

Example 4: OXPHOS-CR: A Coregulated Subset of OXPHOS Genes

One of the overlapping gene sets identified by GSEA is cluster *c*20, defined as a set of genes that are tightly co-regulated across many tissues (see Methods). The partial overlap of OXPHOS with the coregulated cluster led us to ask whether all OXPHOS genes are coordinately regulated, or just a subset. Applicants examined transcriptional co-regulation of mouse homologs of OXPHOS genes across a mouse tissue expression atlas (Su, A.I. et al. Proc Natl Acad Sci U S A 99, 4465-70. (2002)). This revealed a previously unrecognized subset of the OXPHOS biochemical pathway, corresponding to about two-thirds of the OXPHOS genes, that exhibit strong correlation across mouse tissues (r=0.67) (Fig. 3a). Applicants term this subset OXPHOS-CR (OXidative PHOSphorylation Co-Regulated). The remaining OXPHOS genes show little co-regulation with OXHPOS-CR or each other (Fig. 3a). The OXPHOS-CR subset strongly expressed in three of 46 tissues: skeletal muscle, heart, and brown fat. Applicants note that these are the major sites of insulin-mediated glucose disposal in mice.

Applicants next asked whether the downregulation of OXPHOS observed in DM2 was a general property of all OXPHOS genes or was specific to OXPHOS-CR. Interestingly, the bulk of the statistical signal applicants observe in GSEA is accounted for by OXPHOS-CR (Fig. 4). Namely, the OXPHOS-CR subset showed a stronger mean deviation than the remainder of the OXPHOS gene set (Fig. 4), and was itself significant in the GSEA analysis (nominal P-value 0.001, as compared to nominal P=0.226 for the remainder of the OXPHOS

set). To see if these changes were secondary to hyperglycemia *per se*, or preceded the onset of frank diabetes, applicants compared expression of OXPHOS-CR in NGT patients to those with the pre-diabetic state, IGT. Applicants found that expression of OXPHOS-CR is also downregulated in IGT (nominal $P<10^{-4}$). This suggests that downregulation of OXPHOS-CR precedes onset of hyperglycemia. Thus, GSEA allowed us to detect a subset of OXPHOS genes, called OXPHOS-CR, with three key properties: (1) they are members of the oxidative phosphorylation pathway, (2) they are tightly co-regulated across many tissues and are highly expressed in the major sites of insulin mediated glucose disposal, and (3) they exhibit a subtle but consistent decreased expression in muscle from patients with both the pre-diabetic state IGT and type 2 diabetes.

Example 5: PGC-1α can induce expression of OXPHOS-CR

The strong correlation in expression of the OXPHOS-CR genes and their coordinated downregulation in diabetic muscle led us to explore mechanisms that might mediate to this tight control. Applicants reasoned that peroxisome proliferator-activated receptor γ coactivator 1α (PGC-1α), a cold-inducible regulator of mitochondrial biogenesis, thermogenesis, and skeletal muscle fiber type switching (Puigserver, P. et al. Cell 92, 829-39. (1998), Wu, Z. et al. Cell 98, 115-24. (1999), Lin, J. et al. Nature 418, 797-801. (2002)), was a prime candidate for mediating these effects. Consistent with this hypothesis, applicants observed that mean levels of *PGC*-1α transcript were similarly decreased (~20%) in the diabetic muscle, and noted that the promoters of several of the OXPHOS-CR genes have been reported to contain binding sites for nuclear respiratory factor 1, a transcription factor co-activated by PGC-1α (Scarpulla, R.C. Biochim Biophys Acta 1576, 1-14. (2002)).

To test directly whether OXPHOS-CR genes might be transcriptional targets of PGC-1α, applicants expressed PGC-1α in a mouse skeletal muscle cell line using an adenoviral expression vector (Lin, J. et al. Nature 418, 797-801. (2002)) and used DNA microarrays to profile expression of the OXPHOS genes over a 3 day period (see Methods). Applicants found that a subset of OXPHOS genes were strongly upregulated in a time-dependent manner in response to PGC-1α, and that this subset corresponds almost precisely to OXPHOS-CR (Fig. 3b). These *in vitro* results support the hypothesis that PGC-1α plays a role in the regulation of OXPHOS-CR, both across the mouse tissue compendium as well as in the observed downregulation in diabetes.

Example 6: Expression of OXPHOS-CR and Measures of Whole Body Physiology

Metabolic control theory suggests that small increases in many sequential steps of a metabolic pathway can lead to a dramatic change in the total flux through the pathway, whereas large changes in a single enzyme might have no measurable effects (Brown et al. Biochem J 284, 1-13. (1992). To test the hypothesis that subtle differences in OXPHOS-CR gene expression in diabetic patients might be related to changes in total body metabolism, applicants examined the relationships between diabetes status, expression of OXPHOS-CR genes, and VO2max as measured in our patients (Fig. 5). Consistent with previous reports (Eriksson et al. Diabetologia 33, 526-31. (1990)), diabetes and VO2max are correlated in our patients (R_{adj}^2=0.28, P=0.0005). Strikingly, applicants found that the expression of OXPHOS-CR genes in muscle is strongly correlated with VO2max (R_{adj}^2=0.22, P=0.0012) (Fig. 5), a measure of total-body physiology. The top ranking OXPHOS-CR gene, ubiquinol cytochrome *c* reductase binding protein (*UQCRB*), is even a stronger predictor (R_{adj}^2=0.31, P<0.0001). OXPHOS-CR appears to be not solely a proxy for diabetes status, however, because a two-variable regression of VO2max on diabetes status and OXPHOS-CR expression level shows that both variables contribute significantly to the correlation (P=0.05 for the model with both variables as compared to the model with only diabetes status).

It is important to note that these results do not seem secondary to other known predictors of oxidative capacity. Applicants found no relationship between BMI or WHR and OXPHOS-CR gene expression ($R_{adj}^2 < 0.01$ in both cases). In addition, there was no significant relationship between quantitative measures of fiber types and OXPHOS-CR expression. Thus, subtle decrease in expression of OXPHOS-CR genes in muscle appears to be associated with changes in total body aerobic capacity, even beyond their correlation to diabetes status, body habitus, or muscle fiber type.

Second Experimental Series

The following experimental procedures were followed in the second experimental series:

Organelle Purification and Sample Preparation. 6-8 week old male mice were subjected to an 8 hour fast and then euthanized. Brain, heart, kidney, and livers were harvested immediately and placed in ice cold saline. Mitochondria were isolated using differential centrifugation as previously described and purified with a Percoll gradient (Mootha et al. (2003). Proc Natl Acad Sci U S A 100, 605-10). The proteins were then solubilized, size

separated, and digested as previously described (Mootha et al. (2003). Proc Natl Acad Sci U S A 100, 605-10)).

Tandem Mass Spectrometry. Liquid chromatography tandem mass spectrometry (LC-MS/MS) was performed on QSTAR pulsar quadrupole time of flight mass spectrometers (AB/MDS Sciex, Toronto) as described previously (Mootha et al. (2003). Proc Natl Acad Sci U S A 100, 605-10). Tandem mass spectra were searched against the NCBInr database (February 2002) with tryptic constraints and initial mass tolerances <0.13 Da in the search software Mascot (Matrix Sciences, London). Only peptides achieving a Mascot score above 25 and containing a sequence tag of at least three consecutive amino acids were accepted.

Curation of Previously Annotated Mitochondrial Proteins. Two key sources were used to identify previously annotated proteins. First, Applicant downloaded the 308 human and 117 mouse protein sequences at MITOcondria Project (Scharfe et al. (2000). Nucleic Acids Res 28, 155-8). Applicant also downloaded the 199 human and 290 mouse protein sequences annotatated at LocusLink (http://www.ncbi.nlm.nih.gov/LocusLink) as having a mitochondrial subcellular localization based on gene ontology terminology (GO:0005739) (Lewis et al. (2000). Curr Opin Struct Biol 10, 349-54)(January 2003). Also included in the master list the are 13 mtDNA encoded proteins, based on LocusLink annotation.

A Nonredundant List of Mitochondrial Proteins. FASTA sequences corresponding to the previously annotated mitochondrial proteins, newly identified mitochondrial proteins, and the mouse Reference Sequences (Maglott et al. (2000). Nucleic Acids Res 28, 126-8) were merged. These were then collapsed into distinct protein clusters using a downloaded version of blastclust (http://www.ncbi.nlm.nih.gov/BLAST/). Applicants required that members of a cluster demonstrate 70% sequence identity over 50% of the total length, not requiring a reciprocal relationship to exist. Clusters containing multiple Reference Sequences were then broken using a higher stringency blastclust, in which applicants required 90% identity over 50% of the length. Clusters containing hemoglobin, trypsin, and albumin were eliminated as obvious contaminants. When possible the Reference Sequence was selected as the exemplar from the cluster, otherwise another sequence was manually selected. Hence, each cluster is annotated by an exemplar sequence, the protein accessions (and tissues) in which the proteins were found in the proteomics experiments, and the protein accessions corresponding to

annotation sources. Applicant obtained a total of 612 distinct protein clusters (Table 2). The GenPept descriptions of 37 of these exemplars suggested that they are mitochondrial, but simply missed by the automated annotation procedure using the MITOP and LocusLink databases. These exemplars were therefore manually annotated as previously known mitochondrial proteins, to provide a more conservative estimate of our sensitivity measure and newly discovered proteins.

Statistical Analysis. Cluster enrichment was determined using a cumulative hypergeometric distribution. To determine whether two empirical cumulative distributions arise from the same underlying distribution, Applicant used the Kolmogorov-Smirnov test statistic, D. Tail values were obtained using Matlab (Mathworks).

RNA/Protein Concordance Test. the RNA/protein concordance test was developed to determine whether there is significant concordance between protein detection in a proteomics experiment and mRNA abundance in a microarray experiment. Consider the pair of tissues, i,j, where $i,j \in$ {brain, heart, kidney, liver}. For a given gene, G, let M(G,k) represent the gene expression level of gene G in tissue k. Let P(G,k) be an indicator variable that is 0 if the protein product of gene G is not found in tissue k, and 1 if the protein product is found in tissue k. The mRNA and protein expression levels of gene G are concordant in tissues i and j if $M(G,i)>M(G,j)$ when $P(G,i)>P(G,j)$. For a given gene, G, compute the total number of observed concordances (c_G) between all pairs of tissues as well as the expected variance in concordance (v_G) for that gene. The test statistic is simply

$$C = \sum_G c_G \Big/ \sqrt{\sum_G v_G},$$

which has mean 0 and variance 1 and is approximately normal in the null case where there is no concordance between RNA abundance and protein detection.

Compositional Diversity Across Tissues. Mitochondrial gene products show distinct patterns of expression based on protein and RNA expression (Table 5). These patterns of distribution can be used to develop a simple model that describes core mitochondrial proteins versus those that are specialized to any set of cell types.

Consider a set of i+1 tissues, S_{i+1}, as well as a distinct subset S_i, i.e., $S_i \subset S_{i+1}$, where $i>0$. Applicants are interested in the probability that a given gene product is found in S_{i+1} conditional that it is found in S_i, or simply $T(S_{i+1}, S_i)$ = P(gene product is found in S_{i+1}|gene product is found in S_i). Define P_i as the average $T(S_{i+1}, S_i)$ over all selections of $S_i \subset S_{i+1}$. When applicant assessed compositional diversity using RNA expression levels, Applicant interpreted an RNA expression level greater than 200 as present (Su et al. (2002). Proc Natl Acad Sci U S A 99, 4465-70), and an expression below this level as not present. These average conditional probabilities P_i can also be modeled. Imagine that a fraction f of all mitochondrial proteins are ubiquitous (i.e., expressed in all cell types with probability 1) and that a fraction 1-f are not ubiquitous, but rather, appear in a given tissue with probability p. Then $P_{i+1}=(f+(1-f)p^{i+1})/(f+(1-f)p^{i})$.

DNA Microarray Analysis. To identify Affymetrix probe-sets corresponding to each protein cluster, Applicant mapped the exemplar sequence to the Unigene cluster, and then identified the corresponding Affymetrix MG-U74Av2 probe set. The NetAffx website (http://www.affymetrix.com) and its tables were used to perform these mappings (January 2003). The GNF mouse expression atlas (Su et al. (2002). Proc Natl Acad Sci U S A 99, 4465-70) was downloaded from its website (http://www.gnf.org). In comparisons of protein detection and mRNA abundance, the used the mRNA expression level for a given tissue averaged over the replicates, since the GNF mouse expression atlas includes duplicates for each tissue. Because the proteomic survey was performed on whole brain, applicants simply compared to the average expression of all brain samples in the GNF mouse atlas. Hierarchical clustering was performed using DCHIP (Schadt et al. (2001). J Cell Biochem Suppl Suppl, 120-5).

Identification of Ancestral Mitochondrial Genes. The consensus FASTA sequences for the genes represented on the Affymetrix MG-U74Av2 oligonucleotide array were downloaded from the NetAFFX (Liu et al. (2003). Nucleic Acids Res 31, 82-6) website (http://www.affymetrix.com). A blastx comparison of these sequences was performed against the Rickettsia prowazekii protein sequences, downloaded from the NCBI, and then a tblastn comparison of the bacterial protein sequences was performed against the consensus FASTA sequences. An ancestral gene as defined as one achieving a BLASTX E<0.01 and having a reciprocal best match in the BLAST analysis.

Example 7: Proteomic Survey of Mitochondria

Applicants carried out a systematic survey of mitochondrial proteins from brain, heart, kidney, and liver of C57BL6/J mice (see Methods). Each of these tissues provides a rich source of mitochondria. The isolation consisted of density centrifugation followed by Percoll purification. Preparations were tested for purity and for contamination using immunoblotting directed against organelle markers, enzymatic assays to ensure that the mitochondria were intact, and electron microscopy. The liver, heart, and kidney mitochondria were extremely pure. The brain mitochondria tended to show persistent contamination by synaptosomes, which themselves are a rich source of neuronal mitochondria (see Fernandez-Vizarra (2002). Methods 26, 292-7).

Mitochondrial proteins from each tissue were solubilized and size separated by gel filtration chromatography into approximately 20 fractions (see Methods). These proteins were then digested and analyzed by liquid chromatography mass spectrometry/mass spectrometry (LC-MS/MS). More than 100 LC-MS/MS experiments were performed (see Methods).

The acquired tandem mass spectra were then searched against the NCBI nonredundant database consisting of mammalian proteins using a probability-based method (Perkins et al. (1999). Electrophoresis 20, 3551-67. [pii]). Stringent criteria were used for accepting a database hit. Specifically,only peptides corresponding to complete tryptic cleavage specificity with scores greater than 25 were considered (see Methods). Furthermore, only fragmentation spectra which also exhibited a correct, corresponding peptide sequence tag (Mann et al. (1994). Anal Chem 66, 4390-9) consisting of at least three amino acids were considered.

Using these criteria, ~2100 database hits were identified. This list contains a high degree of redundancy, because a protein may have been found in adjacent fractions of the gel and in different tissues. The ~2100 hits collapse to a distinct set of 422 mouse proteins (see Table 4, Figure 6, and Methods).

Example 8: Previously Annotated Mitochondrial Proteins.

A list of previously annotated mouse and human mitochondrial proteins was created by pooling all the mouse and human proteins from MITOchondria Project (MITOP, http://mips.gsf.de/proj/medgen/mitop/), a public database of curated mitochondrial proteins, as well as all proteins annotated as mitochondrial in NCBI's LocusLink database (http://www.ncbi.nlm.nih.gov/LocusLink/) (see Methods). After elimination of redundancy, the list contains 452 distinct mouse proteins that are either directly annotated as mitochondrial or whose human homolog is annotated as mitochondrial (Figure 6A). The human proteins recently reported to be mitochondrial by Taylor et. al. 2003 (in a study published after the construction of Applicant's list of previously annotated proteins) were not included in Applicant's list. These proteins instead serve as a control against which to compare the proteins identified in our proteomic analysis. The list of 452 previously annotated mitochondrial proteins is by no means comprehensive – there are likely many mitochondrial proteins that are simply not annotated by these public databases. However, it does provide a reasonable, high confidence list of previously annotated proteins against which to benchmark Applicant's proteomic survey.

Example 9: Newly Identified Mitochondrial Proteins.

The set of 422 proteins identified in Applicant's proteomic survey include 262 of the 452 proteins previously annotated to be mitochondrial (58%) and 160 proteins not previously annotated as associated with the mitochondria (Figure 6A). The previous and new sets were combined to produce a list of 612 genes whose protein product is physically associated with mitochondria. This set of genes is referred to as mito-P (Table 4).

The 422 proteins identified in the proteomic survey span a wide range of isoelectric points and molecular weights (Figure 6B, 6C), although proteins from the inner mitochondrial membrane are underrepresented (Figure 6D). The incomplete sensitivity (58%) is most likely due to a bias against proteins of low abundance, which is a known feature of the mass spectrometry methodology. This explanation is supported by analysis of RNA expression of the genes encoding the detected and undetected proteins. Considering the subset of the 452 previously annotated genes for which RNA expression was reported in a recent atlas of mRNA expression in mouse (), the distribution of RNA expression level was about 5-fold higher for the genes whose products were detected in our proteomic survey as

compared to those that were not (P=1x10^{-21}) (Figure 6E). This suggests that the proteomics strategy preferentially detected the higher abundance proteins

The 160 proteins not previously annotated as mitochondrial potentially represent new mitochondrial proteins, either in the conventional sense of being present within the organelle or in a broader sense of being tethered to the mitochondrial outer membrane (*e.g.*, tubulin (Heggeness et al. (1978). Proc Natl Acad Sci U S A 75, 3863-6)).

To test this notion, Applicants sought independent evidence that these 160 proteins are actually mitochondrial. First, the list was compared to proteins identified in a recent survey of human heart mitochondria (Taylor et al. (2003). Nat Biotechnol 18, 18). Human homologs of 64 of the 160 proteins were identified in this recently published study. Of the remaining 96 proteins, 24 have strong mitochondrial targeting sequences based on bioinformatic analysis of protein targeting sequences (Table 4 and Methods) (Nakai et al. (1999). Trends Biochem Sci 24, 34-6), a proportion similar to the known mitochondrial proteins. For example polymerase delta interacting protein 38 (encoded by *Pdip38-pending*), which was detected only in liver mitochondria, and the gene product of *Rnaseh1*, which was found only in the kidney, have strong mitochondrial targeting scores. A recent study confirmed that Rnaseh1 can be localized to the mitochondrion, where it plays a critical role in mtDNA homeostasis (Cerritelli et al. (2003). Mol Cell 11, 807-15).

Example 10: Modules of Coregulated Mitochondrial Genes

Applicant also investigated co-regulation of the 612 mito-P genes across different tissues. For 388 of the 612 mito-P genes, mRNA expression levels were available in a mouse gene expression compendium containing data across 47 tissues (Su et al. (2002). Proc Natl Acad Sci U S A 99, 4465-70).

Applicant calculated pairwise correlation and performed hierarchical clustering of these 388 gene expression profiles (Figures 6 and 7). There are several striking mitochondrial gene modules (Figure 6), which are defined here as clusters of genes showing strong expression correlation across the 47 tissues (Table 6). These modules include genes with strong annotation support as well as genes identified in this study as being mitochondrial (see bar labeling in Figure 7). These clusters appear to have properties of scale-free networks, in which a few central nodes are highly correlated with each other (module 6), while most are

correlated with only a few genes or none at all (Barabasi, (2003). Scale-free networks, Sci Am 288, 60-9). As shown in Figure 7, mitochondrial gene expression profiles vary tremendously from tissue to tissue, consistent with the compositional diversity of mitochondria noted above.

Some of these gene modules have no obvious functional relationships, though two appear to be enriched in certain tissues (modules 1,2). Each of these gene modules is characterized by tightly correlated gene expression across the tissue compendium. Members of these genes likely share transcriptional regulatory mechanisms as well as cellular functions. Many of the newly identified mitochondrial genes (black bar in annotation bar of Figure 7) lie within these modules, providing a functional context for their cellular role.

The mitochondria gene modules provide an initial step towards the characterization of some of the newly identified mitochondrial genes, since functionally related genes tend to have correlated gene expression. Of the 104 newly identified mitochondrial proteins that are represented in this microarray dataset, 38 fall within these 7 modules, providing them with a preliminary functional context.

Example 11: Modules Enriched in Genes of Oxidative Phosphorylation.

A striking gene module (module 6) consists of genes related to oxidative phosphorylation (OXPHOS) and β-oxidation and expressed at high levels in brown fat, skeletal muscle, and heart (Figures 6 and 7). The related module 5, enriched in OXPHOS genes but not the β-oxidation genes, is expressed not only in brown fat, heart, and skeletal muscle, but also in colon. Colon is not traditionally considered to be a highly metabolic tissue, but it has high expression of peroxisome proliferative activated receptor-γ, a partner of PGC-1α, a master regulator of mitochondrial biogenesis (Puigserver et al. (2003). Endocr Rev 24, 78-90). In a recent study of human diabetic muscle, Applicant and co-workers demonstrated that the OXPHOS genes in modules 5 and 6 (termed OXPHOS-CR for <u>OX</u>idative <u>PHOS</u>phorylation <u>C</u>o<u>R</u>egulated) show diminished expression in type 2 diabetes, and that these genes are targets of PGC-1α. The current study identifies two modules (modules 5, 6) that contain OXPHOS-CR as well as other mitochondrial genes, including 4 newly identified genes in module 5 and 12 newly mitochondrial genes in module 6. It will be interesting to determine how this expanded set contributes to type 2 diabetes and other measures of whole-body metabolism.

Example 12: Mitochondrial Gene Expression Neighborhood.

Applicant also sought to systematically identify all genes that exhibit correlated expression with the mito-P genes. This was done using the neighborhood index (N_{100}), a previously described statistic that measures a given gene's expression similarity to a target gene set (Mootha et al. (2003). Proc Natl Acad Sci U S A 100, 605-10). For a given gene, the mitochondria neighborhood index is defined as the number of mito-P genes among its nearest 100 expression neighbors. Applicant computed the N_{100} statistic for all genes in the mouse expression atlas (Figure 9).

The 10,043 genes in the mouse expression atlas include 388 of the 612 mito-P genes. If these 388 genes were a random subset, an N_{100} value greater than 10 would be expected to occur by chance 1 in 1000 times, and an N_{100} greater than 50 would be exceedingly rare (P=1.5x10^{-14}).

A total of 806 genes have N_{100} >10. This is defined herein as the expression neighborhood of the mito-P set, and Applicant interprets these genes as being co-regulated with mitochondrial genes (see the entire rank ordered list, Table 7). This group corresponds to only 8% of all the genes studied, but it contains 52% of the mito-P genes (6.5-fold enrichment, P=1.49x10^{-11}). The list includes 59 that are newly mitochondrial, based on the proteomic survey described herein and 25 that were previously known to be mitochondrial but not detected by that proteomic survey.

Importantly, the expression neighborhood includes 605 genes not present in the mito-P set itself. These genes may encode proteins that are physically present in mitochondria but were missed in the proteomic survey or that are functionally related to mitochondria but not physically associated. They provide a catalog of genes that are likely functionally relevant to mitochondrial biology, and are complementary to the proteomic approach that identified proteins resident in this organelle.

Example 13: Transcription Factors and Nutrient Sensors Within the Mitochondrial Neighborhood

Applicant found several genes involved in DNA replication within the mitochondria neighborhood (Table 1). *Essra*, *Pparg*, and *Ppara* encode nuclear receptors that are tightly co-regulated with the mitochondrial genes. This is intriguing since previous studies have

suggested that these nuclear receptors are important partners of the coactivator PGC-1α, a key molecule in mitochondrial biogenesis (Puigserver et al. (2003). Endocr Rev 24, 78-90). While nuclear receptors are critical to mitochondrial biogenesis (Scarpulla, R. C. (2002). Biochim Biophys Acta 1576, 1-14), to our knowledge, none has previously been reported to be co-regulated with the mitochondrial genes themselves. Interestingly, a recent report demonstrated that PGC-1α co-activates *Essra* gene expression (Schreiber et al. (2003). J Biol Chem 278, 9013-8). Applicant's results raise the hypothesis that this may be a general phenomenon, in which PGC-1α is co-activating a number of its own transcriptional partners.

A number of other transcriptional regulators also have expression patterns very tightly regulated with the mitochondrial genes, including *Mdfi*, *Nfix*, *Tbx6*, and *Crsp2*. These are excellent candidate transcription factors that may be targets of PGC-1α, or perhaps are involved in other mechanisms leading to the biogenesis of this organelle.

Surprisingly, the nutrient sensor Sir2 is also found within the mitochondrial expression neighborhood. *Sir2* encodes an NAD(+)-dependent histone deacetylase which is homologous to the yeast silent information regulator 2 (ySir2). Sir2 is involved in gene silencing, chromosomal stability, and aging. Chromatin remodeling enzymes rely on coenzymes derived from metabolic pathways, including those generated by the mitochondrion. These observations suggest that *Sir2* and mitochondrial gene expression are cooperatively regulated, perhaps linking the mitochondrion to the nutrient sensing activities of Sir2.

Third Experimental Series

The following experimental procedures were followed in the third experimental series:

Data Scaling, Visualization, and Annotation Enrichment. Microarray data were acquired and subjected to linear scaling using the median scan as a reference. Data were visualized using the dChip software package (10) and enrichment by ontology terms determined with the GoSurfer tool, using a *P*-value of 0.01 (11). Mitochondrial genes were defined based on a recent proteomic survey of organelle in mouse (12).

Promoter Databases. Applicants used the Reference Sequence annotations of mm3 build of the mouse genome (http://genome.ucsc.edu) and the annotation tables for the Affymetrix

MG-U74Av2 chip (http://www.affymetrix.com) to compile a list of 5034 mouse genes for which there is a 1:1 mapping between Affymetrix probe-set and Reference Sequences. The 'mouse promoter database' consists of 2000bp of genomic sequence centered on the annotated transcription start site of these genes.

Applicants also performed analyses on a 'masked promoter database', consisting of the regions within these 2000bp that are aligned and conserved between mouse and human. Applicants used the mouse/human BLASTZ alignments (mouse mm3 vs. human hg15) (13) and only considered the 5008 promoters for which the alignment contained at least 100bp. Applicants masked the aligned promoters to retain mouse sequence exhibiting at least 70% identity to human across windows of size 10. The median promoter length in the masked database is ~ 1200bp.

Motif discovery. For a given day, genes from the microarray are ordered on the basis of expression difference between GFP and PGC-1α (applicants use the signal to noise ratio as our difference metric). Each gene is annotated for the presence of a motif in the promoter by searching for exact k-mers (where $k = 6, 7, 8$ or 9) or for selected motifs of interest. Applicants use the Mann-Whitney rank sum statistic U to determine whether the distribution of differential expression for those genes with a given motif differs from those genes lacking the motif. When working with promoters of unequal length (*e.g.*, the masked promoter database), a more appropriate null hypothesis for the Mann-Whitney statistic is that the probability of detecting a motif in a promoter is proportional to its length. To assess the significance of a motif with rank sum U that appears in C promoters, applicants use Monte Carlo simulation (with 1000 samples) to estimate the null distribution of U for a sample of C ranks drawn randomly, without replacement, given relative weights proportional to the promoter lengths. For large C (C>10) and a reasonable distribution of promoter lengths, U is approximately normally distributed.
Promoter databases and motifADE source code are available at http://www-genome.wi.mit.edu/mpg/PGC_motifs/.

Example 14: Discovering motifs associated with differential expression.

Systematic identification of transcription factors involved in biological processes in mammals remains a largely unsolved problem (17). A promising approach relates genome-

wide expression profiles to promoter sequences to discover influential *cis*-motifs (18-21). Such methods have yielded impressive results in simple organisms such as yeast, but it has been challenging to extend these algorithms to mammalian genomes, where intergenic regions are large, annotation of gene structure is imperfect, and DNA sequence can be highly repetitive. Most of these methods seek motifs by comparison to a fixed background model of nucleotide composition (which fails to represent the fluctuations seen in large genomes) or by comparison between two sets of genes (which is likely to capture only very sharp differences). Further, many of these methods assume that the expression data are normally distributed, which may not always be true.

To overcome some of these obstacles, applicants devised a simple, nonparametric strategy for identifying motifs associated with differential expression (motifADE) (Fig. 10a). The algorithm involves three steps: (i) ranking genes based on differential expression between two conditions; (ii) given a candidate motif, identifying the subset of genes whose promoter regions contains the motif; and (iii) testing via a nonparametric, rank sum statistic (see Methods) if these genes tend to appear toward the top or bottom of the ranked list (indicating association) or are randomly distributed on the list. motifADE may be applied to a specific candidate motif of interest or to the list of all possible motifs of a given size (in which case the significance level should be adjusted to reflect multiple hypothesis testing). By using a nonparametric scoring procedure (see Methods), applicants do not make assumptions about the distribution of the expression data. Furthermore, by considering the entire rank ordered list, the promoters without the motif implicitly provide a background of DNA composition for comparison, and there is no need to group the genes into clusters. The method can operate on a traditional promoter database or even a database of promoters that have been masked based on evolutionary conservation (see Methods).

Example 15: Binding sites for Errα and Gabpa are the top scoring motifs associated with the PGC-1α transcriptional program.

To identify motifs related to PGC-1α action, applicants infected mouse C2C12 muscle cells with an adenovirus expressing PGC-1α and obtained gene expression profiles for 12,488 genes at 0, 1, 2, and 3 days following infection. Applicants found 649 genes that were induced at least 1.5-fold (nominal $P<0.05$) at day 3. As expected, these were enriched for genes involved in carbohydrate metabolism and the mitochondrion (see (1)). Interestingly,

many genes involved with protein synthesis (GO terms: protein biosynthesis, mitochondrial ribosome and ribosome) are also induced.

Applicants then applied motifADE to study the 5034 mouse genes for which applicants have measures of gene expression as well as reliable annotations of the transcriptional start site (TSS) (see Methods). For each gene, the target region was defined to be a 2kb region centered on the TSS. Applicants then tested all possible *k*-mers ranging in size from *k*=6 to *k*=9 nucleotides for association with differential expression on each of the three days of the timecourse. A total of 20 motifs achieved high statistical significance ($p<0.001$, following Bonferroni correction for multiple hypothesis testing) and these were almost exclusively related to two distinct motifs (see Table 8 and Table 9). The first motif, 5'-TGACCTTG-3' was significant on days 1, 2, and 3 (adjusted $P=2.1\times10^{-6}$, 2.9×10^{-9}, and 7.7×10^{-7}, respectively). It corresponds to the published binding site for the orphan nuclear receptor Errα (22), which is known to be capable of being co-activated by PGC-1-α and -β (23-25). The *Errα* gene is known to be involved in metabolic processes, based on studies showing that knockout mice have reduced body weight and peripheral fat tissue, as well as altered expression of genes involved in metabolic pathways (26). The second motif is 5'-CTTCCG-3' (adjusted $p=8.9\times10^{-9}$), which is the top scoring motif on day 3. It corresponds to the published binding site for Gabpa (27), which complexes with Gabpb (15) to form the heterodimer, nuclear respiratory factor-2 (NRF-2), a factor known to regulate the expression of some OXPHOS genes (28).

Interestingly, the reverse complements of these motifs did not score as well, suggesting a preference for the orientation of these motifs, and some occurrences of the motifs occurred downstream of the TSS. While each of these motifs is individually associated with PGC-1A, our analyses suggest that a gene having both motifs typically ranks higher on the list of differentially expressed genes and genes with only one of the motifs (Figure 12) suggesting that the two motifs might have an additive or synergistic effect.

Example 16: Errα and Gabpa motifs are evolutionarily conserved and enriched upstream of OXPHOS genes.

Applicants next repeated motifADE analysis using a "masked" promoter database (Table 3). Applicants still considered the 2000bp centered on the TSS, but only considered those nucleotides aligned and conserved between mouse and human (see Methods). Still, the top ranking motifs on days 1 and 3 were related to Errα (day 1, $P=4.8\times10^{-6}$; day 3 $P=1.2\times10^{-}$

^{11}) and to Gabpa (day 3 $P=3.1\times10^{-11}$), providing additional support these motifs are biologically relevant.

The Errα and Gabpa motifs are particularly enriched upstream of the OXPHOS-CR genes, which exhibit reduced expression in human diabetes (5, 6). Whereas the top scoring Errα motif (5'-TGACCTTG-3' or its reverse complement) only occurs in 12% of the promoters in the database, in 29% of the PGC-responsive genes (*i.e.*, those genes induced at least 1.5 fold on day 3), and in 27% of the mitochondrial genes, they are found in 52% of the OXPHOS-CR genes (significance of enrichment, $P=1\times10^{-4}$). About one-half of these sites are perfectly conserved in the syntenic region in human. The top scoring Gabpa binding sites (5'-CTTCCG-3' or its reverse complement) are much more common (62% of all promoters of the database and in 79% of the PGC-responsive genes), but they, too, show significant enrichment in the OXPHOS-CR genes (89%, P=0.02).

Example 17: Errα and Gabpa are themselves induced by PGC-1α.

The above results suggest that Errα and Gabpa may be the key transcriptional factors mediating PGC-1α action in muscle. In this connection, it is notable that based on the microarray data, both Errα and Gabpa are themselves induced 2-fold ($P<0.01$) on day 1 following expression PGC-1α consistent with previous studies (2, 23). Moreover, careful analysis of the *Errα* and *Gabpa* genes suggest that each contain potential binding sites for both transcription factors within the vicinity of their promoters. The *Errα* gene has the Errα motif as well as a conserved variant of the Gabpa binding site (27) upstream of the TSS, while the *Gabpa* gene has an Errα site upstream of the TSS and a conserved variant of the Gabpa binding site in its first intron .These results raise the possibility that Errα and Gabpa may regulate their own and each other's expression.

Taken together, the systematic analysis of the transcriptional program driven by PGC-1α in skeletal muscle suggests a model (Fig. 11) in which increases in PGC-1α protein levels (induced, for example, by exercise, e.g. see (29)) results in increased transcriptional activity of Gabpa and Errα on their own promoters, leading to a stable increase in the expression of these two factors via a double positive-feedback loop. These two factors, perhaps in combination with PGC-1α, are then crucial in the induction of downstream target genes, many of which have binding sites for these motifs (Fig. 11). Such a circuit may serve as a regulatory switch, analogous to a feed-forward loop that plays a key role in the early stages of

endomesodermal development in sea urchin (30).

Experiment 18: MotifADE results applied to human diabetic versus normal expression.

Applicants applied the MotifADE method to analyze the transcription factor binding sites that are differentially expressed in diabetic vs. normal human skeletal muscle (previously published data, Mootha et al Nature Genetics 2003). The program identified exactly three motifs achieving an adjusted *P*-value < 0.05. These are AAATCG (adjusted *P*-value 0.003), CCGGAAG (adjusted *P*-value 0.039), and AGCGTTT (adjusted *P*-value 0.011). Applicants note that the second motif is a published binding site for Gabpa (reverse complement of CTTCCG). This results suggest that Gabpa function is altered in diabetic muscle, or that perhaps another transcription factor that binds to this element.

Experiment 6: Identification of human genes having binding sites for Errα, Gabpa or both

Applicants searched for the binding sites motifs (forward or reverse complement) 3 Kb upstream and 1 Kb downstream of the annotated transcription start site. In the accompanying files are the genes with either one motif (forward or reverse complement) or both motifs conserved between human and mouse. The following genes were identified: Table 10: 678 genes with Errα motif conserved between mouse and human. Table 11: 2799 genes with Gabpa motif conserved between mouse and human. Table 12: 354 genes with both motifs conserved between mouse and human.

Discussion of First Experimental Series

In this study, applicants have used a combined genomic and computational strategy to systematically dissect a mammalian transcriptional circuit central to cellular energetics. The results above have computational, biological and medical implications.

First, the motifADE algorithm provides a simple, nonparametric approach for discovering *cis*- elements by considering differential gene expression. It makes very few assumptions about the statistical properties of DNA composition or about the distribution of gene expression. The method is flexible, and as applicants have shown, can easily incorporate "masked" or "phylogenetically footprinted" promoters. With additional cross-species comparisons, it should be possible to interrogate conserved segments of larger upstream

regions (34). Moreover, the method operates on any ordered set of genes and is particularly convenient for discovering motifs associated with human disease states, e.g., "healthy versus sick" or "treated versus control." Clearly, the method has some limitations. For example, in the current study, applicants were confident in the identity of the transcription factors binding the motifs discovered – in general this may not be the case, and experimental strategies will be needed to systematically determine the occupancy of newly identified motifs. Moreover, a motif may be missed if it lies outside the target promoter region, or if a functional binding site is too degenerate for our motif search strategy.

Second, the analyses above indicate that the immediate effects of PGC-1α on OXPHOS genes in muscle are largely mediated through Erra and Gabpa. Recent studies have shown that PGC-1β can also co-activate Erra (25). Together, the data imply a model of gene regulation in which PGC-1α (and likely PGC-1β) initially induces the expression of Erra and Gabpa, via a double positive feedback mechanism (Fig. 11). These transcription factors are then expressed at higher levels and are themselves co-activated by PGC-1 to induce downstream genes such as NRF-1 and members of OXPHOS. Certainly, other transcription factors and regulators, not identified in the current study, are involved in the mitochondrial biogenesis program. Whereas previous studies have shown that PGC-1 interacts with and/or induces 15-20 transcription factors in various physiological settings (including Erra and Gabpa (2, 23-25), the present study points to Erra and Gabpa as being especially important early in the timecourse in muscle and provides a model of how these factors interact in executing the transcriptional program.

Finally, the results suggest a potential approach to the treatment of type 2 diabetes. Recent studies in diabetic and pre-diabetic humans have demonstrated that there is a consistent decrease in the expression of genes of oxidative phosphorylation that are responsive to PGC-1α and PGC-1β and that treatments that induce PGC-1α (such as exercise) lead to increased expression of OXPHOS genes and improved insulin sensitivity (5, 6, 8, 9) . On its face, this might argue for developing therapeutic approaches that raise the transcriptional activity of PGC-1. However, PGC-1 activates many different pathways in many tissues and such approaches may suffer from lack of specificity. For example, global transgenic overexpression of PGC-1β in mice results in resistance to obesity induced by a high-fat diet or by a genetic abnormality, though the contribution of PGC-1β expression in

muscle has not been explored (25). On the other hand, a global knockout of Errα also causes a leaner phenotype and resistance to high-fat diet-induced obesity (26). The identification of the critical roles of Errα and Gabpa in mediating the transcriptional program altered in human diabetic muscle may offer a more specific target. Because Errα is an orphan nuclear receptor, it may be an attractive, "druggable" target for diabetes and for other human metabolic disorders.

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Tables:

Table 1: Clinical and biochemical characteristics of male subjects with normal glucose tolerance (NGT), impaired glucose tolerance (IGT), and type 2 diabetes mellitus (DM2).

	Class			*P*-Value		
	NGT	IGT	DM2	NGT vs. IGT	IGT vs. DM2	NGT vs. DM2
n	17	8	18			

Age (yrs)	66.1 (1.0)	66.4 (1.6)	65.5 (1.8)			
BMI (kg/m^2)	23.6 (3.4)	27.1 (4.8)	27.3 (4.0)			5.70×10^{-3}
WHR	0.91 (0.09)	0.97 (0.04)	0.99 (0.03)	3.00×10^{-2}		3.83×10^{-3}
Trigs (mmol/L)	1.03 (0.40)	1.83 (1.60)	2.04 (1.13)			2.63×10^{-3}
Chol (mmol/L)	5.39 (0.09)	4.60 (1.48)	5.77 (0.97)			
OGTT						
Glucose 0 (mmol/L)	4.67 (0.50)	5.05 (0.46)	7.83 (2.3)		9.22×10^{-5}	2.01×10^{-5}
Insulin 0 (uU/ml)	5.41 (3.3)	13.38 (8.9)	12.0 (6.0)	4.05×10^{-2}		4.10×10^{-4}
Glucose 120 (mmol/L)	6.58 (0.94)	9.15 (0.8)	14.9 (4.0)	2.51×10^{-6}	8.91×10^{-6}	4.90×10^{-8}
Insulin 120 (uU/ml)	33.5 (19.3)	125.1 (66.1)	43.5 (25.6)	5.47×10^{-3}	9.73×10^{-3}	
M-value (mg/kg/min)	8.74 (3.15)	6.32 (3.08)	4.22 (1.72)			2.30×10^{-5}
VO2max (ml O_2/kg/min)	32.1 (5.46)	26.5 (4.6)	24.3 (5.6)	1.72×10^{-2}		3.09×10^{-4}
Glycogen (mmol/kg)	371.1 (77.0)	326.5 (88.0)	350.6 (97.8)			
Type I Fibers						
Number (%)	37.2 (13.5)	33.5 (3.6)	36.4 (9.3)			
Area (%)	39.1 (14.4)	32.7 (0.91)	40.1 (10.7)		2.35×10^{-2}	
Capillaries/Fiber	3.91 (0.72)	4.05 (1.04)	4.14 (0.75)			
Type IIb Fibers						
Number (%)	73.8 (42.1)	60.2 (51.4)	72.2 (36.7)			
Area (%)	31.3 (18.0)	24.7 (18.3)	36.2 (15.4)			
Capillaries/Fiber	2.97 (0.71)	3.05 (0.87)	3.02 (0.65)			

Values are mean (S.D.).
M-value is the total body glucose uptake. VO2max is the total body aerobic capacity.
Only P-values < 0.05 are shown for pairwise comparisons, using a two-sided t-test.

Table 2: 149 gene sets considered in the current analysis.

Pathways Curated at WICGR

FFA Oxidation
Gluconeogenesis
Glycolysis
Glycogen metabolism
GO:0005739
Insulin signaling
Ketone body metabolism
Pyruvate metabolism
Reactive oxygen species
Kreb's cycle
Oxidative phosphorylation (OXPHOS)
human_mitoDB_6_2002
mitochondria keyword

36 GNF Mouse Expression Clusters

cluster *c*0, ..., cluster *c*35

Pathways from NetAFFX (October 2002)

MAP00010_Glycolysis_Gluconeogenesis
MAP00020_Citrate_cycle_TCA_cycle
MAP00030_Pentose_phosphate_pathway
MAP00031_Inositol_metabolism
MAP00040_Pentose_and_glucuronate_interconversions
MAP00051_Fructose_and_mannose_metabolism
MAP00052_Galactose_metabolism
MAP00053_Ascorbate_and_aldarate_metabolism
MAP00061_Fatty_acid_biosynthesis_path_1
MAP00062_Fatty_acid_biosynthesis_path_2
MAP00071_Fatty_acid_metabolism
MAP00072_Synthesis_and_degradation_of_ketone_bodies
MAP00100_Sterol_biosynthesis
MAP00120_Bile_acid_biosynthesis
MAP00130_Ubiquinone_biosynthesis
MAP00140_C21_Steroid_hormone_metabolism
MAP00150_Androgen_and_estrogen_metabolism
MAP00190_Oxidative_phosphorylation
MAP00193_ATP_synthesis
MAP00195_Photosynthesis
MAP00220_Urea_cycle_and_metabolism_of_amino_groups
MAP00230_Purine_metabolism
MAP00240_Pyrimidine_metabolism
MAP00251_Glutamate_metabolism
MAP00252_Alanine_and_aspartate_metabolism
MAP00253_Tetracycline_biosynthesis
MAP00260_Glycine_serine_and_threonine_metabolism
MAP00271_Methionine_metabolism
MAP00272_Cysteine_metabolism
MAP00280_Valine_leucine_and_isoleucine_degradation
MAP00290_Valine_leucine_and_isoleucine_biosynthesis
MAP00300_Lysine_biosynthesis
MAP00310_Lysine_degradation
MAP00330_Arginine_and_proline_metabolism
MAP00340_Histidine_metabolism
MAP00350_Tyrosine_metabolism
MAP00360_Phenylalanine_metabolism
MAP00361_gamma_Hexachlorocyclohexane_degradation
MAP00380_Tryptophan_metabolism
MAP00400_Phenylalanine_tyrosine_and_tryptophan_biosynthesis
MAP00410_beta_Alanine_metabolism

(cont'd)

MAP00430_Taurine_and_hypotaurine_metabolism
MAP00440_Aminophosphonate_metabolism
MAP00450_Selenoamino_acid_metabolism
MAP00460_Cyanoamino_acid_metabolism
MAP00471_D_Glutamine_and_D_glutamate_metabolism
MAP00472_D_Arginine_and_D_ornithine_metabolism
MAP00480_Glutathione_metabolism
MAP00500_Starch_and_sucrose_metabolism
MAP00510_N_Glycans_biosynthesis
MAP00511_N_Glycan_degradation
MAP00512_O_Glycans_biosynthesis
MAP00520_Nucleotide_sugars_metabolism
MAP00521_Streptomycin_biosynthesis
MAP00522_Erythromycin_biosynthesis
MAP00530_Aminosugars_metabolism
MAP00531_Glycosaminoglycan_degradation
MAP00532_Chondroitin_Heparan_sulfate_biosynthesis
MAP00533_Keratan_sulfate_biosynthesis
MAP00550_Peptidoglycan_biosynthesis
MAP00561_Glycerolipid_metabolism
MAP00562_Inositol_phosphate_metabolism
MAP00570_Sphingophospholipid_biosynthesis
MAP00580_Phospholipid_degradation
MAP00590_Prostaglandin_and_leukotriene_metabolism
MAP00600_Sphingoglycolipid_metabolism
MAP00601_Blood_group_glycolipid_biosynthesis_lact_series
MAP00602_Blood_group_glycolipid_biosynthesis_neolact_series
MAP00603_Globoside_metabolism
MAP00620_Pyruvate_metabolism
MAP00625_Tetrachloroethene_degradation
MAP00630_Glyoxylate_and_dicarboxylate_metabolism
MAP00631_1_2_Dichloroethane_degradation
MAP00632_Benzoate_degradation
MAP00640_Propanoate_metabolism
MAP00643_Styrene_degradation
MAP00650_Butanoate_metabolism
MAP00670_One_carbon_pool_by_folate
MAP00680_Methane_metabolism
MAP00710_Carbon_fixation
MAP00720_Reductive_carboxylate_cycle_CO2_fixation
MAP00740_Riboflavin_metabolism
MAP00750_Vitamin_B6_metabolism
MAP00760_Nicotinate_and_nicotinamide_metabolism
MAP00770_Pantothenate_and_CoA_biosynthesis
MAP00780_Biotin_metabolism
MAP00790_Folate_biosynthesis
MAP00830_Retinol_metabolism
MAP00860_Porphyrin_and_chlorophyll_metabolism
MAP00900_Terpenoid_biosynthesis
MAP00910_Nitrogen_metabolism
MAP00920_Sulfur_metabolism
MAP00940_Flavonoids_stilbene_and_lignin_biosynthesis
MAP00950_Alkaloid_biosynthesis_I
MAP00960_Alkaloid_biosynthesis_II
MAP00970_Aminoacyl_tRNA_biosynthesis
MAP03020_RNA_polymerase
MAP03030_DNA_polymerase
MAP03070_Type_III_secretion_system
MAP03090_Type_II_secretion_system

1 **Table 3.** Genes in the mitochondria expression neighborhood with putative roles in DNA maintenance and repair based on Gene Ontology annotations. The gene name, symbol, and neighborhood index (N_{100}) are provided for each gene.

Gene name	Gene symbol	N_{100}
Transcriptional regulators		
MyoD family inhibitor	*Mdfi*	63
nuclear factor I/X	*Nfix*	60
zinc finger protein 288	*Zfp288*	56
T-box 6	*Tbx6*	49
Cofactor required for Sp1 transcriptional activation subunit 2	*Crsp2*	47
RIKEN cDNA 9130025P16 gene	*9130025P16Rik*	46
Kruppel-like factor 9	*Klf9*	43
EGL nine homolog 1	*Egln1*	39
Estrogen related receptor, alpha	*Esrra*	36
nuclease sensitive element binding protein 1	*Nsep1*	34
sirtuin 1 (silent mating type information regulation 2, homolog)	*Sirt1*	31
peroxisome proliferator activated receptor alpha	*Ppara*	29
metastasis associated 1-like 1	*Mta1l1*	28
NK2 transcription factor related, locus 5	*Nkx2-5*	27
cardiac responsive adriamycin protein	*Crap*	24
homeo box D8	*Hoxd8*	21
nuclear receptor subfamily 1, group I, member 2	*Nr1i2*	21
nuclear receptor subfamily 1, group H, member 3	*Nr1h3*	20
cellular nucleic acid binding protein	*Cnbp*	19
transcription factor 2	*Tcf2*	19
Est2 repressor factor	*Erf*	19
nuclear receptor subfamily 5, group A, member 1	*Nr5a1*	18
nuclear factor, erythroid derived 2,-like 1	*Nfe2l1*	18
zinc finger protein 30	*Zfp30*	17
peroxisome proliferator activated receptor gamma	*Pparg*	17
cAMP responsive element binding protein 1	*Creb1*	15
SRY-box containing gene 6	*Sox6*	15
CCAAT/enhancer binding protein (C/EBP), alpha	*Cebpa*	15
DNA repair		
mutL homolog 1	*Mlh1*	29
mutS homolog 5	*Msh5*	24
excision repair cross-complementing rodent repair deficiency, complementation group 1	*Ercc1*	15

Table 4. Annotation and experimental support for the mito-A proteins. The mito-A list of protein clusters consist of proteins that are physically associated with mitochondria, based on previous annotations or based on organelle proteomics. The list is produced by pooling all the individual proteins identified in the organelle proteomics survey with proteins previously annotated as being mitochondrial. These proteins were then clustered into 601 groups using a BLAST procedure (see Methods). Each cluster may be supported by previous annotations, organelle proteomics, or by both (protein accessions are indicated in the appropriate columns). Of the 601 clusters, 10 correspond to expected contaminants and have been flagged. The remaining 591 constitute the mito-A list that is used in the analysis. For each mito-A cluster, an exemplar protein (typically corresponding to a Reference Sequence) accession and description are provided. GenPept or Swissprot accession numbers of the cluster members are provided in the appropriate columns. Of the 591 mito-A clusters, 37 appeared to be obviously mitochondrial based on the description, so these have been flagged as mitochondrial in a dedicated column called "by name."

Exemplar Protein for the Cluster		Previous Mitochondrial Annotations			
Accession	Description	LocusLink Mouse	MITOP Mouse	LocusLink Human	MITOP Human
19354491	1110020P15Rik protein [Mus musculus]				
13385680	2,4-dienoyl CoA reductase 1, mitochondrial [Mus musculus]			4503301	S53352
20071710	2010002H18Rik protein [Mus musculus]				
21630283	2'-5' oligoadenylate synthetase 1A [Mus musculus]		P29080 P11928		P1_A22842 B24359 A91013
21644597	2'-5' oligoadenylate synthetase 2; 2'-5' oligoadenylate synthetase-like 11 [Mus				B42665 A42665
6680233	3-hydroxy-3-methylglutaryl-Coenzyme A lyase [Mus musculus]	25022682 25049209 6680233	HMGL_MOUSE		A45470
31560689	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 [Mus musculus]	27734729 20965433 20874930	B55729	5031751	S51103
31982169	3-hydroxybutyrate dehydrogenase (heart, mitochondrial); 3-hydroxybutyrate			17738292	A42845
21704140	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor; EST AI265272;				D3HI_HUMAN
20149758	3-mercaptopyruvate sulfurtransferase; e [Mus musculus]				ROHU
481864	3-methyl-2-oxobutanoate dehydrogenase (lipoamide) (EC 1.2.4.4) - mouse		S39807	4557353	A37157
18266680	3-oxoacid CoA transferase [Mus musculus]				SCOT_HUMAN

11968160	3-oxoacid CoA transferase 2A; haploid germ cell specific succinyl CoA				
6679066	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1				
20127399	5',3'-deoxyribonucleotidase, mitochondrial [Mus musculus]	20127399		9910372	
18921208	8-oxoguanine DNA-glycosylase 1 [Mus musculus]	18921208			
9910174	A kinase (PRKA) anchor protein 10; protein kinase A anchoring protein [Mus	9910174			
30725845	AAA-ATPase TOB3 [Mus musculus]				
1167982	ABC transporter-7				ABC7_HUMAN
21450129	acetyl-Coenzyme A acetyltransferase 1 precursor [Mus musculus]	21450129		4557237	JH0255
29126205	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A			5174429	S43440
20841184	acetyl-Coenzyme A carboxylase beta [Mus musculus]				
31982520	acetyl-Coenzyme A dehydrogenase, long-chain [Mus musculus]	6680616 25020672	ACDL_MOUSE	4501857	A40559
6680618	acetyl-Coenzyme A dehydrogenase, medium chain [Mus musculus]	6680618	A55724	4557231	I52240
9790059	acid phosphatase 6, lysophosphatidic; acid phosphatase like 1 [Mus musculus]			21359911	
18079339	aconitase 2, mitochondrial [Mus musculus]	18079339		4501867	Q99798
8850209	actin-like [Mus musculus]				
31982522	acyl-Coenzyme A dehydrogenase, short chain; acetyl-Coenzyme A dehydrogenase,	6680620	I49605	4557233	A30605
17647119	acyl-Coenzyme A dehydrogenase, short/branched chain [Mus musculus]			4501859	A55680
23956084	acyl-Coenzyme A dehydrogenase, very long chain [Mus musculus]	23956084 25056160 20881925	ACDV_MOUSE	4557235	ACDB_HUMAN
7656855	acyl-Coenzyme A oxidase 1, palmitoyl; acyl-Coenzyme A oxidase; Acyl-CoA oxidase				
12331400	acyl-Coenzyme A thioesterase 3, mitochondrial; MT-ACT48,p48 [Mus musculus]	12331400 9790025		6912518	
6753074	adaptor protein complex AP-2, mu1; adaptor-related protein complex AP-2, mu1;				
10946936	adenylate kinase 1; cytosolic adenylate kinase [Mus musculus]				

34328230	adenylate kinase 2 [Mus musculus]	8392883			KAD2_HUMAN
23956104	adenylate kinase 3 alpha-like; adenylate kinase 3 alpha like [Mus musculus]				
6753022	adenylate kinase 4 [Mus musculus]	6753022			KIHUA3
16905099	AFG3(ATPase family gene 3)-like 1 [Mus musculus]	16905099		5802970	
6753030	A-kinase anchor protein 1; A kinase anchor protein [Mus musculus]	6753030			I39173
7709978	alanine-glyoxylate aminotransferase; alanine-glyoxylate aminotransferase 1 [Mus	7709978			P21549 XNHUSP
6753036	aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	6753036	I48966	25777732	A40872 DEHUE2
19527258	aldehyde dehydrogenase family 6, subfamily A1 [Mus musculus]				MMSA_HUMAN
20070418	aldehyde dehydrogenase family 7, member A1; aldehyde dehydrogenase 7 family,				
27659728	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase);				
13435924	aldolase 3, C isoform [Mus musculus]				
6678766	alpha-methylacyl-CoA racemase; alpha-methylacyl-Coenzyme A racemase;	6678766		23618869	
31980703	aminoadipate-semialdehyde synthase; lysine oxoglutarate reductase, saccharopine				
33859502	aminolevulinic acid synthase 2, erythroid; erythroid-specific ALAS;	20985872	SYMSAL		SYHUAL SYHUAE
13507620	ankycorbin; NORPEG-like protein [Mus musculus]				
6753058	annexin A10 [Mus musculus]				
21541818	AP endonuclease 2 [Mus musculus]	21541818			
6753110	arginase type II [Mus musculus]	6753110		4502215	ARG2_HUMAN
25089776	ATP synthase D chain, mitochondrial		PN0046		
5834959	ATP synthase F0 subunit 6 [Mus musculus]	5834959	PWMS6	27754208	PWHU6
5834958	ATP synthase F0 subunit 8 [Mus musculus]	5834958	PWMS8		PWHU8
21263432	ATP synthase gamma chain, mitochondrial precursor		PT0095		
31980648	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit; ATP	25052136 7949003	P56480	4502295	A33370
33859512	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	20875157 25020502		21361565	JQ1144
31982497	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9),	6680750	AT91_MOUSE		I38612 S34067 S34066
10181184	ATP synthase, H+ transporting, mitochondrial F0	10181184	P56135		

	complex, subunit f, isoform 2;				
7949005	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F;	7949005	PD0444	18644883	JT0563
31980744	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g; F1F0-ATP				
6680748	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform	6680748	JC1473	4757810	PWHUA
13385484	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit; ATP			5901896	
11602916	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1; F1	11602916		4885079	A49108
20070412	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit [Mus				ATPO_HUMAN
6671592	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e [Mus	6671592	JC1412		
31982864	ATPase inhibitor [Mus musculus]	6671594		7705927	JC7175
6680758	ATPase, Cu++ transporting, beta polypeptide; Wilson protein; toxic milk [Mus				S40525
31560731	ATPase, H+ transporting, V1 subunit A, isoform 1; ATPase, H+ transporting,				
6680756	ATPase, H+ transporting, V1 subunit E isoform 1; ATPase, H+ transporting				
6680612	ATP-binding cassette, sub-family D, member 3; peroxisomal membrane protein, 70				
3766201	ATP-specific succinyl-CoA synthetase beta subunit [Mus musculus]	20876884			
7709988	AU RNA-binding enoyl-coenzyme A hydratase; AU RNA-binding protein/enoyl-coenzyme	7709988 25052987		18426971	
6753168	B-cell leukemia/lymphoma 2 [Mus musculus]	6753168	TVMSA1 B25960		TVHUA1 D37332
6671622	B-cell receptor-associated protein 37; repressor of estrogen receptor activity				
6753198	BCL2/adenovirus E1B 19kDa-interacting protein 1, NIP3; BCL2/adenovirus E1B 19	6753198			
6753200	BCL2/adenovirus E1B 19kDa-interacting protein 3-like; BCL2/adenovirus E1B 19	6753200		4757860	NIPL_HUMAN
6680770	Bcl2-associated X protein [Mus musculus]		BAXA_MOUSE		BAXA_HUMAN
31981887	Bcl2-like [Mus musculus]	6753170		20336335 4502381	BCLX_HUMAN
31981875	benzodiazepine receptor, peripheral [Mus musculus]	6753216	A53405		I38105

31542228	BH3 interacting domain death agonist [Mus musculus]			4557361	BID_HUMAN
9055178	brain protein 44-like; apoptosis-regulating basic protein [Mus musculus]				
33859514	branched chain aminotransferase 2, mitochondrial [Mus musculus]	23597235		4502375	BCAM_HUMAN
31982494	branched chain ketoacid dehydrogenase E1, alpha polypeptide; BCKAD E1[a] [Mus	6671624	S71881	11386135	DEHUXA
6753164	branched chain ketoacid dehydrogenase kinase; branched chain keto acid	6753164		5031609	
16905127	butyryl Coenzyme A synthetase 1; acetyl-Coenzyme A synthetase 3 [Mus musculus]				
6753290	calsequestrin 1 [Mus musculus]				A60424
7381085	carbamoylphosphate synthetase I [Mus musculus]			21361331	JQ1348
6671680	carbonic anhydrase 5a, mitochondrial; carbonic anhydrase 5, mitochondrial;	6671680	S12579	4502521	CRHU5
9506463	carbonic anhydrase 5b, mitochondrial; carbonic anhydrase VB; carbonic anhydrase	9506463		6005723	
6671688	carbonyl reductase 2; lung carbonyl reductase [Mus musculus]	6671688	A28053		
6681009	carnitine acetyltransferase [Mus musculus]	6681009	CACP_MOUSE	21618331 21618334 21618336	A55720
27804309	carnitine palmitoyltransferase 1, liver; L-CPT I [Mus musculus]	20884997 27804309		4503021	I59351
6753512	carnitine palmitoyltransferase 1, muscle; M-CPT I [Mus musculus]			23238254 23238256 4758050 23238258	S70579
6753514	carnitine palmitoyltransferase 2; CPT II [Mus musculus]	6753514	A49362		A39018
6753454	caseinolytic protease X [Mus musculus]	6753454		7242140	CLPX_HUMAN
8393156	caseinolytic protease, ATP-dependent, proteolytic subunit homolog; caseinolytic	8393156			S68421
20847456	caspase 8 [Mus musculus]			15718704 15718706 15718708 15718710 15718712	
6753272	catalase; catalase 1 [Mus musculus]				
6681079	cathepsin B preproprotein [Mus musculus]				

6753556	cathepsin D [Mus musculus]				
11968166	cathepsin Z preproprotein; cathepsin Z precursor; cathepsin X [Mus musculus]				
31560609	ceroid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)			4502889	
6753448	ceroid-lipofuscinosis, neuronal 2 [Mus musculus]				
7304963	chloride intracellular channel 4 (mitochondrial) [Mus musculus]	7304963			
13385942	citrate synthase [Mus musculus]			4758076	
6680816	complement component 1, q subcomponent binding protein [Mus musculus]	6680816			
6681007	coproporphyrinogen oxidase; clone 560 [Mus musculus]	6681007	A48049	20127406	I52444
10946574	creatine kinase, brain [Mus musculus]				
6753428	creatine kinase, mitochondrial 1, ubiquitous [Mus musculus]	6753428	S24612	4502855 10334859	A35756 A30789
6681031	cryptochrome 1 (photolyase-like) [Mus musculus]			4758072	
201006	Cu/Zn-superoxide dismutase				
5834966	cytochrome b [Mus musculus]	5834966	CBMS		CBHU
22094077	cytochrome b-245, alpha polypeptide; cytochrome beta-558; p22 phox [Mus			4557505	
31542440	cytochrome b-245, beta polypeptide [Mus musculus]			6996021	
13385268	cytochrome b-5 [Mus musculus]			4503183	CBHU5 CBHU5E
5834956	cytochrome c oxidase subunit I [Mus musculus]	5834956	ODMS1	27754204	ODHU1
5834957	cytochrome c oxidase subunit II [Mus musculus]	5834957	OBMS2	27754206	OBHU2
5834960	cytochrome c oxidase subunit III [Mus musculus]	5834960	OTMS3		OTHU3
16716379	cytochrome c oxidase subunit IV isoform 2 precursor; Cox IV-2 [Mus musculus]	16716379			
6677977	cytochrome c oxidase subunit VIIa polypeptide 2-like; silica-induced gene 81	6677977			O14548
13384754	cytochrome c oxidase subunit VIIb [Mus musculus]	13384754		4502991	OSHU7B
6753498	cytochrome c oxidase, subunit IVa; cytochrome c oxidase, subunit IV [Mus	6753498	S12142		OLHU4
6680986	cytochrome c oxidase, subunit Va [Mus musculus]	6680986	S05495	4758038	OTHU5A
6753500	cytochrome c oxidase, subunit Vb [Mus musculus]	6753500	A39425		OTHU5B
6680988	cytochrome c oxidase, subunit VI a, polypeptide 1; subunit VIaL (liver-type)	6680988	S52088		OGHU6L
6753502	cytochrome c oxidase, subunit VI a, polypeptide 2; subunit VIaH (heart-type)	6753502	COXD_MOUSE		OGHU6A
13385090	cytochrome c oxidase, subunit VIb [Mus musculus]				OGHU6B

16716343	cytochrome c oxidase, subunit VIc [Mus musculus]		S16083		OGHU6C
6753504	cytochrome c oxidase, subunit VIIa 1; cytochrome c oxidase subunit VIIa 1 [Mus	6753504			
31981830	cytochrome c oxidase, subunit VIIa 2; cytochrome c oxidase subunit VIIa 3;	6753506	I48286		
6680991	cytochrome c oxidase, subunit VIIc; cytochrome c oxidase subunit VIIc [Mus	25025041 25053109 25057077 6680991	COXO_MOUSE S10303		OSHU7C
6680993	cytochrome c oxidase, subunit VIIIa; COX VIII-L [Mus musculus]	6680993	COXR_MOUSE	4758044	OSHU8
6680995	cytochrome c oxidase, subunit VIIIb; COX VIII-H [Mus musculus]	6680995	COXQ_MOUSE		
16758308	cytochrome c oxidase, subunit XVII assembly protein homolog [Rattus norvegicus]				Q14061
6681095	cytochrome c, somatic [Mus musculus]	6753560	CCMS CCMST	11128019	CCHU
13385006	cytochrome c-1 [Mus musculus]			21359867	S00680
231896	Cytochrome P450 11B2, mitochondrial precursor (CYPXIB2) (P450C11) (Steroid			13904853	B34181 S11338
20867579	cytochrome P450, 40 (25-hydroxyvitamin D3 1 alpha-hydroxylase) [Mus musculus]	20867579		4503213	
9789921	cytochrome P450, family 11, subfamily a, polypeptide 1; cytochrome P450, 11a,	9789921		4503189	A25922 S14367
7106287	cytochrome P450, family 11, subfamily b, polypeptide 2;	7106287	A41552		
6681097	cytochrome P450, family 17, subfamily a, polypeptide 1; cytochrome P450, 17;				
6753572	cytochrome P450, family 24, subfamily a, polypeptide 1; cytochrome P450, 24;	6753572	S60033		A47436
30578401	cytochrome P450, family 27, subfamily a, polypeptide 1; cytochrome P450, 27;			4503211	A39740
18875324	DAZ associated protein 1 [Mus musculus]	18875324			
17505907	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 isoform 1; DEAD/DEXH helicase DDX31				
20587962	demethyl-Q 7 [Mus musculus]			25453484	
7304999	deoxyguanosine kinase [Mus musculus]	7304999		18426967 18426963 18426969 18426965	JC6142
21281687	deoxyuridine triphosphatase [Mus musculus]			4503423	DUT_HUMAN

19745150	diaphorase 1 (NADH) [Mus musculus]				RDHUB5
6681137	diazepam binding inhibitor; acyl-CoA binding protein; diazepam-binding inhibitor				
6753610	dihydrolipoamide branched chain transacylase E2; BCKAD E2 [Mus musculus]	6753610	S65760	4503265	A32422
31982856	dihydrolipoamide dehydrogenase [Mus musculus]	6681189	107450	4557525	DEHULP
31542559	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase			21630255	S25665 XXHU
21313536	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	21313536			PN0673
9910194	dihydroorotate dehydrogenase [Mus musculus]	9910194		16753223	PC1219
6753676	dihydropyrimidinase-like 2; collapsin response mediator protein 2 [Mus musculus]				
21311901	dimethylglycine dehydrogenase precursor [Mus musculus]			24797151	M2GD_HUMAN
34328271	direct IAP binding protein with low PI [Mus musculus]	12963593		9845297 21070978 21070976	
34328379	D-lactate dehydrogenase [Mus musculus]				
19527228	DNA segment, Chr 10, ERATO Doi 214, expressed [Mus musculus]				
20070420	DNA segment, Chr 10, Johns Hopkins University 81 expressed [Mus musculus]				JC4913 JC4914
25092662	DNA segment, Chr 11, Wayne State University 68, expressed [Mus musculus]				
27552760	DNA segment, Chr 16, Indiana University Medical 22, expressed [Mus musculus]	27552760			
14861848	DNA segment, Chr 7, Roswell Park 2 complex, expressed; androgen regulated gene				
31560085	DnaJ (Hsp40) homolog, subfamily A, member 3 [Mus musculus]	13994155 25053902			
31981810	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase) [Mus	6753612	S38770	4503267	A55723
31981826	electron transferring flavoprotein, alpha polypeptide; Alpha-ETF [Mus musculus]			4503607	A31998
21313290	electron transferring flavoprotein, dehydrogenase [Mus musculus]				Q16134
6679647	endonuclease G [Mus musculus]	6679647		4758270	NUCG_HUMAN
19923857	endothelial cell growth factor 1; thymidine				P19971

	phosphorylase; gliostatin; platelet				
7949037	enoyl coenzyme A hydratase 1, peroxisomal; peroxisomal/mitochondrial dienoyl-CoA	7949037			
29789289	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial [Mus musculus]			12707570	ECHM_HUMAN
7305125	estradiol 17 beta-dehydrogenase 8; 17-beta-hydroxysteroid dehydrogenase 8;				
18079334	ethanol induced 6 [Mus musculus]				
6679078	expressed in non-metastatic cells 2, protein; expressed in non-metastatic cells				
9790123	expressed in non-metastatic cells 4, protein; nucleoside diphosphate kinase	9790123		4826862	NDKM_HUMAN
21618729	Facl5 protein [Mus musculus]				
31560705	fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme A synthetase;				LCFA_HUMAN JX0202
6679765	ferredoxin 1; ADRENODOXIN [Mus musculus]	6679765	S53524	4758352	AXHU
6679767	ferredoxin reductase [Mus musculus]	6679767	S60028	4758354 13435350	A40487
13385780	ferritin heavy chain 3; mitochondrial ferritin [Mus musculus]	13385780			
20452466	ferrochelatase [Mus musculus]	20452466	A37972		A36403
10946808	fibroblast growth factor (acidic) intracellular binding protein; aFGF			7262378	
33469107	folylpolyglutamyl synthetase [Mus musculus]	20824150	S65755	22024385	A46281
9507187	fractured callus expressed transcript 1; Fracture Callus 1; small zinc	9507187			
6679863	frataxin [Mus musculus]	6679863		4503785	
33859554	fumarate hydratase 1 [Mus musculus]	20831568		19743875	UFHUM
20070402	G elongation factor; mitochondrial [Mus musculus]				
12963633	genes associated with retinoid-IFN-induced mortality 19 [Mus musculus]				
6679957	glioblastoma amplified [Mus musculus]				
31982798	glucokinase; hexokinase 4 [Mus musculus]				A46157 C46157
6680027	glutamate dehydrogenase [Mus musculus]	6680027	S16239	27485958 4885281 6912392	A53719 DEHUE
6754036	glutamate oxaloacetate transaminase 2, mitochondrial; mitochondrial aspartate	6754036	S01174	4504069	XNHUDM
31982332	glutamate-ammonia ligase (glutamine synthase);				

	glutamine synthetase [Mus				
31982847	glutamic acid decarboxylase 1 [Mus musculus]				
6679959	glutaryl-Coenzyme A dehydrogenase [Mus musculus]	6679959	GCDH_MOUSE	4503943 7669494	GCDH_HUMAN
6680075	glutathione peroxidase 1; cellular GPx [Mus musculus]	6680075			
13540480	glutathione peroxidase 4; sperm nuclei glutathione peroxidase; phospholipid	13540480		4504107	
34328489	glutathione reductase 1 [Mus musculus]	13775154			
21313138	glutathione S-transferase class kappa [Mus musculus]				
6754092	glutathione transferase zeta 1 (maleylacetoacetate isomerase);				
6679937	glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]				
6680139	glycerol kinase [Mus musculus]				GKP2_HUMAN GLPK_HUMAN
34536827	glycerol-3-phosphate acyltransferase, mitochondrial [Mus musculus]	6680057			
31981769	glycerol-3-phosphate dehydrogenase 2; glycerol phosphate dehydrogenase 1,	6753970		4504085	GPDM_HUMAN
13385454	glycine amidinotransferase (L-arginine:glycine amidinotransferase) [Mus	13385454		4503933	S41734
31560488	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase);	7305083			
20070408	glycine decarboxylase [Mus musculus]				B39521
6806917	GM2 ganglioside activator protein [Mus musculus]				
6680107	granulin; acrogranulin; progranulin; PC cell-derived growth factor [Mus				
12746414	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration);				
13277394	GrpE-like 1, mitochondrial [Mus musculus]	13277394			
29789124	GrpE-like 2, mitochondrial [Mus musculus]	20878923			
3766203	GTP-specific succinyl-CoA synthetase beta subunit [Mus musculus]	20828815			T08812
2137368	H+-transporting two-sector ATPase (EC 3.6.3.14) chain c - mouse (fragments)		S58660		
6680309	heat shock protein 1 (chaperonin 10); heat shock 10 kDa protein 1 (chaperonin	6680309	A55075 CH10_MOUSE		S47532
31981679	heat shock protein 1 (chaperonin); heat shock protein, 60 kDa; heat shock 60kDa		HHMS60		A32800

6680305	heat shock protein 1, beta; heat shock protein, 84 kDa 1; heat shock 90kDa				
31560686	heat shock protein 2; heat shock protein, 70 kDa 2; heat shock 70kDa protein 2				B45871
6754256	heat shock protein, A; heat shock protein cognate 74; heat shock protein, 74	6754256 25024532	A48127	24234688	B48127
6680277	heat-responsive protein 12 [Mus musculus]				
7305137	heme binding protein 1; heme-binding protein; p22 HBP; heme-binding protein 1				
6680175	hemoglobin alpha, adult chain 1; alpha 1 globin [Mus musculus]				
122513	Hemoglobin beta-1 chain (B1) (Major)				
31982300	hemoglobin, beta adult major chain; beta major globin; beta maj [Mus musculus]				
6754206	hexokinase 1; downeast anemia [Mus musculus]		A35244		A31869 JC2025
20982837	holocarboxylase synthetase; biotin- [propriony-Coenzyme A-carboxylase				BPL1_HUMAN
31542950	holocytochrome c synthetase [Mus musculus]	6680181	CCHL_MOUSE		G02133
6754160	HS1 binding protein [Mus musculus]	6754160		13435356	
12963539	HSCO protein [Mus musculus]				
7949047	hydroxyacyl-Coenzyme A dehydrogenase type II; hydroxyacyl-Coenzyme A				
21704100	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A			4504327	JC2109
33859811	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A			20127408	JC2108
31982273	hydroxysteroid (17-beta) dehydrogenase 4; hydroxysteroid 17-beta dehydrogenase				
6680291	hydroxysteroid dehydrogenase-4, delta-3-beta; 3-beta-hydroxysteroid	20874991 23397415 23621517 6680289 6680291 6680293 7305167 25046137	I49762 3BH3_MOUSE 3BH4_MOUSE 3BH5_MOUSE 3BH6_MOUSE 3BH2_MOUSE		DEHUHS DEHUH2
27754071	hypothetical protein 4833421E05Rik [Mus musculus]				
21311867	hypothetical protein D11Ertd99e [Mus musculus]				
21312020	hypothetical protein D4Ertd765e [Mus musculus]				

22122743	hypothetical protein MGC37245 [Mus musculus]				
21313262	inner membrane protein, mitochondrial [Mus musculus]				
22203753	inorganic pyrophosphatase 2 [Mus musculus]				
14916467	inositol polyphosphate-5-phosphatase E; inositol polyphosphate-5-phosphatase, 72	14916467			
27370516	isocitrate dehydrogenase 2 (NADP+), mitochondrial [Mus musculus]	6680343	IDHP_MOUSE	4504575	S57499
18250284	isocitrate dehydrogenase 3 (NAD+) alpha [Mus musculus]			5031777	S55282
6680345	isocitrate dehydrogenase 3 (NAD+), gamma [Mus musculus]	6680345			IDHG_HUMAN
18700024	isocitrate dehydrogenase 3, beta subunit; isocitrate dehydrogenase 3 beta; N14A			5901982	IDHB_HUMAN
9789985	isovaleryl coenzyme A dehydrogenase; isovaleryl dehydrogenase precursor [Mus			4504799	A37033
6754482	keratin complex 1, acidic, gene 18; keratin 18 [Mus musculus]				
6754488	keratin complex 2, basic, gene 6b [Mus musculus]				
19482166	kidney expressed gene 1 [Mus musculus]				
25031694	kinesin family member 1B [Mus musculus]	20850523 25031694			
19527030	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) [Mus musculus]				
6754408	kynurenine aminotransferase II [Mus musculus]				
6680163	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain; hydroxylacyl-Coenzyme A	6680163	JC4210	4885387	JC4879
21703764	lactamase, beta 2 [Mus musculus]				
13507666	lactamase, beta; serine beta lactamase-like protein; mitochondrial ribosomal	13507666			
31981147	leucine aminopeptidase 3; leucine aminopeptidase [Mus musculus]				
9789997	leucine zipper-EF-hand containing transmembrane protein 1; leucine				
21389320	leucine-rich PPR motif-containing protein; leucine rich protein LRP130 [Mus				
23346617	leucyl-tRNA synthetase [Mus musculus]				SYLM_HUMAN
13277380	lipoic acid synthetase [Mus musculus]	13277380			
6678716	low density lipoprotein receptor-related protein 5; low density				

21539585	low molecular mass ubiquinone-binding protein; ubiquinol-cytochrome c reductase	21539585			
31541815	L-specific multifunctional beta-oxdiation protein [Mus musculus]				
6678760	lysophospholipase 1; phospholipase 1a; lysophopholipase 1 [Mus musculus]				
8393739	lysozyme [Mus musculus]				
13654245	major urinary protein 1 [Mus musculus]				
31982186	malate dehydrogenase, mitochondrial [Mus musculus]	6678916	DEMSMM		MDHM_HUMAN
21703972	malic enzyme 2, NAD(+)-dependent, mitochondrial [Mus musculus]			4505145	A39503
31542169	malic enzyme 3, NADP(+)-dependent, mitochondrial [Mus musculus]				S53351
9910434	malonyl-CoA decarboxylase [Mus musculus]			6912498	DCMC_HUMAN
6754760	mature T-cell proliferation 1 [Mus musculus]	6754760			
7305291	metaxin 1; metaxin [Mus musculus]	7305291			MTXN_HUMAN
31543274	metaxin 2 [Mus musculus]	7949084			
31981013	methionine sulfoxide reductase A [Mus musculus]				
31980706	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) [Mus musculus]	12965187			
6678952	methylenetetrahydrofolate dehydrogenase (NAD+ dependent),	6678952	A33267	5729935	DEHUMT
20270275	methylenetetrahydrofolate dehydrogenase 1; C1-tetrahydrofolate synthase [Mus			13699868	A31903
6678970	methylmalonyl-Coenzyme A mutase [Mus musculus]	6678970	S08680	4557767	S40622
31981068	microsomal glutathione S-transferase 1 [Mus musculus]				B28083
30794474	mitchondrial ribosomal protein S7; ribosomal protein, mitochondrial, S7 [Mus				JC7165
19527402	mitochondrial acyl-CoA thioesterase 1 [Mus musculus]	19527402			
13386040	mitochondrial ATP synthase regulatory component factor B [Mus musculus]	13386040			
15011842	mitochondrial capsule selenoprotein; sperm mitochondria associated cysteine-rich	15011842	A37199		MCS_HUMAN
9790055	mitochondrial carrier homolog 2 [Mus musculus]				
28076953	mitochondrial intermediate peptidase [Mus musculus]			5174567	
27502349	mitochondrial matrix processing protease, alpha subunit [Mus musculus]				Q10713
31559891	mitochondrial Rho 1 [Mus musculus]				
22164792	mitochondrial ribosomal protein L12 [Mus musculus]				RM12_HUMAN

16716447	mitochondrial ribosomal protein L27 [Mus musculus]	16716447			
31981470	mitochondrial ribosomal protein L3 [Mus musculus]				R5HUL3 R5HUL3
13385266	mitochondrial ribosomal protein L33 [Mus musculus]				
16716449	mitochondrial ribosomal protein L34 [Mus musculus]	16716449			
31560438	mitochondrial ribosomal protein L39; ribosomal protein, mitochondrial, L5 [Mus	8393021			
13385752	mitochondrial ribosomal protein L49; neighbor of fau 1 [Mus musculus]	13385752			
30519921	mitochondrial ribosomal protein L50 [Mus musculus]				
29789253	mitochondrial ribosomal protein L9 [Mus musculus]	20874698			
17157979	mitochondrial ribosomal protein S11 [Mus musculus]	17157979			
6755360	mitochondrial ribosomal protein S12; ribosomal protein, mitochondrial, S12;	6755360			RT12_HUMAN
13384894	mitochondrial ribosomal protein S14 [Mus musculus]				
13384968	mitochondrial ribosomal protein S15 [Mus musculus]	13384968			
13384844	mitochondrial ribosomal protein S16 [Mus musculus]	13384844			
13384854	mitochondrial ribosomal protein S17 [Mus musculus]	13384854			
31543265	mitochondrial ribosomal protein S2 [Mus musculus]				
17505220	mitochondrial ribosomal protein S21 [Mus musculus]	17505220			
31981257	mitochondrial ribosomal protein S25 [Mus musculus]	13385024			
10181116	mitochondrial ribosomal protein S31; islet mitochondrial antigen, 38 kD [Mus	10181116		5031787	
17157985	mitochondrial ribosomal protein S5 [Mus musculus]				
23956244	mitochondrial ribosomal protein S6 [Mus musculus]	23956244			
19526984	mitochondrial translational initiation factor 2 [Mus musculus]			4505277	A55628
31981857	mitochondrial translational release factor 1 [Mus musculus]			4758744	RF1M_HUMAN
27804325	monoamine oxidase A [Mus musculus]	20983270 27804325	I48342		A36175
19073795	MTO1 [Mus musculus]	19073795			
6754732	myeloperoxidase [Mus musculus]				OPHUM
22003874	N-acetylglutamate synthase; amino-acid N-acetyltransferase [Mus musculus]	22003874			
9055168	N-acylsphingosine amidohydrolase 2; neutral/alkaline; neutral/alkaline			9845267	
13195624	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10 [Mus musculus]				O95299
9506911	NADH dehydrogenase (ubiquinone) 1 alpha	9506911			O15239

	subcomplex, 1 (7.5kD, MWFE); NADH				
31981600	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2; NADH dehydrogenase				O43678
33563266	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4; NADH dehydrogenase		NUML_MOUSE		NUML_HUMAN
13386100	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 [Mus musculus]				NUFM_Human
13385492	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14); NADH dehydrogenase				P56556
12963571	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a); NADH				AAD05427
21312012	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 [Mus musculus]			7657369	NUPM_HUMAN
13384720	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 [Mus musculus]				NUEM_HUMAN
31980802	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1; NADH	27229088			
13385054	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3 [Mus musculus]			4505361	O43676
13385558	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8 [Mus musculus]				JE0382
13386096	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 [Mus musculus]				
27754144	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5; NADH dehydrogenase				O43674
13385322	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 [Mus musculus]				NB8M_HUMAN
29789148	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 [Mus musculus]				
27754007	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1 [Mus musculus]				T00741
13384946	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 [Mus musculus]				O43677
21704020	NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]				S17854
23346461	NADH dehydrogenase (ubiquinone) Fe-S protein 2; NADH-coenzyme Q reductase [Mus				JE0193
6754814	NADH dehydrogenase (ubiquinone) Fe-S protein 4; NADH dehydrogenase (ubiquinone)				NUYM_HUMAN

19527334	NADH dehydrogenase (ubiquinone) Fe-S protein 5; NADH dehydrogenase Fe-S protein				O43920
21312950	NADH dehydrogenase (ubiquinone) Fe-S protein 7 [Mus musculus]				O75251
21450107	NADH dehydrogenase (ubiquinone) Fe-S protein 8 [Mus musculus]				NUIM_HUMAN
19526814	NADH dehydrogenase (ubiquinone) flavoprotein 1; NADH dehydrogenase flavoprotein				A44362
20900762	NADH dehydrogenase (ubiquinone) flavoprotein 2 [Mus musculus]	20900762			A30113
5834954	NADH dehydrogenase subunit 1 [Mus musculus]	5834954	QXMS1M		DNHUN1
5834955	NADH dehydrogenase subunit 2 [Mus musculus]	5834955	QXMS2M		DNHUN2
5834961	NADH dehydrogenase subunit 3 [Mus musculus]	5834961	QXMS3M		DNHUN3
5834963	NADH dehydrogenase subunit 4 [Mus musculus]	5834963	QXMS4M		DNHUN4
5834962	NADH dehydrogenase subunit 4L [Mus musculus]	5834962	QXMS4L		DNHUNL
7770109	NADH dehydrogenase subunit 5 [Mus musculus domesticus]				DNHUN5
5834964	NADH dehydrogenase subunit 5 [Mus musculus]	5834964	QXMS5M		
5834965	NADH dehydrogenase subunit 6 [Mus musculus]	5834965	DEMSN6	27754188	DEHUN6
21314826	NADH:ubiquinone oxidoreductase B15 subunit [Mus musculus]				O95168
21539587	NADH-ubiquinone oxidoreductase B9 subunit; Complex I-B9; CI-B9 [Mus musculus]	21539587			O95167
13507612	NADPH-dependent retinol dehydrogenase/reductase [Mus musculus]				
6754870	neighbor of Cox4 [Mus musculus]			5174615	
200022	neurofilament protein				
9506933	neuronal protein 15.6 [Mus musculus]				
31543330	nicotinamide nucleotide transhydrogenase [Mus musculus]	6679088	S54876		G02257
13385084	NIPSNAP-related protein [Mus musculus]				
12963555	Nit protein 2 [Mus musculus]				
21313484	nitrogen fixation cluster-like [Mus musculus]				
6754846	nitrogen fixation gene, yeast homolog 1; nifS-like (sic) [Mus musculus]	25058437 6754846		26006849	
6679146	nth (endonuclease III)-like 1; thymine glycol DNA glycosylase/AP lyase [Mus	6679146			
31543343	nuclear respiratory factor 1 [Mus musculus]				A54868
27753998	nudix (nucleoside diphosphate linked moiety X)-type	27753998			

	motif 9 [Mus musculus]				
19526960	optic atrophy 1 homolog [Mus musculus]	19526960			T00336
8393866	ornithine aminotransferase [Mus musculus]	8393866	XNMSO	4557809	XNHUO
6679184	ornithine transcarbamylase; sparse fur [Mus musculus]	6679184	OWMS	9257234	OWHU
33563270	oxoglutarate dehydrogenase (lipoamide); alpha-ketoglutarate dehydrogenase [Mus	20853413 25025547	I48884 ODO1_MOUSE		A38234
11528520	p53 apoptosis effector related to Pmp22; p53 apoptosis-associated target [Mus	11528520			
19527310	peptidylprolyl isomerase F (cyclophilin F); peptidyl-prolyl cis-trans isomerase;	19527310			A41581
6680690	peroxiredoxin 3; anti-oxidant protein 1; mitochondrial Trx dependent peroxide	6680690	JQ0064		TDXM_HUMAN
7948999	peroxiredoxin 4; antioxidant enzyme AOE372; Prx IV [Mus musculus]				
6755114	peroxiredoxin 5 precursor; peroxiredoxin 6; peroxisomal membrane protein 20;	6755114		6912238	
18875408	peroxisomal acyl-CoA thioesterase 1 [Mus musculus]				
31980804	peroxisomal trans 2-enoyl CoA reductase; perosisomal 2-enoyl-CoA reductase [Mus				
21450279	PET112-like [Mus musculus]			4758894	GATB_HUMAN
10946832	phorbol-12-myristate-13-acetate-induced protein 1; Noxa protein [Mus musculus]	10946832			
33667036	phosphatidylethanolamine N-methyltransferase [Mus musculus]	7110685			PEMT_HUMAN
6755090	phospholipase A2, group IB, pancreas [Mus musculus]				PSHU
7242175	phospholipase A2, group IIA (platelets, synovial fluid); modifier of Min1;		I48342		
6679369	phospholipase A2, group IVA (cytosolic, calcium-dependent); phospholipase A2,				A39329
7657467	polymerase (DNA directed), gamma 2, accessory subunit; mitochondrial polymerase	7657467			
8567392	polymerase (DNA directed), gamma; polymerase, gamma; Pol gamma; polymerase	8567392	DPOG_MOUSE	4505937	G02750
14780884	polymerase delta interacting protein 38 [Mus musculus]				
6755004	programmed cell death 8; programmed cell death 8 (apoptosis inducing factor);	6755004		4757732 22202629 22202631	
6679299	prohibitin [Mus musculus]				
6755178	proline dehydrogenase [Mus musculus]	25053948			

		6755178			
13385310	propionyl Coenzyme A carboxylase, beta polypeptide [Mus musculus]			4557044	A53020
21450241	propionyl-Coenzyme A carboxylase, alpha polypeptide; propionyl CoA-carboxylase			4557833	A27883
34328185	prosaposin [Mus musculus]				
31980991	protease, serine, 25; serine protease OMI [Mus musculus]	9790135			
6679437	protective protein for beta-galactosidase [Mus musculus]				
6679445	protoporphyrinogen oxidase [Mus musculus]	6679445	S68367	4506001	PPOX_HUMAN
21553115	putative mitochondrial solute carrier [Mus musculus]	21553115			
31543280	putative prostate cancer tumor suppressor; cDNA sequence BC003311 [Mus musculus]				
21450149	pyrroline-5-carboxylate reductase 1; hypothetical protein MGC11688 [Mus				A41770
24025659	pyrroline-5-carboxylate synthetase; glutamate gamma-semialdehyde synthetase [Mus	9790061 24025659			
6679237	pyruvate carboxylase; pyruvate decarboxylase [Mus musculus]	6679237	A47255	11761615 4505627	JC2460
18152793	pyruvate dehydrogenase (lipoamide) beta [Mus musculus]			4505687	DEHUPB
28201978	pyruvate dehydrogenase complex, component X; dihydrolipoamide			4505699	
6679261	pyruvate dehydrogenase E1 alpha 1; pyruvate dehydrogenase E1alpha subunit [Mus	6679263 6679261	S23507 S23506	4505685	DEHUPA DEHUPT
19526816	pyruvate dehydrogenase kinase, isoenzyme 2; pyruvate dehydrogenase 2 [Mus	19526816			I70159
21704122	pyruvate dehydrogenase kinase, isoenzyme 3 [Mus musculus]			4885545	I70160
7305375	pyruvate dehydrogenase kinase, isoenzyme 4; pyruvate dehydrogenase kinase 4 [Mus	7305375		4505693	Q16654
31981562	pyruvate kinase 3 [Mus musculus]				
31543608	reticulon 4 interacting protein 1; NOGO-interacting mitochondrial protein;	18700036			
22267464	retinoic acid inducible protein 3 [Mus musculus]				
6755334	ribonuclease H1 [Mus musculus]				
12584986	ribosomal protein L23 [Mus musculus]				RL23_HUMAN
13384904	ribosomal protein, mitochondrial, S22 [Mus musculus]	13384904			

21311883	RIKEN cDNA 0610007O07 [Mus musculus]				
21311967	RIKEN cDNA 0610008C08 [Mus musculus]				
21536220	RIKEN cDNA 0610008F14 [Mus musculus]				S22348
21313679	RIKEN cDNA 0610009D10 [Mus musculus]				
21312004	RIKEN cDNA 0610009I16 [Mus musculus]				S32482
13385656	RIKEN cDNA 0610010D20 [Mus musculus]				
21311853	RIKEN cDNA 0610012H03 [Mus musculus]				
21313618	RIKEN cDNA 0610041L09 [Mus musculus]				
13385662	RIKEN cDNA 0610042E07 [Mus musculus]				
27754146	RIKEN cDNA 0710001P09 [Mus musculus]				
21312028	RIKEN cDNA 1110006I11 [Mus musculus]				
13384742	RIKEN cDNA 1110018B13 [Mus musculus]				
13384766	RIKEN cDNA 1110021D01 [Mus musculus]				
12963697	RIKEN cDNA 1110025H10 [Mus musculus]				
13385298	RIKEN cDNA 1300002A08 [Mus musculus]	13385298			
21311845	RIKEN cDNA 1300006L01 [Mus musculus]	21311845			
33859744	RIKEN cDNA 1500032D16 [Mus musculus]				NUOM_HUMAN
18859597	RIKEN cDNA 1810004I06 [Mus musculus]				O95298
20876012	RIKEN cDNA 1810020M02 [Mus musculus]				I38079
20897872	RIKEN cDNA 1810058I14 [Mus musculus]				
21624609	RIKEN cDNA 2010012D11 [Mus musculus]				
13385436	RIKEN cDNA 2010100O12 [Mus musculus]				
21312554	RIKEN cDNA 2010107E04 [Mus musculus]	21312554	P56379		68MP_HUMAN
13385042	RIKEN cDNA 2010309E21 [Mus musculus]				
27370092	RIKEN cDNA 2300002G02 [Mus musculus]		PD0441	21359837	I53499 S62767
31980955	RIKEN cDNA 2310005D12 [Mus musculus]				
33859690	RIKEN cDNA 2310005O14 [Mus musculus]				
21312348	RIKEN cDNA 2310020P08 [Mus musculus]	21312348			
13384950	RIKEN cDNA 2310039H17 [Mus musculus]				
21313468	RIKEN cDNA 2310050B20 [Mus musculus]	21313468		21361280	I84606
13385998	RIKEN cDNA 2410002K23 [Mus musculus]	13385998			
31560255	RIKEN cDNA 2410005O16 [Mus musculus]				
27228985	RIKEN cDNA 2410011G03 [Mus musculus]				
30794396	RIKEN cDNA 2410021P16 [Mus musculus]				
21312594	RIKEN cDNA 2610205H19; EST AA108335 [Mus musculus]				
13195670	RIKEN cDNA 2610207I16 [Mus musculus]				
21313080	RIKEN cDNA 2700085E05 [Mus musculus]				
22267456	RIKEN cDNA 2810431B21 [Mus musculus]			5729820	

21312204	RIKEN cDNA 2810435D12 [Mus musculus]			
19526848	RIKEN cDNA 2810484M10 [Mus musculus]			
31541932	RIKEN cDNA 2900026G05 [Mus musculus]		17921985 17921987	
21312153	RIKEN cDNA 2900070E19 [Mus musculus]			
13386046	RIKEN cDNA 3010027G13 [Mus musculus]	13386046		
27229021	RIKEN cDNA 3110001M13 [Mus musculus]		4506865	DHSD_HUMAN
20822904	RIKEN cDNA 3110004O18 [Mus musculus]	20822904 25031957	4758734	O75439
30424808	RIKEN cDNA 3110021G18 [Mus musculus]		15011910	A40141
25072051	RIKEN cDNA 3110065L21 [Mus musculus]			
21312006	RIKEN cDNA 3632410G24 [Mus musculus]	21312006	4759286	UCP4_HUMAN
21311988	RIKEN cDNA 4121402D02 [Mus musculus]			
13385168	RIKEN cDNA 4430402G14 [Mus musculus]			UCRI_HUMAN
31981207	RIKEN cDNA 4432405K22 [Mus musculus]			
19527276	RIKEN cDNA 4921526O06 [Mus musculus]			
21312894	RIKEN cDNA 4930483N21 [Mus musculus]			
30424611	RIKEN cDNA 4932416F07 [Mus musculus]			
13386066	RIKEN cDNA 5730591C18 [Mus musculus]	13386066	4758424	GCHUH
27370158	RIKEN cDNA 6430520C02 [Mus musculus]		5454070	Q92581
28077029	RIKEN cDNA 9130022B02 [Mus musculus]		4758886	S69546
13386062	RIKEN cDNA 9430083G14 [Mus musculus]			
27369922	RIKEN cDNA 9630020E24 [Mus musculus]			
27370474	RIKEN cDNA 9630038C02 [Mus musculus]			GABT_HUMAN
22122359	RIKEN cDNA A330009E03 [Mus musculus]		5031709	
21450203	RIKEN cDNA A330035H04; long-chain acyl-CoA synthetase [Mus musculus]			
21704204	RIKEN cDNA A930031O08 [Mus musculus]		4759068	
34328415	RIKEN cDNA A930035F14 gene [Mus musculus]			PUT2_HUMAN
21311919	RIKEN cDNA B430104H02 [Mus musculus]			
27369966	RIKEN cDNA D530020C15 [Mus musculus]		4505689	I55465
27369748	RIKEN cDNA D630032B01 [Mus musculus]			
19527384	RIKEN cDNA D930010J01 [Mus musculus]			
28893421	RIKEN cDNA E430012M05 gene [Mus musculus]			
22267442	RIKubiquinol cytochrome c reductase core protein 2 [Mus musculus]	22267442		A32629
31982720	SA rat hypertension-associated homolog [Mus musculus]			
20149748	sarcosine dehydrogenase [Mus musculus]			

15030102	Sdha protein [Mus musculus]			4759080	
984837	secretory group II phospholipase A2				PSHUYF
6677943	serine hydroxymethyl transferase 1 (soluble) [Mus musculus]				
21312298	serine hydroxymethyl transferase 2 (mitochondrial) [Mus musculus]			19923315	B46746
15147224	sideroflexin 1; flexed tail [Mus musculus]	15147224 16716499			
31981486	sideroflexin 2 [Mus musculus]	16716497			
16716501	sideroflexin 4 [Mus musculus]	16716501			
20895140	similar to aminomethyltransferase [Mus musculus]			4502083	I54192
25052664	similar to Cytochrome c oxidase assembly protein COX11, mitochondrial precursor			4758034	COXZ_HUMAN
28478945	similar to Glutaminase, kidney isoform, mitochondrial precursor (GLS)			20336214	
28526374	similar to NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) complex I 13K-A chain		NUMM_MOUSE		O75380
20825073	similar to NADH-ubiquinone oxidoreductase B17 subunit (Complex I-B17) (CI-B17)				O95139
20916351	single-stranded DNA binding protein 1 [Mus musculus]			4507231	JN0568
27229283	small fragment nuclease [Mus musculus]				T14770
13540709	sodium channel, voltage-gated, type 1, alpha polypeptide; sodium channel,				
6678001	solute carrier family 1, member 1 [Mus musculus]		EAT3_MOUSE		
7106409	solute carrier family 1, member 2; glial high affinity glutamate transporter				EAT2_HUMAN
24233554	solute carrier family 1, member 3; glial high affinity glutamate transporter				JC2084
9790129	solute carrier family 22 member 4; solute carrier family (organic cation				
28544699	solute carrier family 25 (mitochondrial carrier), member 18 [Mus musculus]	20342202 20831383 25022813			
6755544	solute carrier family 25 (mitochondrial carrier, brain), member 14; solute	6755544 13385736		4507009 13259543	O95258
7657583	solute carrier family 25 (mitochondrial carrier; adenine nucleotide	7657583		21361103 7657581	Y14494
7305501	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter),	7305501			

6754952	solute carrier family 25 (mitochondrial carrier; ornithine transporter), member	6754952			
21312994	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member	21312994			A56650
29789024	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein),	20902883			
19526818	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3;	19526818		6031192 4505775	A53737 B53737
21313024	solute carrier family 25 (mitochondrial deoxynucleotide carrier), member 19 [Mus	21313024			
23943838	solute carrier family 25, member 1; DiGeorge syndrome gene j; solute carrier	20346164 20891945 23943838 25025453			TXTP_HUMAN
22094075	solute carrier family 25, member 5; adenine nucleotide translocator 2,	20863388 22094075	S31814 S37210	4502097	A29132 A44778 S03894
6755548	solute carrier family 27 (fatty acid transporter), member 2; very long-chain				
31981977	spastic paraplegia 7 homolog; paraplegin; spastic paraplegia 7 [Mus musculus]			4507173	
13507712	sphingosine-1-phosphate phosphatase 1; sphingosine-1-phosphate phosphatase [Mus	13507712			
10946984	START domain containing 3; es64 protein; steroidogenic acute regulatory protein				S60682
31543776	steroidogenic acute regulatory protein [Mus musculus]	19920319	A55455	4507251	I38896
28545662	sterol carrier protein 2, liver [Mus musculus]	20841062	JU0157 A40015		B40407
12963591	stomatin-like protein 2 [Mus musculus]				
13384690	succinate dehydrogenase complex, subunit C, integral membrane protein [Mus	13384690		4506863	
20908717	succinate dehydrogenase Fp subunit [Mus musculus]				JX0336
34328286	succinate dehydrogenase Ip subunit [Mus musculus]		PT0094	9257242	A34045
9845299	succinate-CoA ligase, GDP-forming, alpha subunit; succinyl-CoA synthetase [Mus	9845299		11321581	P53597
31981549	sulfide quinone reductase-like; flavo-binding protein; sulfide				
30424565	sulfite oxidase [Mus musculus]				S55874
31980762	superoxide dismutase 2, mitochondrial; manganese SOD; manganese superoxide	7305511	I57023	10835187	DSHUN
31088872	suppressor of var1, 3-like 1 [Mus musculus]			4507315	

7363455	surfeit gene 1 [Mus musculus]	7363455	B25394		S57749
6678179	syntaxin binding protein 1; unc18 homolog (C. elegans); UNC-18 homolog (C.				
15809030	synuclein, beta [Mus musculus]				
31442416	tafazzin [Mus musculus]				TFZ_HUMAN
13384998	tetratricopeptide repeat domain 11 [Mus musculus]				
13385260	thioesterase superfamily member 2 [Mus musculus]				
6755911	thioredoxin 1; thioredoxin [Mus musculus]				
9903609	thioredoxin 2; thioredoxin nuclear gene encoding mitochondrial protein;	9903609			THI2_HUMAN
7305603	thioredoxin reductase 2; human EST 573010; EST AA118373; TR beta [Mus musculus]	7305603		22035672 22035670 22035668	
6678449	thiosulfate sulfurtransferase, mitochondrial [Mus musculus]	6678449	THTR_MOUSE		
6678357	thymidine kinase 1 [Mus musculus]				KIHUT
10835111	thymidine kinase 2, mitochondrial; thymidine kinase 2 [Mus musculus]	10835111		10281330	
6678417	thyroid peroxidase [Mus musculus]				OPHUIT
6678303	transcription factor A, mitochondrial [Mus musculus]	6678303			JC1496
26006865	transcription termination factor, mitochondrial-like [Mus musculus]			5902010	
7305573	translocase of inner mitochondrial membrane 10 homolog [Mus musculus]				
7305575	translocase of inner mitochondrial membrane 13 homolog a [Mus musculus]				
12025536	translocase of inner mitochondrial membrane 23 homolog [Mus musculus]	12025536			
7305577	translocase of inner mitochondrial membrane 8 homolog a [Mus musculus]	7305577			U66035
7305579	translocase of inner mitochondrial membrane 8 homolog b [Mus musculus]				
7305581	translocase of inner mitochondrial membrane 9 homolog [Mus musculus]				
13324686	translocase of outer mitochondrial membrane 20 homolog [Mus musculus]				S66619
8394480	translocase of outer mitochondrial membrane 40 homolog; mitochondrial outer	8394480			
19705563	translocator of inner mitochondrial membrane 44 [Mus	19705563			IM44_HUMAN

	musculus]	25024735 25070554			
33468943	translocator of inner mitochondrial membrane a; translocator of inner	25030423 20910363			IM17_HUMAN
20270297	trimethyllysine hydroxylase, epsilon; epsilon-trimethyllysine 2-oxoglutarate	20270297			
33859692	tRNA nucleotidyl transferase, CCA-adding, 1; tRNA adenylyltransferase,	20829254			
16716569	trypsinogen 16 [Mus musculus]				
31543952	tryptophanyl tRNA synthetase 2 (mitochondrial) [Mus musculus]	21362271		7710154	
6678469	tubulin, alpha 6; tubulin alpha 6 [Mus musculus]				
12963615	tubulin, beta 3 [Mus musculus]				
31981925	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon				143E_HUMAN
6756041	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta		JC5384		PSHUAM
22122769	tyrosine aminotransferase [Mus musculus]				S10887
21539599	ubiquinol cytochrome c reductase hinge protein; mitochondrial hinge protein;	21539599			S00219
13385726	ubiquinol-cytochrome c reductase binding protein [Mus musculus]	13385726			A32450
13384794	ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	13384794 25030421			A48043
13385112	ubiquinol-cytochrome c reductase subunit [Mus musculus]				
21070950	ubiquitin C; polyubiquitin C [Mus musculus]				
6678497	uncoupling protein 1, mitochondrial; uncoupling protein, mitochondrial [Mus	6678497	A31106	11225256	A60793
31543920	uncoupling protein 2, mitochondrial [Mus musculus]	6755933			UCP2_HUMAN
6678495	uncoupling protein 3, mitochondrial [Mus musculus]	6678495			
12836291	unnamed protein product [Mus musculus]			21396489	S42366
12832533	unnamed protein product [Mus musculus]				O75489
12832556	unnamed protein product [Mus musculus]				O96000
26343407	unnamed protein product [Mus musculus]			14790138	
26346947	unnamed protein product [Mus musculus]				S63453
12834221	unnamed protein product [Mus musculus]				
12834781	unnamed protein product [Mus musculus]				
12835668	unnamed protein product [Mus musculus]				

12835711	unnamed protein product [Mus musculus]				
12836533	unnamed protein product [Mus musculus]				
12836798	unnamed protein product [Mus musculus]				
12841269	unnamed protein product [Mus musculus]				
12842244	unnamed protein product [Mus musculus]				
12845262	unnamed protein product [Mus musculus]				
12846164	unnamed protein product [Mus musculus]				
12855263	unnamed protein product [Mus musculus]				
12855887	unnamed protein product [Mus musculus]				
12860092	unnamed protein product [Mus musculus]				
12861374	unnamed protein product [Mus musculus]				
26363071	unnamed protein product [Mus musculus]				
13128954	upregulated during skeletal muscle growth 5 [Mus musculus]				
6755941	uracil-DNA glycosylase [Mus musculus]	6755941	UNG_MOUSE		A60472
6678509	urate oxidase; uricase [Mus musculus]				
6678519	uroporphyrinogen III synthase; URO-synthase; uroporphyrinogen-III synthase;				A40483
34328204	valyl-tRNA synthetase 2 [Mus musculus]				
31559883	very-long-chain acyl-CoA dehydrogenase VLCAD homolog [Mus musculus]				
6755963	voltage-dependent anion channel 1 [Mus musculus]	6755963		4507879	MMHUP3
6755965	voltage-dependent anion channel 2 [Mus musculus]	6755965			B44422
6755967	voltage-dependent anion channel 3 [Mus musculus]				S59547
31980962	WW-domain oxidoreductase [Mus musculus]	9625012			

Table 5. Tiers of evidence supporting the 163 newly identified mito-A proteins. The protein accession and description of each of the newly identified mito-A proteins is shown along with each of the GenPept accessions of the proteins identified in the tissue proteomics experiments. For each mito-A protein cluster, the top scoring human homologue from the study, the PSORT targeting prediction, the mitochondrial neighborhood index, and the results of epitope tagging experiments, when available, are shown. For the BLASTP analyses, only the top scoring match from the study by MitoKor is provided, using a threshold of $E<1x10^{-5}$. The PSORT targeting prediction and probability were obtained for the exemplar protein sequence. The neighborhood indices (N_{50}, N_{100}, and N_{250}) are provided, when available. Due to probe-set duplicity, some proteins have more than one corresponding probe-set, and others have no probe-set. An $N_{50}\geq6$, $N_{100}\geq10$, and $N_{250}\geq19$ each correspond to a nominal P=0.001, assuming that mito-A genes are randomly distributed in expression space. In the final column, the subcellular localization based on immunofluorescence microscopy is indicated for the five proteins shown in Figure 2

Exemplar Protein for the Cluster		Proteomics				BLASTP against MitoKor		
Accession	Description	Liver	Brain	Heart	Kidney	Match	Score	Expect
21313679	RIKEN cDNA 0610009D10 [Mus musculus]	12832313 220904	12832313	12832313	12832313 220904	5453559	283	1.00E-78
21312594	RIKEN cDNA 2610205H19; EST AA108335 [Mus musculus]	12848292 730248	12848292	12848292 730248	730248	7661602	249	2.00E-68
13128954	upregulated during skeletal muscle growth 5 [Mus musculus]	12842476 6851054	13128954 12842476	12842476	12842476	14249376	105	2.00E-25
6671622	B-cell receptor-associated protein 37; repressor of estrogen receptor activity	6005854 6671622	6005854	6005854	6005854	6005854	568	e-164
27228985	RIKEN cDNA 2410011G03 [Mus musculus]	10092657 13384978	13384978	13384978	13384978	10092657	297	6.00E-83
13384766	RIKEN cDNA 1110021D01 [Mus musculus]	13384766 12842709	13384766	12842709	13384766	NO MATCH		
19354491	1110020P15Rik protein [Mus musculus]	136701	9297078 136701 3891857 6094658	136701	136701	9297078	116	5.00E-29

9789997	leucine zipper-EF-hand containing transmembrane protein 1; leucine	9789997	9789997	9789997	9789997	6912482	1209	0
13385260	thioesterase superfamily member 2 [Mus musculus]	13385260	13385260	13385260	13385260	4210351	209	2.00E-56
19527228	DNA segment, Chr 10, ERATO Doi 214, expressed [Mus musculus]	8923930	8923930	8923930	8923930	8923930	206	1.00E-55
12842244	unnamed protein product [Mus musculus]	12842244	12842244	12842244	12842244	17455445	210	1.00E-56
12963633	genes associated with retinoid-IFN-induced mortality 19 [Mus musculus]	12963633 12833386 12833406	12963633 12833406	12963633 12833386 12833406	12963633 12833386 7705734 12833406	12005918	260	1.00E-71
6679066	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1	6679066 12850319	4505399 6679066 12850319	6679066	12803135 4505399 6679066 12850319	4503937	429	e-122
7949047	hydroxyacyl-Coenzyme A dehydrogenase type II; hydroxyacyl-Coenzyme A	7949047 12850643 13182962 3183025	7949047	7949047 12850643 13182962	7949047 13182962	14764202	421	e-120
23956104	adenylate kinase 3 alpha-like; adenylate kinase 3 alpha like [Mus musculus]	12837588 6978479 6707707		12837588	12836369 12837588 6707707	12735226	428	e-122
20149748	sarcosine dehydrogenase [Mus musculus]	13097441 3283373 4928113		13097441	13097441 3283373	13775158	185	3.00E-48
31980804	peroxisomal trans 2-enoyl CoA reductase; perosisomal 2-enoyl-CoA reductase [Mus	12963715 13506791		12963715	12845570 12963715 13506791	4503301	143	5.00E-36
21624609	RIKEN cDNA 2010012D11 [Mus musculus]	12833236 12857234		12857234	12833236 4757862	NO MATCH		
21389320	leucine-rich PPR motif-containing protein; leucine rich protein LRP130 [Mus	12851540		1730078 12851540	12851540	1730078	1938	0
21313618	RIKEN cDNA 0610041L09 [Mus musculus]		12839842	12832121 8923390	12832121	8923390	411	e-117

30424611	RIKEN cDNA 4932416F07 [Mus musculus]	7513021		7513021	7513021	NO MATCH		
27369748	RIKEN cDNA D630032B01 [Mus musculus]	1711535	1711535		1711535	13630862	608	e-176
34328379	D-lactate dehydrogenase [Mus musculus]	12852638		12852638	12852638	NO MATCH		
19526848	RIKEN cDNA 2810484M10 [Mus musculus]	3747107	3747107		3747107	NO MATCH		
19482166	kidney expressed gene 1 [Mus musculus]	12832283		12832283	12832283	NO MATCH		
6754092	glutathione transferase zeta 1 (maleylacetoacetate isomerase);	6754092		6754092	6754092	NO MATCH		
21312153	RIKEN cDNA 2900070E19 [Mus musculus]	12851249	12851249		12851249	12735430	101	6.00E-24
13384742	RIKEN cDNA 1110018B13 [Mus musculus]		13384742	13384742	13384742	15150811	175	2.00E-46
12835711	unnamed protein product [Mus musculus]	12835711		12835711	12835711	14211923	290	1.00E-80
13507612	NADPH-dependent retinol dehydrogenase/reductase [Mus musculus]	13097510		13507612 12832859	11559414	12804319	51	1.00E-08
34328185	prosaposin [Mus musculus]	7242191 91281 557967 6981424 881390 9438805 1360694 11386147	6981424 881390		91281 881390	NO MATCH		
13540709	sodium channel, voltage-gated, type 1, alpha polypeptide; sodium channel,	13540709		13540709		NO MATCH		
21070950	ubiquitin C; polyubiquitin C [Mus musculus]	9790277	9790277 1050930 136670			11024714	449	e-128

31980703	aminoadipate-semialdehyde synthase; lysine oxoglutarate reductase, saccharopine	13529344 8393730		13027640 13529344 4938304 8393730	NO MATCH		
6753272	catalase; catalase 1 [Mus musculus]	6753272		115704 6753272 115698 229299	NO MATCH		
31541815	L-specific multifunctional beta-oxdiation protein [Mus musculus]	12836375		1706569 11434714 12836375	14730775	293	9.00E-81
7656855	acyl-Coenzyme A oxidase 1, palmitoyl; acyl-Coenzyme A oxidase; Acyl-CoA oxidase	6429156 7656855		6429156 7656855	13653049	55	3.00E-09
9790129	solute carrier family 22 member 4; solute carrier family (organic cation	9790129	9790129		NO MATCH		
6680756	ATPase, H+ transporting, V1 subunit E isoform 1; ATPase, H+ transporting		6680756 313014	6680756	NO MATCH		
201006	Cu/Zn-superoxide dismutase	201006		134614 1351080 226471 7433299	1237406	266	2.00E-73
9055178	brain protein 44-like; apoptosis-regulating basic protein [Mus musculus]	12852262 7706369 9055178	12852262 12852283		14755192	216	1.00E-58
7305125	estradiol 17 beta-dehydrogenase 8; 17-beta-hydroxysteroid dehydrogenase 8;	7305125 1103844		1103844	14041699	418	e-119
12963539	HSCO protein [Mus musculus]	12832819		12963539 12832819	4885389	70	3.00E-14
21312020	hypothetical protein D4Ertd765e [Mus musculus]	12836667		12836667 12847441	4502327	300	2.00E-83
12963697	RIKEN cDNA 1110025H10 [Mus musculus]	12963697		12963697 12834868	NO MATCH		

6681137	diazepam binding inhibitor; acyl-CoA binding protein; diazepam-binding inhibitor	13937379 6681137			13937379	12052810	76	1.00E-16
13507620	ankycorbin; NORPEG-like protein [Mus musculus]		13507620	13507620		14771689	100	2.00E-22
16905127	butyryl Coenzyme A synthetase 1; acetyl-Coenzyme A synthetase 3 [Mus musculus]	5019275			15487300	6996429	137	6.00E-34
22122743	hypothetical protein MGC37245 [Mus musculus]			3127193	3127193	6996429	123	7.00E-30
22203753	inorganic pyrophosphatase 2 [Mus musculus]	12834464			12834464	11526789	525	e-151
13385656	RIKEN cDNA 0610010D20 [Mus musculus]	13385656 12846589			13385656	NO MATCH		
33859690	RIKEN cDNA 2310005O14 [Mus musculus]	3252827		3252827		3252827	578	e-167
21311919	RIKEN cDNA B430104H02 [Mus musculus]	7705608			12836847	NO MATCH		
21703764	lactamase, beta 2 [Mus musculus]	13278495			13278495	NO MATCH		
13385662	RIKEN cDNA 0610042E07 [Mus musculus]	13376007			13376007	NO MATCH		
10946936	adenylate kinase 1; cytosolic adenylate kinase [Mus musculus]			729865	125152	4502011	347	6.00E-98
6680277	heat-responsive protein 12 [Mus musculus]	6680277			6680277	5032215	226	3.00E-61
21312028	RIKEN cDNA 1110006I11 [Mus musculus]	12834206			12834206	NO MATCH		
13385436	RIKEN cDNA 2010100O12 [Mus musculus]	13385436			13385436	NO MATCH		
12836533	unnamed protein product [Mus musculus]			12836533	12836533	NO MATCH		
6677943	serine hydroxymethyl transferase 1 (soluble) [Mus musculus]	232178	232178			NO MATCH		
12834221	unnamed protein product [Mus musculus]	12834221			12834221	14211939	283	1.00E-78
6681097	cytochrome P450, family 17, subfamily a, polypeptide 1; cytochrome P450, 17;	2148066		2506241		NO MATCH		

6753676	dihydropyrimidinase-like 2; collapsin response mediator protein 2 [Mus musculus]		1351260 3122018	13645618	825	0
79937	glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	6679937 229279 65987 9838358		7669492	637	0
13435924	aldolase 3, C isoform [Mus musculus]		11231095 12836758	312137	716	0
31982332	glutamate-ammonia ligase (glutamine synthase); glutamine synthetase [Mus		2144562 4504027 6680023 2144563	NO MATCH		
6681079	cathepsin B preproprotein [Mus musculus]	227293 6681079 12832453 3929817		NO MATCH		
13654245	major urinary protein 1 [Mus musculus]	13276755 127531		NO MATCH		
27369922	RIKEN cDNA 9630020E24 [Mus musculus]		12052944	7513022	108	4.00E-25
6680305	heat shock protein 1, beta; heat shock protein, 84 kDa 1; heat shock 90kDa		1170383 3642691	72222	1415	0
31982847	glutamic acid decarboxylase 1 [Mus musculus]	416884 1082397 1352214		NO MATCH		
31981147	leucine aminopeptidase 3; leucine aminopeptidase [Mus musculus]	12845995 7705688 12833083		NO MATCH		
6753556	cathepsin D [Mus musculus]	6753556 115720 8886526		4503143	697	0
31560731	ATPase, H+ transporting, V1 subunit A, isoform 1; ATPase, H+ transporting,		108733 6680752	114549	116	1.00E-27

6680107	granulin; acrogranulin; progranulin; PC cell-derived growth factor [Mus	191767 6680107				1335064	57	8.00E-10
31982720	SA rat hypertension-associated homolog [Mus musculus]				2135243 5032065	6996429	161	2.00E-41
6753448	ceroid-lipofuscinosis, neuronal 2 [Mus musculus]	13786206 6753448				NO MATCH		
6754408	kynurenine aminotransferase II [Mus musculus]				6754408 8393641	NO MATCH		
14780884	polymerase delta interacting protein 38 [Mus musculus]	7661672 12834531				NO MATCH		
31543280	putative prostate cancer tumor suppressor; cDNA sequence BC003311 [Mus musculus]				1353701	NO MATCH		
12963555	Nit protein 2 [Mus musculus]				12963555 12835765	NO MATCH		
27754146	RIKEN cDNA 0710001P09 [Mus musculus]		12853604 12839157			14150134	301	8.00E-84
27754071	hypothetical protein 4833421E05Rik [Mus musculus]				12837739 12847330	NO MATCH		
31981013	methionine sulfoxide reductase A [Mus musculus]				12844852 12857997	NO MATCH		
13384998	tetratricopeptide repeat domain 11 [Mus musculus]				13384998 7705632	14747249	288	4.00E-80
9506933	neuronal protein 15.6 [Mus musculus]			9506933		13938442	220	8.00E-60
21311867	hypothetical protein D11Ertd99e [Mus musculus]				12859025 7661732	7661732	174	4.00E-46
6678716	low density lipoprotein receptor-related protein 5; low density			7513560		1335064	53	3.00E-08
34328204	valyl-tRNA synthetase 2 [Mus musculus]				6755953	7678804	191	5.00E-50
30794396	RIKEN cDNA 2410021P16 [Mus musculus]				12846107	13653049	141	6.00E-35
31982273	hydroxysteroid (17-beta) dehydrogenase 4; hydroxysteroid 17-beta dehydrogenase				12836373	14041699	100	1.00E-22

21450203	RIKEN cDNA A330035H04; long-chain acyl-CoA synthetase [Mus musculus]	4336604				11276083	981	0
31981207	RIKEN cDNA 4432405K22 [Mus musculus]			12232451		NO MATCH		
6680612	ATP-binding cassette, sub-family D, member 3; peroxisomal membrane protein, 70				105161	NO MATCH		
31559883	very-long-chain acyl-CoA dehydrogenase VLCAD homolog [Mus musculus]		12849737			10436258	1056	0
6755548	solute carrier family 27 (fatty acid transporter), member 2; very long-chain				3087820	15559516	61	4.00E-11
21311988	RIKEN cDNA 4121402D02 [Mus musculus]				12853862	NO MATCH		
6678179	syntaxin binding protein 1; unc18 homolog (C. elegans); UNC-18 homolog (C.		6981602			NO MATCH		
30725845	AAA-ATPase TOB3 [Mus musculus]				13752413	11095436	57	8.00E-10
31981562	pyruvate kinase 3 [Mus musculus]		6755074			107554	1032	0
11968160	3-oxoacid CoA transferase 2A; haploid germ cell specific succinyl CoA				11968160	4557817	709	0
20070418	aldehyde dehydrogenase family 7, member A1; aldehyde dehydrogenase 7 family,	12836597				12803387	953	0
13195670	RIKEN cDNA 2610207I16 [Mus musculus]	13195670				14150062	374	e-105
19527030	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) [Mus musculus]	11024672				NO MATCH		
6679437	protective protein for beta-galactosidase [Mus musculus]				12860234	NO MATCH		
31981549	sulfide quinone reductase-like; flavo-binding protein; sulfide				12842384	10864011	812	0
6753074	adaptor protein complex AP-2, mu1; adaptor-related protein complex AP-2, mu1;		6753074			NO MATCH		
28893421	RIKEN cDNA E430012M05 gene [Mus musculus]		12654733			NO MATCH		

19527276	RIKEN cDNA 4921526O06 [Mus musculus]				7705586	NO MATCH		
27659728	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase);	13384704				NO MATCH		
14861848	DNA segment, Chr 7, Roswell Park 2 complex, expressed; androgen regulated gene				14861848	NO MATCH		
12963591	stomatin-like protein 2 [Mus musculus]	12963591				7513076	603	e-174
6753058	annexin A10 [Mus musculus]		6274497			4826643	271	1.00E-74
12834781	unnamed protein product [Mus musculus]	12834781 12856019				NO MATCH		
18875408	peroxisomal acyl-CoA thioesterase 1 [Mus musculus]				4885565	NO MATCH		
11968166	cathepsin Z preproprotein; cathepsin Z precursor; cathepsin X [Mus musculus]	12835144				NO MATCH		
31560255	RIKEN cDNA 2410005O16 [Mus musculus]	13384896				16307164	511	e-147
6678509	urate oxidase; uricase [Mus musculus]	6678509				NO MATCH		
31980955	RIKEN cDNA 2310005D12 [Mus musculus]	13195640				12654521	474	e-136
21313080	RIKEN cDNA 2700085E05 [Mus musculus]	12840992				NO MATCH		
6755334	ribonuclease H1 [Mus musculus]				3004981	NO MATCH		
6679957	glioblastoma amplified [Mus musculus]			6679957		4503937	540	e-156
7948999	peroxiredoxin 4; antioxidant enzyme AOE372; Prx IV [Mus musculus]	12407849				14768743	464	e-133
13386062	RIKEN cDNA 9430083G14 [Mus musculus]				13386062	17461670	414	e-118
21311883	RIKEN cDNA 0610007O07 [Mus musculus]	12858578				NO MATCH		

21312204	RIKEN cDNA 2810435D12 [Mus musculus]	12850490				13654294	400	e-113
13385084	NIPSNAP-related protein [Mus musculus]	13385084				14743031	416	e-118
19527384	RIKEN cDNA D930010J01 [Mus musculus]			12653017		12653017	458	e-131
6678760	lysophospholipase 1; phospholipase 1a; lysophopholipase 1 [Mus musculus]				6678760	14747375	249	3.00E-68
21312894	RIKEN cDNA 4930483N21 [Mus musculus]		12854111			8922629	56	5.00E-10
21313138	glutathione S-transferase class kappa [Mus musculus]	12832811				7705704	350	1.00E-98
21311853	RIKEN cDNA 0610012H03 [Mus musculus]				12832709	NO MATCH		
21311967	RIKEN cDNA 0610008C08 [Mus musculus]				12832215	12001992	287	1.00E-79
13384950	RIKEN cDNA 2310039H17 [Mus musculus]			13384950		NO MATCH		
12746414	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration);	7670387				NO MATCH		
6806917	GM2 ganglioside activator protein [Mus musculus]				479912	NO MATCH		
7305137	heme binding protein 1; heme-binding protein; p22 HBP; heme-binding protein 1				4886904	NO MATCH		
25092662	DNA segment, Chr 11, Wayne State University 68, expressed [Mus musculus]				13386160	NO MATCH		
21313484	nitrogen fixation cluster-like [Mus musculus]				12843563	NO MATCH		
18079334	ethanol induced 6 [Mus musculus]				12834045	NO MATCH		
6679078	expressed in non-metastatic cells 2, protein; expressed in non-metastatic cells		13929192			1421609	311	5.00E-87

13385042	RIKEN cDNA 2010309E21 [Mus musculus]	13385042				NO MATCH		
15809030	synuclein, beta [Mus musculus]		464424			NO MATCH		
6755911	thioredoxin 1; thioredoxin [Mus musculus]				12841560	14740403	196	1.00E-52
20841184	acetyl-Coenzyme A carboxylase beta [Mus musculus]			3080546		NO MATCH		
25072051	RIKEN cDNA 3110065L21 [Mus musculus]		4758012			NO MATCH		
20071710	2010002H18Rik protein [Mus musculus]			7678804		7678804	954	0
200022	neurofilament protein				205686	14742600	301	4.00E-83
21618729	Facl5 protein [Mus musculus]				10800088	7706449	1193	0
17505907	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 isoform 1; DEAD/DEXH helicase DDX31			12232467		NO MATCH		
12855263	unnamed protein product [Mus musculus]				12855263	NO MATCH		
12855887	unnamed protein product [Mus musculus]	12855887				NO MATCH		
26363071	unnamed protein product [Mus musculus]		12843537			14771689	107	4.00E-25
12836798	unnamed protein product [Mus musculus]			12836798		NO MATCH		
12846164	unnamed protein product [Mus musculus]	12846164				NO MATCH		
12845262	unnamed protein product [Mus musculus]				12845262	14770968	326	3.00E-91
12860092	unnamed protein product [Mus musculus]	12860092				11545863	316	2.00E-88
20897872	RIKEN cDNA 1810058I14 [Mus musculus]				12841742	NO MATCH		
12841269	unnamed protein product [Mus musculus]	12841269				NO MATCH		
12835668	unnamed protein product [Mus musculus]	12835668				NO MATCH		
12861374	unnamed protein product [Mus musculus]				12861374	NO MATCH		
22267464	retinoic acid inducible protein 3 [Mus musculus]				13436248	NO MATCH		

Table 6. The ordered gene list for Figures 7 and 8. The list is ordered based on Figures 7 and 8, and each row includes the corresponding Affymetrix probe-set ID, protein accession, the gene symbol, evidence (white, previously annotated; gray, detected in proteomics; black, previously annotated and detected in proteomics), the module annotation, and the description

Row	Probe Set	Protein Exemplar	Description	Symbol
1	104560_at	21553115	putative mitochondrial solute carrier [Mus musculus]	Mrs3/4-pending
2	97868_at	31560085	DnaJ (Hsp40) homolog, subfamily A, member 3 [Mus musculus]	Dnaja3
3	95608_at	6681079	cathepsin B preproprotein [Mus musculus]	Ctsb
4	95359_at	6680305	heat shock protein 1, beta; heat shock protein, 84 kDa 1; heat shock 90kDa	Hspcb
5	104103_at	30725845	AAA-ATPase TOB3 [Mus musculus]	TOB3
6	96861_at	30519921	mitochondrial ribosomal protein L50 [Mus musculus]	D4Wsu125e
7	95438_at	31559891	mitochondrial Rho 1 [Mus musculus]	2210403N23Rik
8	95431_at	27552760	DNA segment, Chr 16, Indiana University Medical 22, expressed [Mus musculus]	D16Ium22e
9	93808_at	6671688	carbonyl reductase 2; lung carbonyl reductase [Mus musculus]	Cbr2
10	103044_g_at	6754760	mature T-cell proliferation 1 [Mus musculus]	Mtcp1
11	104747_at	6678001	solute carrier family 1, member 1 [Mus musculus]	Slc1a1
12	104748_s_at	6678001	solute carrier family 1, member 1 [Mus musculus]	Slc1a1
13	104700_at	6677943	serine hydroxymethyl transferase 1 (soluble) [Mus musculus]	Shmt1
14	98470_at	6755544	solute carrier family 25 (mitochondrial carrier, brain), member 14; solute	Slc25a14
15	97935_at	21311988	RIKEN cDNA 4121402D02 [Mus musculus]	---
16	103061_at	31982847	glutamic acid decarboxylase 1 [Mus musculus]	Gad1
17	95432_f_at	27552760	DNA segment, Chr 16, Indiana University Medical 22, expressed [Mus musculus]	D16Ium22e
18	95746_at	31560731	ATPase, H+ transporting, V1 subunit A, isoform 1; ATPase, H+ transporting,	B230379M23Rik
19	93126_at	10946574	creatine kinase, brain [Mus musculus]	Ckb
20	97983_s_at	6678179	syntaxin binding protein 1; unc18 homolog (C. elegans); UNC-18 homolog (C.	Stxbp1
21	100510_at	15809030	synuclein, beta [Mus musculus]	Sncb
22	93362_at	6753074	adaptor protein complex AP-2, mu1; adaptor-related protein complex AP-2, mu1;	Ap2m1
23	97544_at	6756041	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta	Ywhaz

24	AFFX-GapdhMur/-M32599_3_st	6679937	glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	
25	100551_r_at	16716343	cytochrome c oxidase, subunit VIc [Mus musculus]	Cox6c
26	99124_at	9507187	fractured callus expressed transcript 1; Fracture Callus 1; small zinc	Fxc1
27	92876_at	6754814	NADH dehydrogenase (ubiquinone) Fe-S protein 4; NADH dehydrogenase (ubiquinone)	Ndufs4
28	96760_at	7305573	translocase of inner mitochondrial membrane 10 homolog [Mus musculus]	Timm10
29	94421_r_at	6681031	cryptochrome 1 (photolyase-like) [Mus musculus]	Cry1
30	93359_at	18859597	RIKEN cDNA 1810004I06 [Mus musculus]	1810004I06Rik
31	98832_at	6678417	thyroid peroxidase [Mus musculus]	Tpo
32	96857_at	6680816	complement component 1, q subcomponent binding protein [Mus musculus]	C1qbp
33	98117_at	9506911	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (7.5kD, MWFE); NADH	Ndufa1
34	100046_at	6678952	methylenetetrahydrofolate dehydrogenase (NAD+ dependent),	Mthfd2
35	103806_at	6678716	low density lipoprotein receptor-related protein 5; low density	Lrp5
36	97372_at	18875324	DAZ associated protein 1 [Mus musculus]	Dazap1
37	102416_at	6681097	cytochrome P450, family 17, subfamily a, polypeptide 1; cytochrome P450, 17;	Cyp17
38	94850_at	12331400	acyl-Coenzyme A thioesterase 3, mitochondrial; MT-ACT48,p48 [Mus musculus]	Acate3-pending
39	103471_at	31981207	RIKEN cDNA 4432405K22 [Mus musculus]	4432405K22Rik
40	92810_at	21704122	pyruvate dehydrogenase kinase, isoenzyme 3 [Mus musculus]	Pdk3
41	93062_at	31560438	mitochondrial ribosomal protein L39; ribosomal protein, mitochondrial, L5 [Mus	Mrpl39
42	97884_at	17157979	mitochondrial ribosomal protein S11 [Mus musculus]	Mrps11
43	94420_f_at	6681031	cryptochrome 1 (photolyase-like) [Mus musculus]	Cry1
44	99027_at	31981887	Bcl2-like [Mus musculus]	Bcl2l
45	100619_r_at	22094075	solute carrier family 25, member 5; adenine nucleotide translocator 2,	Slc25a5
46	102007_at	31542950	holocytochrome c synthetase [Mus musculus]	Hccs
47	95354_at	7657583	solute carrier family 25 (mitochondrial carrier; adenine nucleotide	Slc25a13
48	99543_s_at	7304999	deoxyguanosine kinase [Mus musculus]	Dguok
49	98903_at	21312028	RIKEN cDNA 1110006I11 [Mus musculus]	1110006I11Rik
50	96032_at	31982497	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9),	Atp5g1
51	95734_at	31981470	mitochondrial ribosomal protein L3 [Mus musculus]	Mrpl3
52	102128_f_at	31981257	mitochondrial ribosomal protein S25 [Mus musculus]	Mrps25

53	94210_at	7305581	translocase of inner mitochondrial membrane 9 homolog [Mus musculus]	Timm9
54	103622_at	9910434	malonyl-CoA decarboxylase [Mus musculus]	Mlycd
55	96289_at	12963591	stomatin-like protein 2 [Mus musculus]	Stoml2
56	AFFX-PyruCarbMur/-L09192_5_at	6679237	pyruvate carboxylase; pyruvate decarboxylase [Mus musculus]	
57	95645_at	21313484	nitrogen fixation cluster-like [Mus musculus]	2310020H20Rik
58	96916_at	13385266	mitochondrial ribosomal protein L33 [Mus musculus]	Mrpl33
59	94012_at	7305575	translocase of inner mitochondrial membrane 13 homolog a [Mus musculus]	Timm13a
60	93859_at	19526984	mitochondrial translational initiation factor 2 [Mus musculus]	2410112O06Rik
61	96202_at	7106409	solute carrier family 1, member 2; glial high affinity glutamate transporter	Slc1a2
62	96650_at	7709988	AU RNA-binding enoyl-coenzyme A hydratase; AU RNA-binding protein/enoyl-coenzyme	Auh
63	98120_at	16716447	mitochondrial ribosomal protein L27 [Mus musculus]	Mrpl27
64	93048_at	8393156	caseinolytic protease, ATP-dependent, proteolytic subunit homolog; caseinolytic	Clpp
65	94852_at	31982332	glutamate-ammonia ligase (glutamine synthase); glutamine synthetase [Mus	Glul
66	98909_at	13277380	lipoic acid synthetase [Mus musculus]	Lias
67	103646_at	6681009	carnitine acetyltransferase [Mus musculus]	Crat
68	98984_f_at	31981769	glycerol-3-phosphate dehydrogenase 2; glycerol phosphate dehydrogenase 1,	Gpd2
69	98099_at	27753998	nudix (nucleoside diphosphate linked moiety X)-type motif 9 [Mus musculus]	Nudt9
70	94897_at	13540480	glutathione peroxidase 4; sperm nuclei glutathione peroxidase; phospholipid	Gpx4
71	97369_g_at	6753030	A-kinase anchor protein 1; A kinase anchor protein [Mus musculus]	Akap1
72	99636_at	14780884	polymerase delta interacting protein 38 [Mus musculus]	1300003F06Rik
73	95215_f_at	21070950	ubiquitin C; polyubiquitin C [Mus musculus]	Ubc
74	96095_i_at	13195670	RIKEN cDNA 2610207I16 [Mus musculus]	2610207I16Rik
75	93114_at	10181184	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2;	Atp5j2
76	100527_at	21311867	hypothetical protein D11Ertd99e [Mus musculus]	D11Ertd99e
77	92625_at	6679078	expressed in non-metastatic cells 2, protein; expressed in non-metastatic cells	Nme2
78	96653_at	21311883	RIKEN cDNA 0610007O07 [Mus musculus]	0610007O07Rik
79	96856_at	6680816	complement component 1, q subcomponent binding protein [Mus musculus]	C1qbp
80	98545_at	6671622	B-cell receptor-associated protein 37; repressor of estrogen receptor activity	Bcap37
81	96858_at	6755004	programmed cell death 8; programmed cell death 8 (apoptosis inducing	Pdcd8

			factor);	
82	94855_at	6679299	prohibitin [Mus musculus]	Phb
83	99148_at	33859554	fumarate hydratase 1 [Mus musculus]	Fh1
84	96898_at	33859512	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	Atp5f1
85	AFFX-GapdhMur/-M32599_5_st	6679937	glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	
86	AFFX-GapdhMur/-M32599_M_st	6679937	glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	
87	93392_at	6678495	uncoupling protein 3, mitochondrial [Mus musculus]	Ucp3
88	94379_at	25031694	kinesin family member 1B [Mus musculus]	Kif1b
89	102426_at	6753290	calsequestrin 1 [Mus musculus]	Casq1
90	96801_at	10946936	adenylate kinase 1; cytosolic adenylate kinase [Mus musculus]	Ak1
91	96066_s_at	31981562	pyruvate kinase 3 [Mus musculus]	Pkm2
92	101214_f_at	6679937	glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	Gapd
93	AFFX-GapdhMur/-M32599_3_at	6679937	glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	
94	AFFX-GapdhMur/-M32599_5_at	6679937	glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	
95	AFFX-GapdhMur/-M32599_M_at	6679937	glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]	
96	94279_at	21536220	RIKEN cDNA 0610008F14 [Mus musculus]	0610008F14Rik
97	95498_at	13384968	mitochondrial ribosomal protein S15 [Mus musculus]	Mrps15
98	98130_at	9903609	thioredoxin 2; thioredoxin nuclear gene encoding mitochondrial protein;	Txn2
99	96626_at	27370092	RIKEN cDNA 2300002G02 [Mus musculus]	2300002G02Rik
100	99658_f_at	12963697	RIKEN cDNA 1110025H10 [Mus musculus]	1110025H10Rik
101	97342_at	13384894	mitochondrial ribosomal protein S14 [Mus musculus]	Mrps14
102	95472_f_at	13385726	ubiquinol-cytochrome c reductase binding protein [Mus musculus]	2210415M14Rik
103	94062_at	20900762	NADH dehydrogenase (ubiquinone) flavoprotein 2 [Mus musculus]	Ndufv2
104	99661_r_at	6680991	cytochrome c oxidase, subunit VIIc; cytochrome c oxidase subunit VIIc [Mus	Cox7c
105	95718_f_at	13128954	upregulated during skeletal muscle growth 5 [Mus musculus]	Usmg5
106	101580_at	13384754	cytochrome c oxidase subunit VIIb [Mus musculus]	Cox7b
107	96887_at	9506933	neuronal protein 15.6 [Mus musculus]	Np15
108	96280_at	31981600	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2; NADH dehydrogenase	Ndufa2
109	95131_f_at	13386096	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 [Mus musculus]	1810011O01Rik

110	95132_r_at	13386096	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 [Mus musculus]	1810011O01Rik
111	99660_f_at	6680991	cytochrome c oxidase, subunit VIIc; cytochrome c oxidase subunit VIIc [Mus	Cox7c
112	93014_at	31980744	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g; F1F0-ATP	Atp5l
113	99678_f_at	31980744	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g; F1F0-ATP	Atp5l
114	97512_at	21312554	RIKEN cDNA 2010107E04 [Mus musculus]	2010107E04Rik
115	100550_f_at	16716343	cytochrome c oxidase, subunit VIc [Mus musculus]	Cox6c
116	93820_at	31981830	cytochrome c oxidase, subunit VIIa 2; cytochrome c oxidase subunit VIIa 3;	Cox7a2
117	99115_at	21539599	ubiquinol cytochrome c reductase hinge protein; mitochondrial hinge protein;	2610041P16Rik
118	94909_at	13384854	mitochondrial ribosomal protein S17 [Mus musculus]	Mrps17
119	96686_i_at	13385436	RIKEN cDNA 2010100O12 [Mus musculus]	2010100O12Rik
120	96687_f_at	13385436	RIKEN cDNA 2010100O12 [Mus musculus]	2010100O12Rik
121	94526_at	19527228	DNA segment, Chr 10, ERATO Doi 214, expressed [Mus musculus]	D10Ertd214e
122	97880_at	21313536	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	4930529O08Rik
123	96096_f_at	13195670	RIKEN cDNA 2610207I16 [Mus musculus]	2610207I16Rik
124	94866_at	13384844	mitochondrial ribosomal protein S16 [Mus musculus]	Mrps16
125	93582_at	20587962	demethyl-Q 7 [Mus musculus]	Coq7
126	94860_at	33468943	translocator of inner mitochondrial membrane a; translocator of inner	Timm17a
127	100892_at	31980802	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1; NADH	Ndufaf1
128	102097_f_at	21539587	NADH-ubiquinone oxidoreductase B9 subunit; Complex I-B9; CI-B9 [Mus musculus]	1010001M12Rik
129	97874_at	33859744	RIKEN cDNA 1500032D16 [Mus musculus]	1500032D16Rik
130	93562_at	13385054	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3 [Mus musculus]	2700033I16Rik
131	94534_at	18250284	isocitrate dehydrogenase 3 (NAD+) alpha [Mus musculus]	Idh3a
132	98929_at	13384742	RIKEN cDNA 1110018B13 [Mus musculus]	1110018B13Rik
133	95058_f_at	21312594	RIKEN cDNA 2610205H19; EST AA108335 [Mus musculus]	2610205H19Rik
134	99666_at	13385942	citrate synthase [Mus musculus]	Cs
135	94080_at	20908717	succinate dehydrogenase Fp subunit [Mus musculus]	Sdha
136	93029_at	6680345	isocitrate dehydrogenase 3 (NAD+), gamma [Mus musculus]	Idh3g
137	94912_at	17505220	mitochondrial ribosomal protein S21 [Mus musculus]	Mrps21
138	93531_at	21312012	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 [Mus musculus]	0610033L03Rik
139	93754_at	7949037	enoyl coenzyme A hydratase 1, peroxisomal; peroxisomal/mitochondrial dienoyl-CoA	Ech1

140	92581_at	6680618	acetyl-Coenzyme A dehydrogenase, medium chain [Mus musculus]	Acadm
141	96112_at	31981826	electron transferring flavoprotein, alpha polypeptide; Alpha-ETF [Mus musculus]	Etfa
142	97869_at	21313290	electron transferring flavoprotein, dehydrogenase [Mus musculus]	0610010I20Rik
143	95072_at	13385006	cytochrome c-1 [Mus musculus]	Cyc1
144	96267_at	19526814	NADH dehydrogenase (ubiquinone) flavoprotein 1; NADH dehydrogenase flavoprotein	Ndufv1
145	101989_at	13384794	ubiquinol-cytochrome c reductase core protein 1 [Mus musculus]	Uqcrc1
146	94806_at	18152793	pyruvate dehydrogenase (lipoamide) beta [Mus musculus]	Pdhb
147	93815_at	21313618	RIKEN cDNA 0610041L09 [Mus musculus]	0610041L09Rik
148	96268_at	9845299	succinate-CoA ligase, GDP-forming, alpha subunit; succinyl-CoA synthetase [Mus	Suclg1
149	102749_at	6753504	cytochrome c oxidase, subunit VIIa 1; cytochrome c oxidase subunit VIIa 1 [Mus	Cox7a1
150	95698_at	13385322	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 [Mus musculus]	1110002H15Rik
151	93119_at	6753500	cytochrome c oxidase, subunit Vb [Mus musculus]	Cox5b
152	96909_at	27754007	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1 [Mus musculus]	2610003B19Rik
153	99128_at	20070412	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit [Mus	Atp5o
154	100753_at	6680748	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform	Atp5a1
155	93596_i_at	13385484	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit; ATP	2410043G19Rik
156	93844_at	21539585	low molecular mass ubiquinone-binding protein; ubiquinol-cytochrome c reductase	Uqcrb
157	96915_f_at	21539587	NADH-ubiquinone oxidoreductase B9 subunit; Complex I-B9; CI-B9 [Mus musculus]	1010001M12Rik
158	99618_at	13385112	ubiquinol-cytochrome c reductase subunit [Mus musculus]	0710008D09Rik
159	100079_at	29789148	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 [Mus musculus]	Ndufb9
160	93581_at	13385558	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8 [Mus musculus]	2900010I05Rik
161	96870_at	18079339	aconitase 2, mitochondrial [Mus musculus]	Aco2
162	98102_at	6679261	pyruvate dehydrogenase E1 alpha 1; pyruvate dehydrogenase E1alpha subunit [Mus	Pdha1
163	95425_at	31982520	acetyl-Coenzyme A dehydrogenase, long-chain [Mus musculus]	Acadl
164	96913_at	21704100	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A	4930479F15Rik
165	93972_at	23346461	NADH dehydrogenase (ubiquinone) Fe-S protein 2; NADH-coenzyme Q reductase [Mus	Ndufs2

166	94216_at	13384690	succinate dehydrogenase complex, subunit C, integral membrane protein [Mus	0610010E03Rik
167	97502_at	31982856	dihydrolipoamide dehydrogenase [Mus musculus]	Dld
168	92574_at	27229021	RIKEN cDNA 3110001M13 [Mus musculus]	3110001M13Rik
169	102000_f_at	22267442	RIKubiquinol cytochrome c reductase core protein 2 [Mus musculus]	1500004O06Rik
170	96321_at	13384720	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 [Mus musculus]	1010001N11Rik
171	97201_s_at	13386100	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 [Mus musculus]	2900002J19Rik
172	93764_at	12963633	genes associated with retinoid-IFN-induced mortality 19 [Mus musculus]	Grim19-pending
173	97307_f_at	27754144	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5; NADH dehydrogenase	Ndufb5
174	92798_at	11602916	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1; F1	Atp5c1
175	92799_g_at	11602916	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1; F1	Atp5c1
176	93572_at	21704020	NADH dehydrogenase (ubiquinone) Fe-S protein 1 [Mus musculus]	---
177	93780_at	13385260	thioesterase superfamily member 2 [Mus musculus]	0610006O17Rik
178	99593_at	19527334	NADH dehydrogenase (ubiquinone) Fe-S protein 5; NADH dehydrogenase Fe-S protein	Ndufs5
179	96746_at	31542559	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase	Dlat
180	95441_at	12025536	translocase of inner mitochondrial membrane 23 homolog [Mus musculus]	Timm23
181	102049_at	7305375	pyruvate dehydrogenase kinase, isoenzyme 4; pyruvate dehydrogenase kinase 4 [Mus	Pdk4
182	95485_at	6680163	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain; hydroxylacyl-Coenzyme A	Hadhsc
183	95426_at	29789289	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial [Mus musculus]	Echs1
184	95064_at	29126205	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A	D18Ertd240e
185	96947_at	21312004	RIKEN cDNA 0610009I16 [Mus musculus]	0610009I16Rik
186	96757_at	20070420	DNA segment, Chr 10, Johns Hopkins University 81 expressed [Mus musculus]	D10Jhu81e
187	98128_at	7949005	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F;	Atp5j
188	94531_at	33859690	RIKEN cDNA 2310005O14 [Mus musculus]	2310005O14Rik
189	99667_at	6753502	cytochrome c oxidase, subunit VI a, polypeptide 2; subunit VIaH (heart-type)	Cox6a2
190	102402_at	6679957	glioblastoma amplified [Mus musculus]	Gbas
191	99631_f_at	6680988	cytochrome c oxidase, subunit VI a, polypeptide 1; subunit VIaL (liver-type)	Cox6a1
192	96670_at	21313138	glutathione S-transferase class kappa [Mus musculus]	0610025I19Rik
193	94940_at	31980706	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) [Mus musculus]	Mccc1

194	AFFX-PyruCarbMur/-L09192_MB_at	6679237	pyruvate carboxylase; pyruvate decarboxylase [Mus musculus]	
195	AFFX-PyruCarbMur/-L09192_3_at	6679237	pyruvate carboxylase; pyruvate decarboxylase [Mus musculus]	
196	93308_s_at	6679237	pyruvate carboxylase; pyruvate decarboxylase [Mus musculus]	Pcx
197	103401_at	31982522	acyl-Coenzyme A dehydrogenase, short chain; acetyl-Coenzyme A dehydrogenase,	Acads
198	94807_at	23943838	solute carrier family 25, member 1; DiGeorge syndrome gene j; solute carrier	Slc25a1
199	97248_at	6681137	diazepam binding inhibitor; acyl-CoA binding protein; diazepam-binding inhibitor	Dbi
200	94507_at	31560705	fatty acid Coenzyme A ligase, long chain 2; acetyl-Coenzyme A synthetase;	Facl2
201	104057_at	13277394	GrpE-like 1, mitochondrial [Mus musculus]	Grpel1
202	97279_at	21704140	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor; EST AI265272;	AI265272
203	99613_at	6678970	methylmalonyl-Coenzyme A mutase [Mus musculus]	Mut
204	96035_at	31982494	branched chain ketoacid dehydrogenase E1, alpha polypeptide; BCKAD E1[a] [Mus	Bckdha
205	101045_at	7949047	hydroxyacyl-Coenzyme A dehydrogenase type II; hydroxyacyl-Coenzyme A	Hadh2
206	98966_at	6753610	dihydrolipoamide branched chain transacylase E2; BCKAD E2 [Mus musculus]	Dbt
207	104212_at	21389320	leucine-rich PPR motif-containing protein; leucine rich protein LRP130 [Mus	3110001K13Rik
208	92845_at	18266680	3-oxoacid CoA transferase [Mus musculus]	Oxct
209	99009_at	31543330	nicotinamide nucleotide transhydrogenase [Mus musculus]	Nnt
210	97367_at	6753030	A-kinase anchor protein 1; A kinase anchor protein [Mus musculus]	Akap1
211	93042_at	31981875	benzodiazepine receptor, peripheral [Mus musculus]	Bzrp
212	92754_at	6679767	ferredoxin reductase [Mus musculus]	Fdxr
213	92587_at	6679765	ferredoxin 1; ADRENODOXIN [Mus musculus]	Fdx1
214	92213_at	31543776	steroidogenic acute regulatory protein [Mus musculus]	Star
215	96256_at	6680690	peroxiredoxin 3; anti-oxidant protein 1; mitochondrial Trx dependent peroxide	Prdx3
216	92829_at	6680309	heat shock protein 1 (chaperonin 10); heat shock 10 kDa protein 1 (chaperonin	Hspe1
217	93277_at	31981679	heat shock protein 1 (chaperonin); heat shock protein, 60 kDa; heat shock 60kDa	Hspd1
218	100977_at	27369966	RIKEN cDNA D530020C15 [Mus musculus]	D530020C15Rik
219	101096_s_at	6754160	HS1 binding protein [Mus musculus]	Hs1bp1

220	95065_at	6754846	nitrogen fixation gene, yeast homolog 1; nifS-like (sic) [Mus musculus]	Nfs1
221	AFFX-PyruCarbMur/-L09192_MA_at	6679237	pyruvate carboxylase; pyruvate decarboxylase [Mus musculus]	
222	98137_at	6671680	carbonic anhydrase 5a, mitochondrial; carbonic anhydrase 5, mitochondrial;	Car5a
223	98459_at	6677943	serine hydroxymethyl transferase 1 (soluble) [Mus musculus]	Shmt1
224	92586_at	6680027	glutamate dehydrogenase [Mus musculus]	Glud
225	97450_s_at	20070418	aldehyde dehydrogenase family 7, member A1; aldehyde dehydrogenase 7 family,	Aldh7a1
226	97515_at	31982273	hydroxysteroid (17-beta) dehydrogenase 4; hydroxysteroid 17-beta dehydrogenase	Hsd17b4
227	103085_at	7305137	heme binding protein 1; heme-binding protein; p22 HBP; heme-binding protein 1	Hebp1
228	98533_at	13385268	cytochrome b-5 [Mus musculus]	Cyb5
229	104086_at	21311901	dimethylglycine dehydrogenase precursor [Mus musculus]	1200014D15Rik
230	96890_at	13385298	RIKEN cDNA 1300002A08 [Mus musculus]	1300002A08Rik
231	93026_at	31981068	microsomal glutathione S-transferase 1 [Mus musculus]	Mgst1
232	96763_at	20149748	sarcosine dehydrogenase [Mus musculus]	Sardh
233	93278_at	28545662	sterol carrier protein 2, liver [Mus musculus]	Scp2
234	101515_at	7656855	acyl-Coenzyme A oxidase 1, palmitoyl; acyl-Coenzyme A oxidase; Acyl-CoA oxidase	Acox1
235	93625_at	7709978	alanine-glyoxylate aminotransferase; alanine-glyoxylate aminotransferase 1 [Mus	Agxt
236	96326_at	22122769	tyrosine aminotransferase [Mus musculus]	Tat
237	101910_f_at	13654245	major urinary protein 1 [Mus musculus]	Mup1
238	92606_at	6678509	urate oxidase; uricase [Mus musculus]	Uox
239	102096_f_at	13654245	major urinary protein 1 [Mus musculus]	Mup1
240	93320_at	27804309	carnitine palmitoyltransferase 1, liver; L-CPT I [Mus musculus]	Cpt1a
241	96057_at	6753036	aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	Aldh2
242	96058_s_at	6753036	aldehyde dehydrogenase 2, mitochondrial [Mus musculus]	Aldh2
243	92800_i_at	11602916	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1; F1	Atp5c1
244	100617_at	22094075	solute carrier family 25, member 5; adenine nucleotide translocator 2,	Slc25a5
245	100618_f_at	22094075	solute carrier family 25, member 5; adenine nucleotide translocator 2,	Slc25a5
246	97207_f_at	6678760	lysophospholipase 1; phospholipase 1a; lysophopholipase 1 [Mus musculus]	Lypla1
247	98473_at	6753110	arginase type II [Mus musculus]	Arg2

248	98112_r_at	31981147	leucine aminopeptidase 3; leucine aminopeptidase [Mus musculus]	Lap3
249	100633_at	19526848	RIKEN cDNA 2810484M10 [Mus musculus]	2810484M10Rik
250	92848_at	8393866	ornithine aminotransferase [Mus musculus]	Oat
251	104007_at	6754952	solute carrier family 25 (mitochondrial carrier; ornithine transporter), member	Slc25a15
252	96336_at	13385454	glycine amidinotransferase (L-arginine:glycine amidinotransferase) [Mus	Gatm
253	93595_at	6753448	ceroid-lipofuscinosis, neuronal 2 [Mus musculus]	Cln2
254	104153_at	9789985	isovaleryl coenzyme A dehydrogenase; isovaleryl dehydrogenase precursor [Mus	Ivd
255	94005_at	20822904	RIKEN cDNA 3110004O18 [Mus musculus]	3110004O18Rik
256	103881_at	22203753	inorganic pyrophosphatase 2 [Mus musculus]	1110013G13Rik
257	101944_at	6678760	lysophospholipase 1; phospholipase 1a; lysophopholipase 1 [Mus musculus]	Lypla1
258	101945_g_at	6678760	lysophospholipase 1; phospholipase 1a; lysophopholipase 1 [Mus musculus]	Lypla1
259	101946_at	6678760	lysophospholipase 1; phospholipase 1a; lysophopholipase 1 [Mus musculus]	Lypla1
260	99112_at	7305501	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter),	Slc25a10
261	99521_at	6753022	adenylate kinase 4 [Mus musculus]	Ak4
262	96069_at	27659728	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase);	Afar
263	96231_at	21624609	RIKEN cDNA 2010012D11 [Mus musculus]	2010012D11Rik
264	97525_at	6680139	glycerol kinase [Mus musculus]	Gyk
265	102192_r_at	31982720	SA rat hypertension-associated homolog [Mus musculus]	Sah
266	93435_at	6753572	cytochrome P450, family 24, subfamily a, polypeptide 1; cytochrome P450, 24;	Cyp24
267	99959_at	6753022	adenylate kinase 4 [Mus musculus]	Ak4
268	98123_at	6754408	kynurenine aminotransferase II [Mus musculus]	Kat2
269	96629_at	14861848	DNA segment, Chr 7, Roswell Park 2 complex, expressed; androgen regulated gene	D7Rp2e
270	92869_at	6680291	hydroxysteroid dehydrogenase-4, delta-3-beta; 3-beta-hydroxysteroid	Hsd3b4
271	96910_at	22122743	hypothetical protein MGC37245 [Mus musculus]	MGC37245
272	96938_at	19482166	kidney expressed gene 1 [Mus musculus]	Keg1
273	95588_at	6678766	alpha-methylacyl-CoA racemase; alpha-methylacyl-Coenzyme A racemase;	Amacr
274	97316_at	31541815	L-specific multifunctional beta-oxdiation protein [Mus musculus]	1300002P22Rik
275	97258_at	21703764	lactamase, beta 2 [Mus musculus]	Cgi-83-pending
276	97257_at	21703764	lactamase, beta 2 [Mus musculus]	Cgi-83-pending
277	96048_at	6680277	heat-responsive protein 12 [Mus musculus]	Hrsp12
278	103389_at	31980703	aminoadipate-semialdehyde synthase; lysine oxoglutarate reductase, saccharopine	Aass
279	100967_at	6755548	solute carrier family 27 (fatty acid transporter), member 2; very long-chain	Slc27a2

280	96678_at	13507612	NADPH-dependent retinol dehydrogenase/reductase [Mus musculus]	D14Ucla2
281	92492_at	23956104	adenylate kinase 3 alpha-like; adenylate kinase 3 alpha like [Mus musculus]	Ak3l
282	99659_r_at	12963697	RIKEN cDNA 1110025H10 [Mus musculus]	1110025H10Rik
283	102761_at	29789124	GrpE-like 2, mitochondrial [Mus musculus]	Grpel2
284	94961_at	6753454	caseinolytic protease X [Mus musculus]	Clpx
285	103354_at	10181116	mitochondrial ribosomal protein S31; islet mitochondrial antigen, 38 kD [Mus	Mrps31
286	93506_at	19526818	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3;	Slc25a3
287	93495_at	7948999	peroxiredoxin 4; antioxidant enzyme AOE372; Prx IV [Mus musculus]	Prdx4
288	97477_at	7305579	translocase of inner mitochondrial membrane 8 homolog b [Mus musculus]	Timm8b
289	94515_at	31981549	sulfide quinone reductase-like; flavo-binding protein; sulfide	Sqrdl
290	95660_at	12963539	HSCO protein [Mus musculus]	0610025L15Rik
291	92807_at	6755911	thioredoxin 1; thioredoxin [Mus musculus]	Txn1
292	93749_at	27804325	monoamine oxidase A [Mus musculus]	Maoa
293	93984_at	31982864	ATPase inhibitor [Mus musculus]	Atpi
294	96849_at	7305577	translocase of inner mitochondrial membrane 8 homolog a [Mus musculus]	Timm8a
295	104283_at	31981207	RIKEN cDNA 4432405K22 [Mus musculus]	4432405K22Rik
296	99513_at	6679369	phospholipase A2, group IVA (cytosolic, calcium-dependent); phospholipase A2,	Pla2g4a
297	100957_at	20916351	single-stranded DNA binding protein 1 [Mus musculus]	---
298	99335_at	6754206	hexokinase 1; downeast anemia [Mus musculus]	Hk1
299	92735_at	7242175	phospholipase A2, group IIA (platelets, synovial fluid); modifier of Min1;	Pla2g2a
300	98902_at	21312028	RIKEN cDNA 1110006I11 [Mus musculus]	1110006I11Rik
301	94284_at	19745150	diaphorase 1 (NADH) [Mus musculus]	Dia1
302	92792_at	31543920	uncoupling protein 2, mitochondrial [Mus musculus]	Ucp2
303	95676_at	18700024	isocitrate dehydrogenase 3, beta subunit; isocitrate dehydrogenase 3 beta; N14A	Idh3b
304	99176_at	10946808	fibroblast growth factor (acidic) intracellular binding protein; aFGF	Fibp
305	98613_at	21313080	RIKEN cDNA 2700085E05 [Mus musculus]	2700085E05Rik
306	96641_at	6754870	neighbor of Cox4 [Mus musculus]	Noc4
307	97825_at	11528520	p53 apoptosis effector related to Pmp22; p53 apoptosis-associated target [Mus	Perp-pending
308	92860_at	6680993	cytochrome c oxidase, subunit VIIIa; COX VIII-L [Mus musculus]	Cox8a
309	99172_at	6678303	transcription factor A, mitochondrial [Mus musculus]	Tfam
310	99836_at	20867579	cytochrome P450, 40 (25-hydroxyvitamin D3 1 alpha-hydroxylase) [Mus musculus]	Cyp40
311	103043_at	6754760	mature T-cell proliferation 1 [Mus musculus]	Mtcp1

312	104102_at	31980991	protease, serine, 25; serine protease OMI [Mus musculus]	Prss25
313	97398_at	28077029	RIKEN cDNA 9130022B02 [Mus musculus]	9130022B02Rik
314	96353_at	13384766	RIKEN cDNA 1110021D01 [Mus musculus]	1110021D01Rik
315	100300_at	31542440	cytochrome b-245, beta polypeptide [Mus musculus]	Cybb
316	99114_r_at	13385090	cytochrome c oxidase, subunit VIb [Mus musculus]	2010000G05Rik
317	96255_at	6753200	BCL2/adenovirus E1B 19kDa-interacting protein 3-like; BCL2/adenovirus E1B 19	Bnip3l
318	92768_s_at	33859502	aminolevulinic acid synthase 2, erythroid; erythroid-specific ALAS;	Alas2
319	100414_s_at	6754732	myeloperoxidase [Mus musculus]	Mpo
320	92595_r_at	20452466	ferrochelatase [Mus musculus]	Fech
321	98505_i_at	6681007	coproporphyrinogen oxidase; clone 560 [Mus musculus]	Cpo
322	98506_r_at	6681007	coproporphyrinogen oxidase; clone 560 [Mus musculus]	Cpo
323	104234_at	31981257	mitochondrial ribosomal protein S25 [Mus musculus]	Mrps25
324	97373_at	21313024	solute carrier family 25 (mitochondrial deoxynucleotide carrier), member 19 [Mus	Slc25a19
325	94501_at	13507712	sphingosine-1-phosphate phosphatase 1; sphingosine-1-phosphate phosphatase [Mus	---
326	101557_at	6753164	branched chain ketoacid dehydrogenase kinase; branched chain keto acid	Bckdk
327	100443_at	33859514	branched chain aminotransferase 2, mitochondrial [Mus musculus]	Bcat2
328	94034_at	27229283	small fragment nuclease [Mus musculus]	Smfn
329	102058_at	29789253	mitochondrial ribosomal protein L9 [Mus musculus]	Mrpl9
330	103045_at	6754760	mature T-cell proliferation 1 [Mus musculus]	Mtcp1
331	93836_at	6753198	BCL2/adenovirus E1B 19kDa-interacting protein 1, NIP3; BCL2/adenovirus E1B 19	Bnip3
332	99544_at	7304999	deoxyguanosine kinase [Mus musculus]	Dguok
333	96848_at	14916467	inositol polyphosphate-5-phosphatase E; inositol polyphosphate-5-phosphatase, 72	Inpp5e
334	102659_at	31560609	ceroid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	Cln3
335	94541_at	21314826	NADH:ubiquinone oxidoreductase B15 subunit [Mus musculus]	0610006N12Rik
336	97368_at	6753030	A-kinase anchor protein 1; A kinase anchor protein [Mus musculus]	Akap1
337	96745_at	31542559	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase	Dlat
338	95607_at	10946984	START domain containing 3; es64 protein; steroidogenic acute regulatory protein	Stard3
339	101407_at	6679863	frataxin [Mus musculus]	Frda
340	95896_at	6680991	cytochrome c oxidase, subunit VIIc; cytochrome c oxidase subunit VIIc [Mus	---

341	101356_at	10835111	thymidine kinase 2, mitochondrial; thymidine kinase 2 [Mus musculus]	Tk2
342	100059_at	22094077	cytochrome b-245, alpha polypeptide; cytochrome beta-558; p22 phox [Mus	Cyba
343	93536_at	6680770	Bcl2-associated X protein [Mus musculus]	Bax
344	101036_at	13324686	translocase of outer mitochondrial membrane 20 homolog [Mus musculus]	1810060K07Rik
345	97472_at	29789024	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein),	Slc25a17
346	92494_at	6753058	annexin A10 [Mus musculus]	Anxa10
347	96028_at	9055178	brain protein 44-like; apoptosis-regulating basic protein [Mus musculus]	Brp44l
348	94254_at	7304963	chloride intracellular channel 4 (mitochondrial) [Mus musculus]	Clic4
349	94255_g_at	7304963	chloride intracellular channel 4 (mitochondrial) [Mus musculus]	Clic4
350	94256_at	7304963	chloride intracellular channel 4 (mitochondrial) [Mus musculus]	Clic4
351	99141_at	6806917	GM2 ganglioside activator protein [Mus musculus]	Gm2a
352	101055_at	6679437	protective protein for beta-galactosidase [Mus musculus]	Ppgb
353	92633_at	11968166	cathepsin Z preproprotein; cathepsin Z precursor; cathepsin X [Mus musculus]	Ctsz
354	102328_at	20847456	caspase 8 [Mus musculus]	Casp8
355	103608_at	22267456	RIKEN cDNA 2810431B21 [Mus musculus]	2810431B21Rik
356	93699_at	7657467	polymerase (DNA directed), gamma 2, accessory subunit; mitochondrial polymerase	Polg2
357	96287_at	21281687	deoxyuridine triphosphatase [Mus musculus]	Dutp
358	94283_at	13385752	mitochondrial ribosomal protein L49; neighbor of fau 1 [Mus musculus]	Mrpl49
359	98547_at	6755360	mitochondrial ribosomal protein S12; ribosomal protein, mitochondrial, S12;	Mrps12
360	93251_at	6679066	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1	Nipsnap1
361	100589_at	21313262	inner membrane protein, mitochondrial [Mus musculus]	Immt
362	104132_at	6754870	neighbor of Cox4 [Mus musculus]	Noc4
363	94368_at	31088872	suppressor of var1, 3-like 1 [Mus musculus]	---
364	96036_at	13384998	tetratricopeptide repeat domain 11 [Mus musculus]	2010003O14Rik
365	100335_at	6680758	ATPase, Cu++ transporting, beta polypeptide; Wilson protein; toxic milk [Mus	Atp7b
366	103683_at	9910194	dihydroorotate dehydrogenase [Mus musculus]	Dhodh
367	97256_at	27228985	RIKEN cDNA 2410011G03 [Mus musculus]	2410011G03Rik
368	102031_at	6755334	ribonuclease H1 [Mus musculus]	Rnaseh1
369	96906_at	18079334	ethanol induced 6 [Mus musculus]	Etohi6
370	93561_at	27754146	RIKEN cDNA 0710001P09 [Mus musculus]	0710001P09Rik
371	94962_g_at	6753454	caseinolytic protease X [Mus musculus]	Clpx
372	98433_at	31542228	BH3 interacting domain death agonist [Mus musculus]	Bid

373	96904_at	30794474	mitchondrial ribosomal protein S7; ribosomal protein, mitochondrial, S7 [Mus	Mrps7
374	103386_at	18875408	peroxisomal acyl-CoA thioesterase 1 [Mus musculus]	Pte1
375	93355_at	6754036	glutamate oxaloacetate transaminase 2, mitochondrial; mitochondrial aspartate	Got2
376	98139_at	6755963	voltage-dependent anion channel 1 [Mus musculus]	Vdac1
377	95738_at	24025659	pyrroline-5-carboxylate synthetase; glutamate gamma-semialdehyde synthetase [Mus	Pycs
378	98298_at	6753676	dihydropyrimidinase-like 2; collapsin response mediator protein 2 [Mus musculus]	Dpysl2
379	95603_at	20070408	glycine decarboxylase [Mus musculus]	D19Wsu57e
380	97993_at	6678519	uroporphyrinogen III synthase; URO-synthase; uroporphyrinogen-III synthase;	Uros
381	99159_at	19527310	peptidylprolyl isomerase F (cyclophilin F); peptidyl-prolyl cis-trans isomerase;	AW457192
382	98118_at	9506911	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 (7.5kD, MWFE); NADH	Ndufa1
383	98106_at	19705563	translocator of inner mitochondrial membrane 44 [Mus musculus]	Timm44
384	103625_at	16905099	AFG3(ATPase family gene 3)-like 1 [Mus musculus]	Afg3l1
385	92497_at	9790129	solute carrier family 22 member 4; solute carrier family (organic cation	Slc22a4
386	93385_at	6679146	nth (endonuclease III)-like 1; thymine glycol DNA glycosylase/AP lyase [Mus	Nthl1

Table 7. The 643 genes in the mitochondria expression neighborhood. For each gene, the Affymetrix probe-set ID, neighborhood index (N_{100}), protein exemplar (if the gene was in mito-A), gene symbol, description, and electronic annotations are provided.

Probe Set	N_{100}	mito-A Exemplar	Gene		Electronic Annotations	
			Symbol	Title	INTERPRO	PFAM
97201_s_at	69	13386100	2900002J19Rik	RIKEN cDNA 2900002J19 gene	---	---
102561_at	68		---	---	---	---
92574_at	68	27229021	3110001M13Rik	RIKEN cDNA 3110001M13 gene	---	---
96321_at	68	13384720	1010001N11Rik	RIKEN cDNA 1010001N11 gene	---	---
99128_at	68	20070412	Atp5o	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	IPR000711 // H+-transporting two-sector ATPase, delta (OSCP) subunit	OSCP // ATP synthase delta (OSCP) subunit;5.6e-64
100892_at	67	31980802	Ndufaf1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	---	---
102000_f_at	67	22267442	1500004O06Rik	RIKEN cDNA 1500004O06 gene	IPR001431 // Insulinase-like peptidase, family M16 /// IPR001478 // PDZ/DHR/GLGF domain	Peptidase_M16 // Insulinase (Peptidase family M16);1.5e-40
93764_at	67	12963633	Grim19-pending	genes associated with retinoid-IFN-induced mortality 19	---	---
96112_at	67	31981826	Etfa	electron transferring flavoprotein, alpha polypeptide	IPR001308 // Electron transfer flavoprotein, alpha subunit	ETF_alpha // Electron transfer flavoprotein alpha subuni;3.5e-149
96611_at	67		2010012C24Rik	RIKEN cDNA 2010012C24 gene	---	---
97502_at	67	31982856	Dld	dihydrolipoamide dehydrogenase	IPR001327 // FAD-dependent pyridine nucleotide-disulphide oxidoreductase /// IPR004099 // Pyridine nucleotide-disulphide	pyr_redox_dim // Pyridine nucleotide-disulphide oxidored;2.5e-61 /// pyr_redox // Pyridine nucleotide-disulphide oxidored;1.2e-92

					oxidoreductase dimerisation domain /// IPR000815 // Mercuric reductase /// IPR001100 // Pyridine nucleotide-disulphide oxidoreductase, class I	
99106_at	67		Cops6	COP9 (constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana)	IPR003640 // Mov34 family, subtype 2 /// IPR000555 // Mov34 family	---
99618_at	67	13385112	0710008D09Rik	RIKEN cDNA 0710008D09 gene	---	---
100753_at	66	6680748	Atp5a1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	IPR005294 // ATP synthase F1, alpha subunit /// IPR000793 // H+-transporting two-sector ATPase, alpha/beta subunit, C-terminal /// IPR004100 // H+-transporting two-sector ATPase, alpha/beta subunit,N-terminal /// IPR000790 // H+-transporting two-sector ATPase, alpha subunit, C-terminal /// IPR000194 // H+-transporting two-sector ATPase, alpha/beta subunit, central region	ATP-synt_ab_N // ATP synthase alpha/beta family, beta-ba;8.4e-19 /// ATP-synt_ab // ATP synthase alpha/beta family, nucleot;3e-162 /// ATP-synt_ab_C // ATP synthase alpha/beta chain, C termin;4e-37
102228_at	66		Lat	linker for activation of T cells	---	---
92581_at	66	6680618	Acadm	acetyl-Coenzyme A dehydrogenase, medium chain	IPR006089 // Acyl-CoA dehydrogenase /// IPR006092 // Acyl-	Acyl-CoA_dh_M // Acyl-CoA dehydrogenase,

					CoA dehydrogenase, N-terminal /// IPR006091 // Acyl-CoA dehydrogenase, middle domain /// IPR006090 // Acyl-CoA dehydrogenase, C-terminal	middle domain;3.1e-66 /// Acyl-CoA_dh // Acyl-CoA dehydrogenase, C-terminal doma;4.5e-68 /// Acyl-CoA_dh_N // Acyl-CoA dehydrogenase, N-terminal doma;2.1e-53
94912_at	66	17505220	Mrps21	mitochondrial ribosomal protein S21	IPR001911 // Ribosomal protein S21	---
97307_f_at	66	27754144	Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	---	---
97914_at	66		Hspa9a	heat shock protein, A	IPR002048 // Calcium-binding EF-hand /// IPR001023 // Heat shock protein Hsp70	HSP70 // Hsp70 protein;0
99666_at	66	13385942	Cs	citrate synthase	IPR002020 // Citrate synthase	citrate_synt // Citrate synthase;4.4e-233
100079_at	65	29789148	Ndufb9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	---	---
93991_at	65		Mor1	malate dehydrogenase, mitochondrial	IPR001236 // Lactate/malate dehydrogenase /// IPR001252 // Malate dehydrogenase	ldh_C // lactate/malate dehydrogenase, alpha/beta C-t;2e-72 /// ldh // lactate/malate dehydrogenase, NAD binding do;3.1e-73
94461_at	65		Pbef-pending	pre-B-cell colony-enhancing factor	IPR002088 // Protein prenyltransferase, alpha subunit	---
94907_f_at	65		1110001J03Rik	RIKEN cDNA 1110001J03 gene	---	---
95053_s_at	65		0710008N11Rik	RIKEN cDNA 0710008N11 gene	IPR006058 // 2Fe-2S Ferredoxin /// IPR001450 // 4Fe-4S ferredoxin, iron-sulfur binding domain /// IPR001041 //	fer2 // 2Fe-2S iron-sulfur cluster binding domain;0.057

					Ferredoxin /// IPR004489 // Succinate dehydrogenase/fumarate reductase iron-sulfur protein	
95072_at	65	13385006	Cyc1	cytochrome c-1	IPR002326 // Cytochrome c1 /// IPR000345 // Cytochrome c heme-binding site	Cytochrome_C1 // Cytochrome C1 family;6.4e-165
98132_at	65		Cycs	cytochrome c, somatic	---	cytochrome_c // Cytochrome c;3.9e-38
99140_at	65		Mrpl16	mitochondrial ribosomal protein L16	IPR000114 // Ribosomal protein L16	Ribosomal_L16 // Ribosomal protein L16;1.9e-07
92799_g_at	64	11602916	Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	IPR000131 // H+-transporting two-sector ATPase, gamma subunit	ATP-synt // ATP synthase;6.9e-132
93119_at	64	6753500	Cox5b	cytochrome c oxidase, subunit Vb	IPR002124 // Cytochrome c oxidase, subunit Vb	COX5B // Cytochrome c oxidase subunit Vb;2.4e-58
93562_at	64	13385054	2700033I16Rik	RIKEN cDNA 2700033I16 gene	---	---
94080_at	64	20908717	Sdha	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	IPR003952 // Fumarate reductase/succinate dehydrogenase, FAD-binding site /// IPR001327 // FAD-dependent pyridine nucleotide-disulphide oxidoreductase /// IPR004112 // Fumarate reductase/succinate dehydrogenase flavoprotein, C-terminal ///	---

					IPR001100 // Pyridine nucleotide-disulphide oxidoreductase, class I /// IPR003953 // Fumarate reductase/succinate dehydrogenase flavoprotein, N-terminal	
95058_f_at	64	21312594	2610205H19Rik	RIKEN cDNA 2610205H19 gene	IPR005336 // Protein of unknown function UPF0041	UPF0041 // Uncharacterised protein family (UPF0041);1.5e-33
95132_r_at	64	13386096	1810011O01Rik	RIKEN cDNA 1810011O01 gene	---	---
96291_f_at	64		---	ESTs, Highly similar to NUMM_MOUSE NADH-ubiquinone oxidoreductase 13 kDa-A subunit (Complex I-13KD-A) (CI-13KD-A) [M.musculus]	---	---
96899_at	64		Ndufs3	NADH dehydrogenase (ubiquinone) Fe-S protein 3	IPR001268 // NADH dehydrogenase (ubiquinone), 30 kDa subunit	---
96909_at	64	27754007	2610003B19Rik	RIKEN cDNA 2610003B19 gene	IPR003231 // Acyl carrier protein (ACP) /// IPR002048 // Calcium-binding EF-hand /// IPR006162 // Phosphopantetheine attachment site /// IPR006163 // Phosphopantetheine-binding domain	pp-binding // Phosphopantetheine attachment site;1.6e-17
97869_at	64	21313290	0610010I20Rik	RIKEN cDNA 0610010I20 gene	IPR000103 // Pyridine nucleotide-disulphide oxidoreductase, class-II	---

100432_f_at	63		Mdfi	MyoD family inhibitor	---	---
100628_at	63		Ndufc1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	---	---
101525_at	63		0610011B04Rik	RIKEN cDNA 0610011B04 gene	---	---
101989_at	63	13384794	Uqcrc1	ubiquinol-cytochrome c reductase core protein 1	IPR001431 // Insulinase-like peptidase, family M16	Peptidase_M16 // Insulinase (Peptidase family M16);2e-71
93581_at	63	13385558	2900010I05Rik	RIKEN cDNA 2900010I05 gene	---	---
93582_at	63	20587962	Coq7	demethyl-Q 7	IPR004916 // Ubiquinone biosyntheis protein COQ7	COQ7 // Ubiquinone biosynthesis protein COQ7;2.9e-107
93815_at	63	21313618	0610041L09Rik	RIKEN cDNA 0610041L09 gene	---	---
93972_at	63	23346461	Ndufs2	NADH dehydrogenase (ubiquinone) Fe-S protein 2	IPR001135 // NADH-ubiquinone oxidoreductase, chain 49kDa	complex1_49Kd // Respiratory-chain NADH dehydrogenase, 4;3.2e-205
94078_at	63		1110020P15Rik	RIKEN cDNA 1110020P15 gene	---	---
94216_at	63	13384690	0610010E03Rik	RIKEN cDNA 0610010E03 gene	IPR000701 // Succinate dehydrogenase, cytochrome b subunit	Sdh_cyt // Succinate dehydrogenase cytochrome b subunit;1.6e-44
94526_at	63	19527228	D10Ertd214e	DNA segment, Chr 10, ERATO Doi 214, expressed	---	---
94566_at	63		G2a-pending	G protein-coupled receptor G2A	IPR005388 // G2A lysophosphatidylcholine receptor /// IPR000276 // Rhodopsin-like GPCR superfamily	7tm_1 // 7 transmembrane receptor (rhodopsin family);6.7e-38
95517_i_at	63		BC004004	cDNA sequence BC004004	---	---
95652_at	63		Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	---	---
96042_at	63		Sod2	superoxide dismutase 2, mitochondrial	IPR001189 // Manganese and iron	sodfe_C // Iron/manganese

					superoxide dismutase	superoxide dismutases, C-term;1.8e-77 /// sodfe // Iron/manganese superoxide dismutases, alpha-;1.5e-47
96082_at	63		Mrpl30	mitochondrial ribosomal protein L30	IPR000517 // Ribosomal protein L30	---
96267_at	63	19526814	Ndufv1	NADH dehydrogenase (ubiquinone) flavoprotein 1	IPR001949 // Respiratory-chain NADH dehydrogenase, 51 kDa subunit	Complex1_51K // Respiratory-chain NADH dehydrogenase 51;5.4e-183
96292_r_at	63		---	ESTs, Highly similar to NUMM_MOUSE NADH-ubiquinone oxidoreductase 13 kDa-A subunit (Complex I-13KD-A) (CI-13KD-A) [M.musculus]	---	---
96900_at	63		AI267078	expressed sequence AI267078	---	---
96913_at	63	21704100	4930479F15Rik	RIKEN cDNA 4930479F15 gene	IPR002155 // Thiolase /// IPR000408 // Regulator of chromosome condensation, RCC1	thiolase_C // Thiolase, C-terminal domain;1.1e-78 /// thiolase // Thiolase, N-terminal domain;1.4e-131
96915_f_at	63	21539587	1010001M12Rik	RIKEN cDNA 1010001M12 gene	---	---
97874_at	63	33859744	1500032D16Rik	RIKEN cDNA 1500032D16 gene	---	---
99150_at	63		Ict1	immature colon carcinoma transcript 1	IPR000352 // Class I peptide chain release factor domain	RF-1 // Peptidyl-tRNA hydrolase domain;7e-30
93029_at	62	6680345	Idh3g	isocitrate dehydrogenase 3 (NAD+), gamma	IPR001804 // Isocitrate/isopropylmalate dehydrogenase /// IPR004434 // Isocitrate dehydrogenase NAD-dependent,	isodh // Isocitrate/isopropylmalate dehydrogenase;4.7e-85

					mitochondrial	
93844_at	62	21539585	Uqcrb	ubiquinol-cytochrome c reductase binding protein	IPR004205 // UcrQ family	UcrQ // UcrQ family;1.9e-45
94005_at	62	20822904	3110004O18Rik	RIKEN cDNA 3110004O18 gene	IPR001431 // Insulinase-like peptidase, family M16	---
95472_f_at	62	13385726	2210415M14Rik	RIKEN cDNA 2210415M14 gene	IPR003197 // Cytochrome bd ubiquinol oxidase, 14 kDa subunit	UCR_14kD // Ubiquinol-cytochrome C reductase complex 14k;4.3e-58
96268_at	62	9845299	Suclg1	succinate-CoA ligase, GDP-forming, alpha subunit	IPR005811 // ATP-citrate lyase/succinyl-CoA ligase /// IPR005810 // Succinyl-CoA ligase, alpha subunit /// IPR003781 // CoA Binding Domain	ligase-CoA // CoA-ligase;3.9e-65 /// CoA_binding // CoA binding domain;5e-72
96626_at	62	27370092	2300002G02Rik	RIKEN cDNA 2300002G02 gene	---	GTP_EFTU_D2 // Elongation factor Tu domain 2;3.2e-24 /// GTP_EFTU_D3 // Elongation factor Tu C-terminal domain;6.1e-41 /// GTP_EFTU // Elongation factor Tu GTP binding domain;1.4e-89
96652_at	62		Mrpl28	mitochondrial ribosomal protein L28	---	---
98102_at	62	6679261	Pdha1	pyruvate dehydrogenase E1 alpha 1	IPR001017 // Dehydrogenase, E1 component	E1_dehydrog // Dehydrogenase E1 component;3.6e-183
102749_at	61	6753504	Cox7a1	cytochrome c oxidase, subunit VIIa 1	IPR003177 // Cytochrome c oxidase, subunit VIIa	COX7a // Cytochrome c oxidase subunit VIIa;7.4e-56
103001_at	61		Vegfb	vascular endothelial growth factor	IPR002400 // Growth	PDGF // Platelet-

				B	factor, cystine knot /// IPR000072 // Platelet-derived growth factor (PDGF)	derived growth factor (PDGF);4.3e-20
93455_s_at	61		Bmp4	bone morphogenetic protein 4	IPR001111 // Transforming growth factor beta (TGFb), N-terminal /// IPR001839 // Transforming growth factor beta (TGFb)	TGF-beta // Transforming growth factor beta like;1.8e-62 /// TGFb_propeptide // TGF-beta propeptide;2.4e-95
93501_f_at	61		Sucla2	succinate-Coenzyme A ligase, ADP-forming, beta subunit	IPR005811 // ATP-citrate lyase/succinyl-CoA ligase /// IPR005809 // Succinyl-CoA synthetase, beta subunit /// IPR003135 // ATP-dependent carboxylate-amine ligase-like, ATP-grasp	---
94062_at	61	20900762	Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	IPR002023 // NADH dehydrogenase (ubiquinone), 24 kDa subunit	---
94806_at	61	18152793	Pdhb	pyruvate dehydrogenase (lipoamide) beta	IPR005476 // Transketolase, C terminal /// IPR005475 // Transketolase, central region	transketolase_C // Transketolase, C-terminal domain;4.1e-55 /// transket_pyr // Transketolase, pyridine binding domai;1.5e-73
95698_at	61	13385322	1110002H15Rik	RIKEN cDNA 1110002H15 gene	---	---
99593_at	61	19527334	Ndufs5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	---	---
100307_at	60		---	Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length enriched library,	---	---

				clone:B430214H24 product:nuclear factor I/X, full insert sequence.		
102097_f_at	60	21539587	1010001M12Rik	RIKEN cDNA 1010001M12 gene	---	---
103406_at	60		2410004J02Rik	RIKEN cDNA 2410004J02 gene	IPR003593 // AAA ATPase /// IPR004130 // Conserved hypothetical ATP binding protein	ATP-bind // Conserved hypothetical ATP binding protein;6.4e-114
92798_at	60	11602916	Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	IPR000131 // H+-transporting two-sector ATPase, gamma subunit	ATP-synt // ATP synthase;6.9e-132
93502_r_at	60		Sucla2	succinate-Coenzyme A ligase, ADP-forming, beta subunit	IPR005811 // ATP-citrate lyase/succinyl-CoA ligase /// IPR005809 // Succinyl-CoA synthetase, beta subunit /// IPR003135 // ATP-dependent carboxylate-amine ligase-like, ATP-grasp	---
93572_at	60	21704020	---	Mus musculus, clone IMAGE:1380460, mRNA	IPR001467 // Prokaryotic molybdopterin oxidoreductase /// IPR001041 // Ferredoxin /// IPR000283 // Respiratory-chain NADH dehydrogenase 75 Kd subunit	fer2 // 2Fe-2S iron-sulfur cluster binding domain;1.7e-11
94537_at	60		1500001M02Rik	RIKEN cDNA 1500001M02 gene	IPR002048 // Calcium-binding EF-hand	efhand // EF hand;1.3e-13

94860_at	60	33468943	Timm17a	translocator of inner mitochondrial membrane 17 kDa, a	IPR005678 // Mitochondrial import inner membrane translocase, subunit Tim17 /// IPR003397 // Mitochondrial import inner membrane translocase, subunit Tim17/22	---
95483_at	60		Psmd1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	---	---
96686_i_at	60	13385436	2010100O12Rik	RIKEN cDNA 2010100O12 gene	---	---
99658_f_at	60	12963697	1110025H10Rik	RIKEN cDNA 1110025H10 gene	IPR002529 // Fumarylacetoacetate (FAA) hydrolase	FAA_hydrolase // Fumarylacetoacetate (FAA) hydrolase fam;5.8e-79
99660_f_at	60	6680991	Cox7c	cytochrome c oxidase, subunit VIIc	IPR004202 // Cytochrome c oxidase subunit VIIc	COX7C // Cytochrome c oxidase subunit VIIc;4e-33
101023_f_at	59		0610010E21Rik	RIKEN cDNA 0610010E21 gene	---	---
101094_at	59		Hig1-pending	hypoxia induced gene 1	---	---
102022_at	59		1110007A04Rik	RIKEN cDNA 1110007A04 gene	IPR004360 // Glyoxalase/Bleomycin resistance protein/dioxygenase domain	---
92615_at	59		2010003O02Rik	RIKEN cDNA 2010003O02 gene	---	---
93596_i_at	59	13385484	2410043G19Rik	RIKEN cDNA 2410043G19 gene	---	---
95485_at	59	6680163	Hadhsc	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	IPR006180 // 3-hydroxyacyl-CoA dehydrogenase /// IPR000205 // NAD binding site /// IPR006108 // 3-hydroxyacyl-CoA dehydrogenase, C-terminal domain /// IPR006176 // 3-	3HCDH_N // 3-hydroxyacyl-CoA dehydrogenase, NAD binding;8.9e-105 /// 3HCDH // 3-hydroxyacyl-CoA dehydrogenase, C-terminal;2e-45

					hydroxyacyl-CoA dehydrogenase, NAD binding domain	
96879_at	59		Ogdh	oxoglutarate dehydrogenase (lipoamide)	IPR001017 // Dehydrogenase, E1 component /// IPR005475 // Transketolase, central region	---
103331_at	58		C030006K11Rik	RIKEN cDNA C030006K11 gene	IPR000834 // Zinc carboxypeptidase A metalloprotease (M14) /// IPR002086 // Aldehyde dehydrogenase	---
92568_at	58		Hkp1	house-keeping protein 1	IPR001737 // Ribosomal RNA adenine dimethylase	RrnaAD // Ribosomal RNA adenine dimethylase;8.2e-06
93531_at	58	21312012	0610033L03Rik	RIKEN cDNA 0610033L03 gene	---	---
93787_f_at	58		1010001C05Rik	RIKEN cDNA 1010001C05 gene	---	---
95736_at	58		Mrpl4	mitochondrial ribosomal protein L4	IPR002136 // Ribosomal protein L4/L1e	Ribosomal_L4 // Ribosomal protein L4/L1 family;5.1e-07
96687_f_at	58	13385436	2010100O12Rik	RIKEN cDNA 2010100O12 gene	---	---
96757_at	58	20070420	D10Jhu81e	DNA segment, Chr 10, Johns Hopkins University 81 expressed	IPR002818 // Family of unknown function ThiJ/PfpI	DJ-1_PfpI // DJ-1/PfpI family;2.3e-28
99166_at	58		0610012G03Rik	RIKEN cDNA 0610012G03 gene	---	---
102124_f_at	57		Cox4a	cytochrome c oxidase, subunit IVa	IPR004203 // Cytochrome c oxidase subunit IV	COX4 // Cytochrome c oxidase subunit IV;1.2e-68
95105_at	57		2010110M21Rik	RIKEN cDNA 2010110M21 gene	---	---
95131_f_at	57	13386096	1810011O01Rik	RIKEN cDNA 1810011O01 gene	---	---
95425_at	57	31982520	Acadl	acetyl-Coenzyme A dehydrogenase, long-chain	IPR006089 // Acyl-CoA dehydrogenase /// IPR006092 // Acyl-CoA dehydrogenase, N-terminal /// IPR006091 // Acyl-	Acyl-CoA_dh_N // Acyl-CoA dehydrogenase, N-terminal doma;9.6e-47 /// Acyl-CoA_dh // Acyl-CoA

					CoA dehydrogenase, middle domain /// IPR006090 // Acyl-CoA dehydrogenase, C-terminal	dehydrogenase, C-terminal doma;1.2e-62 /// Acyl-CoA_dh_M // Acyl-CoA dehydrogenase, middle domain;5.4e-61
96870_at	57	18079339	Aco2	aconitase 2, mitochondrial	IPR000573 // Aconitate hydratase, C-terminal /// IPR002155 // Thiolase /// IPR001030 // Aconitate hydratase, N-terminal	aconitase // Aconitase family (aconitate hydratase);2.1e-272 /// Aconitase_C // Aconitase C-terminal domain;1.8e-86
97880_at	57	21313536	4930529O08Rik	RIKEN cDNA 4930529O08 gene	IPR001078 // Catalytic domain of components of various dehydrogenase complexes /// IPR003016 // 2-oxo acid dehydrogenase, acyltransferase component, lipoyl-binding /// IPR000089 // Biotin/lipoyl attachment	biotin_lipoyl // Biotin-requiring enzyme;1.7e-27 /// 2-oxoacid_dh // 2-oxo acid dehydrogenases acyltransfera;1.8e-132
99471_at	57		AL022671	expressed sequence AL022671	IPR002913 // Lipid-binding START	START // START domain;1.5e-07
104212_at	56	21389320	3110001K13Rik	RIKEN cDNA 3110001K13 gene	IPR002885 // PPR repeat	PPR // PPR repeat;3e-30
92763_at	56		Abcb7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	IPR003439 // ABC transporter /// IPR003593 // AAA ATPase /// IPR001140 // ABC transporter, transmembrane	---

					region	
94534_at	56	18250284	Idh3a	isocitrate dehydrogenase 3 (NAD+) alpha	IPR001804 // Isocitrate/isopropylmalate dehydrogenase /// IPR004434 // Isocitrate dehydrogenase NAD-dependent, mitochondrial	isodh // Isocitrate/isopropylmalate dehydrogenase;2.5e-173
94780_at	56		Zfp288	zinc finger protein 288	IPR000210 // BTB/POZ domain /// IPR000822 // Zn-finger, C2H2 type	zf-C2H2 // Zinc finger, C2H2 type;9.7e-32 /// BTB // BTB/POZ domain;3.9e-27
95441_at	56	12025536	Timm23	translocase of inner mitochondrial membrane 23 homolog (yeast)	IPR005681 // Mitochondrial import inner membrane translocase, subunit Tim23	---
95690_at	56		1110030L07Rik	RIKEN cDNA 1110030L07 gene	---	---
96280_at	56	31981600	Ndufa2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	---	---
96746_at	56	31542559	Dlat	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	IPR004167 // E3 binding domain /// IPR001078 // Catalytic domain of components of various dehydrogenase complexes /// IPR001412 // Aminoacyl-tRNA synthetase, class I /// IPR003016 // 2-oxo acid dehydrogenase, acyltransferase component, lipoyl-binding /// IPR000089 // Biotin/lipoyl	2-oxoacid_dh // 2-oxo acid dehydrogenases acyltransfera;3.8e-127 /// e3_binding // e3 binding domain;2.9e-19 /// biotin_lipoyl // Biotin-requiring enzyme;3.8e-29

					attachment	
96945_at	56		Snap23	synaptosomal-associated protein, 23kD	IPR000928 // SNAP-25 family /// IPR000727 // Target SNARE coiled-coil domain	SNAP-25 // SNAP-25 family;1.3e-24
101472_s_at	55		Pklr	pyruvate kinase liver and red blood cell	IPR001697 // Pyruvate kinase	PK_C // Pyruvate kinase, alpha/beta domain;5.9e-71 /// PK // Pyruvate kinase, barrel domain;1e-252
103261_at	55		Gspt2	G1 to phase transition 2	IPR004160 // Elongation factor Tu, C-terminal /// IPR004161 // Elongation factor Tu, domain 2 /// IPR000795 // Elongation factor, GTP-binding	GTP_EFTU // Elongation factor Tu GTP binding domain;8.1e-93 /// GTP_EFTU_D3 // Elongation factor Tu C-terminal domain;1.4e-30 /// GTP_EFTU_D2 // Elongation factor Tu domain 2;7.5e-11
103849_at	55		Crkl	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	IPR001452 // SH3 domain /// IPR000980 // SH2 motif	SH2 // SH2 domain;5.7e-31 /// SH3 // SH3 domain;1.2e-20
93014_at	55	31980744	Atp5l	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g	---	---
93780_at	55	13385260	0610006O17Rik	RIKEN cDNA 0610006O17 gene	IPR003736 // Phenylacetic acid degradation-related protein	DUF157 // Uncharacterized protein Paal, COG2050;2.9e-10
94562_at	55		Gnpat	glyceronephosphate O-acyltransferase	IPR002123 // Phospholipid/glycerol acyltransferase	Acyltransferase // Acyltransferase;6.2e-33
95611_at	55		Lpl	lipoprotein lipase	IPR002330 // Lipoprotein lipase /// IPR001024 //	lipase // Lipase;1.1e-173 /// PLAT // PLAT/LH2

					Lipoxygenase, LH2 domain /// IPR000734 // Lipase /// IPR000379 // Esterase/lipase/thioesterase, active site	domain;5.8e-37
95658_at	55		Murr1	U2af1-rs1 region 1	---	---
97422_at	55		2010002H18Rik	RIKEN cDNA 2010002H18 gene	IPR002300 // Aminoacyl-tRNA synthetase, class Ia	---
94279_at	54	21536220	0610008F14Rik	RIKEN cDNA 0610008F14 gene	IPR001469 // H+-transporting two-sector ATPase, delta/epsilon subunit	ATP-synt_DE // ATP synthase, Delta/Epsilon chain, long;0.011 /// ATP-synt_DE_N // ATP synthase, Delta/Epsilon chain, beta;4.5e-31
94908_r_at	54		1110001J03Rik	RIKEN cDNA 1110001J03 gene	---	---
98130_at	54	9903609	Txn2	thioredoxin 2	IPR000063 // Thioredoxin type domain /// IPR005746 // Thioredoxin	thiored // Thioredoxin;3.4e-28
98539_at	54		Cops2	COP9 (constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis thaliana)	IPR000717 // Domain in components of the proteasome, COP9-complex and eIF3 (PCI)	PCI // PCI domain;3.4e-25
98929_at	54	13384742	1110018B13Rik	RIKEN cDNA 1110018B13 gene	---	---
99237_at	54		U55872	cDNA sequence U55872	IPR001288 // Initiation factor 3	IF3 // Translation initiation factor IF-3;2.5e-34
101045_at	53	7949047	Hadh2	hydroxyacyl-Coenzyme A dehydrogenase type II	IPR002198 // Short-chain dehydrogenase/reductase SDR /// IPR002347 // Glucose/ribitol dehydrogenase	adh_short // short chain dehydrogenase;7.4e-49

92625_at	53	6679078	Nme2	expressed in non-metastatic cells 2, protein (NM23B) (nucleoside diphosphate kinase)	IPR000834 // Zinc carboxypeptidase A metalloprotease (M14) /// IPR001564 // Nucleoside diphosphate kinase /// IPR003599 // Immunoglobulin subtype /// IPR003598 // Immunoglobulin C-2 type /// IPR003006 // Immunoglobulin/major histocompatibility complex /// IPR003596 // Immunoglobulin V-type	NDK // Nucleoside diphosphate kinase;1.9e-116
93754_at	53	7949037	Ech1	enoyl coenzyme A hydratase 1, peroxisomal	IPR001753 // Enoyl-CoA hydratase/isomerase	ECH // Enoyl-CoA hydratase/isomerase family;1.4e-43
94829_at	53		1110020A09Rik	RIKEN cDNA 1110020A09 gene	---	---
95646_at	53		Cpt2	carnitine palmitoyltransferase 2	IPR000542 // Acyltransferase ChoActase/COT/CPT	Carn_acyltransf // Choline/Carnitine o-acyltransferase;4.4e-289
99594_at	53		Mrpl51	mitochondrial ribosomal protein L51	---	---
100886_f_at	52		Mrpl45	mitochondrial ribosomal protein L45	---	---
94866_at	52	13384844	Mrps16	mitochondrial ribosomal protein S16	IPR000307 // Ribosomal protein S16	Ribosomal_S16 // Ribosomal protein S16;5.4e-17
94909_at	52	13384854	Mrps17	mitochondrial ribosomal protein S17	IPR000266 // Ribosomal protein S17	Ribosomal_S17 // Ribosomal protein S17;0.0021
95941_at	52		AI853514	expressed sequence AI853514	IPR000569 // HECT domain (Ubiquitin-protein ligase)	---

99613_at	52	6678970	Mut	methylmalonyl-Coenzyme A mutase	IPR006100 // Methylmalonyl-CoA mutase subfamily /// IPR006159 // Methylmalonyl-CoA mutase, C-terminal /// IPR006158 // Coenzyme B12-binding /// IPR006099 // Methylmalonyl-CoA mutase /// IPR006098 // Methylmalonyl-CoA mutase, N-terminal domain	MM_CoA_mutase // Methylmalonyl-CoA mutase;0 /// B12-binding // B12 binding domain;1.7e-20
102624_at	51		Stc2	stanniocalcin 2	IPR004978 // Stanniocalcin	Stanniocalcin // Stanniocalcin family;5.7e-193
94327_at	51		Mrps18a	mitochondrial ribosomal protein S18A	IPR001648 // Ribosomal protein S18	Ribosomal_S18 // Ribosomal protein S18;0.0013
94667_at	51		---	ESTs	---	---
94940_at	51	31980706	Mccc1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	IPR005482 // Biotin carboxylase, C-terminal /// IPR005481 // Carbamoyl-phosphate synthetase large chain, N-terminal /// IPR001882 // Biotin-requiring enzyme, attachment site /// IPR000089 // Biotin/lipoyl attachment /// IPR005479 // Carbamoyl-phosphate synthase L chain, ATP-binding	CPSase_L_chain // Carbamoyl-phosphate synthase L chain,;2.9e-53 /// biotin_lipoyl // Biotin-requiring enzyme;3.5e-14 /// Biotin_carb_C // Biotin carboxylase C-terminal domain;1e-43 /// CPSase_L_D2 // Carbamoyl-phosphate synthase L chain,;2.2e-100

96756_at	51		1110007M04Rik	RIKEN cDNA 1110007M04 gene	---	---
96871_at	51		2310042G06Rik	RIKEN cDNA 2310042G06 gene	---	---
98892_at	51		Lpin1	lipin 1	---	---
101867_at	50		Gpam	glycerol-3-phosphate acyltransferase, mitochondrial	IPR002123 // Phospholipid/glycerol acyltransferase	Acyltransferase // Acyltransferase;5.3e-36
94855_at	50	6679299	Phb	prohibitin	IPR001107 // Band 7 protein /// IPR000163 // Prohibitin	Band_7 // SPFH domain / Band 7 family;3.7e-61
96744_at	50		Acp6	acid phosphatase 6, lysophosphatidic	IPR000560 // Histidine acid phosphatase	acid_phosphat // Histidine acid phosphatase;2.4e-07
96858_at	50	6755004	Pdcd8	programmed cell death 8	IPR001327 // FAD-dependent pyridine nucleotide-disulphide oxidoreductase /// IPR001100 // Pyridine nucleotide-disulphide oxidoreductase, class I	pyr_redox // Pyridine nucleotide-disulphide oxidoreducta;2.6e-52
96898_at	50	33859512	Atp5f1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	---	---
100550_f_at	49	16716343	Cox6c	cytochrome c oxidase, subunit VIc	IPR004204 // Cytochrome c oxidase subunit VIc	COX6C // Cytochrome c oxidase subunit VIc;2.5e-50
103780_at	49		1700021F05Rik	RIKEN cDNA 1700021F05 gene	---	---
104153_at	49	9789985	Ivd	isovaleryl coenzyme A dehydrogenase	IPR006089 // Acyl-CoA dehydrogenase /// IPR006092 // Acyl-CoA dehydrogenase, N-terminal /// IPR006091 // Acyl-CoA dehydrogenase, middle domain /// IPR006090 // Acyl-CoA dehydrogenase, C-terminal	Acyl-CoA_dh_N // Acyl-CoA dehydrogenase, N-terminal doma;4.7e-58 /// Acyl-CoA_dh // Acyl-CoA dehydrogenase, C-terminal doma;3e-55 /// Acyl-CoA_dh_M // Acyl-CoA dehydrogenase,

						middle domain;9.3e-71
92364_at	49		Celsr2	cadherin EGF LAG seven-pass G-type receptor 2	IPR002126 // Cadherin /// IPR001881 // EGF-like calcium-binding /// IPR001368 // TNFR/CD27/30/40/95 cysteine-rich region /// IPR000561 // EGF-like domain /// IPR000742 // EGF-like domain, subtype 2 /// IPR000203 // GPS domain /// IPR000152 // Aspartic acid and asparagine hydroxylation site /// IPR002049 // Laminin-type EGF-like domain /// IPR000832 // G-protein coupled receptors family 2 (secretin-like) /// IPR001791 // Laminin G /// IPR001879 // Hormone receptor, extracellular	laminin_G // Laminin G domain;1.2e-18 /// EGF // EGF-like domain;1.6e-21 /// GPS // Latrophilin/CL-1-like GPS domain;1.3e-26 /// cadherin // Cadherin domain;2.9e-209 /// 7tm_2 // 7 transmembrane receptor (Secretin family);1.8e-58 /// HRM // Hormone receptor domain;6.2e-17
93399_at	49		Rai2	retinoic acid induced 2	---	---
93611_at	49		Tbx6	T-box 6	IPR001699 // Transcription factor, T-box /// IPR002070 // Transcription factor, Brachyury	T-box // T-box;1.1e-125
94531_at	49	33859690	2310005O14Rik	RIKEN cDNA 2310005O14 gene	---	---
96096_f_at	49	13195670	2610207I16Rik	RIKEN cDNA 2610207I16 gene	IPR002198 // Short-chain	adh_short // short chain

					dehydrogenase/reductase SDR /// IPR003033 // Sterol-binding /// IPR002347 // Glucose/ribitol dehydrogenase	dehydrogenase;1.2e-29 /// SCP2 // SCP-2 sterol transfer family;1.5e-27
96261_at	49		2310028O11Rik	RIKEN cDNA 2310028O11 gene	---	---
99148_at	49	33859554	Fh1	fumarate hydratase 1	IPR000362 // Fumarate lyase	---
104710_at	48		Bak1	BCL2-antagonist/killer 1	IPR000712 // Apoptosis regulator Bcl-2 protein, BH /// IPR002475 // BCL2-like apoptosis inhibitor	Bcl-2 // Apoptosis regulator proteins, Bcl-2 family;2.3e-39
96095_i_at	48	13195670	2610207I16Rik	RIKEN cDNA 2610207I16 gene	IPR002198 // Short-chain dehydrogenase/reductase SDR /// IPR003033 // Sterol-binding /// IPR002347 // Glucose/ribitol dehydrogenase	adh_short // short chain dehydrogenase;1.2e-29 /// SCP2 // SCP-2 sterol transfer family;1.5e-27
97397_at	48		D5Ertd33e	DNA segment, Chr 5, ERATO Doi 33, expressed	IPR004033 // UbiE/COQ5 methyltransferase /// IPR000051 // SAM (and some other nucleotide) binding motif /// IPR004034 // Ubiquinone/menaquinone biosynthesis methyltransferase /// IPR001601 // Generic methyltransferase	Ubie_methyltran // ubiE/COQ5 methyltransferase family;1.4e-116
103294_at	47		Rgs5	regulator of G-protein signaling 5	IPR000342 // Regulator of G protein	---
103646_at	47	6681009	Crat	carnitine acetyltransferase	IPR000542 //	Carn_acyltransf //

					Acyltransferase ChoActase/COT/CPT	Choline/Carnitine o-acyltransferase;0
94508_at	47		1810020E01Rik	RIKEN cDNA 1810020E01 gene	---	---
95939_i_at	47		9830126M18	hypothetical protein 9830126M18	---	---
96035_at	47	31982494	Bckdha	branched chain ketoacid dehydrogenase E1, alpha polypeptide	IPR001017 // Dehydrogenase, E1 component	E1_dehydrog // Dehydrogenase E1 component;1.8e-162
96296_at	47		Mrpl15	mitochondrial ribosomal protein L15	IPR001196 // Ribosomal protein L15	---
96670_at	47	21313138	0610025I19Rik	RIKEN cDNA 0610025I19 gene	IPR004287 // 2-hydroxychromene-2-carboxylate isomerase	HCCA_isomerase // 2-hydroxychromene-2-carboxylate isomer;1.8e-110
97796_at	47		Crsp2	cofactor required for Sp1 transcriptional activation subunit 2	---	---
98128_at	47	7949005	Atp5j	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	---	---
100527_at	46	21311867	D11Ertd99e	DNA segment, Chr 11, ERATO Doi 99, expressed	---	---
101027_s_at	46		Pttg1	pituitary tumor-transforming 1	---	---
104215_at	46		9130025P16Rik	RIKEN cDNA 9130025P16 gene	---	---
104767_f_at	46		Mrps18a	mitochondrial ribosomal protein S18A	IPR001648 // Ribosomal protein S18	Ribosomal_S18 // Ribosomal protein S18;0.0013
93346_at	46		Pgk1	phosphoglycerate kinase 1	IPR001576 // Phosphoglycerate kinase	PGK // Phosphoglycerate kinase;8.4e-296
93539_at	46		1810004D07Rik	RIKEN cDNA 1810004D07 gene	---	---
95498_at	46	13384968	Mrps15	mitochondrial ribosomal protein S15	IPR005290 // Ribosomal protein S15, bacterial chloroplast and mitochondrial type /// IPR000589 // Ribosomal protein S15	Ribosomal_S15 // Ribosomal protein S15;1.1e-08
96947_at	46	21312004	0610009I16Rik	RIKEN cDNA 0610009I16 gene	IPR000049 //	ETF_beta // Electron

					Electron transfer flavoprotein beta-subunit /// IPR006162 // Phosphopantetheine attachment site	transfer flavoprotein beta subunit;3.3e-124
103401_at	45	31982522	Acads	acetyl-Coenzyme A dehydrogenase, short chain	IPR006089 // Acyl-CoA dehydrogenase /// IPR006092 // Acyl-CoA dehydrogenase, N-terminal /// IPR006091 // Acyl-CoA dehydrogenase, middle domain /// IPR006090 // Acyl-CoA dehydrogenase, C-terminal	Acyl-CoA_dh_M // Acyl-CoA dehydrogenase, middle domain;9e-64 /// Acyl-CoA_dh_N // Acyl-CoA dehydrogenase, N-terminal doma;1.9e-60 /// Acyl-CoA_dh // Acyl-CoA dehydrogenase, C-terminal doma;3.9e-77
104057_at	45	13277394	Grpel1	GrpE-like 1, mitochondrial	IPR000740 // GrpE protein	GrpE // GrpE;3.8e-76
95064_at	45	29126205	D18Ertd240e	DNA segment, Chr 18, ERATO Doi 240, expressed	---	---
96180_at	45		Rgs5	regulator of G-protein signaling 5	IPR000342 // Regulator of G protein	---
96887_at	45	9506933	Np15	nuclear protein 15.6	---	---
97706_at	45		---	ESTs	---	---
96322_at	44		Edf1	endothelial differentiation-related factor 1	IPR001387 // Helix-turn-helix motif	HTH_3 // Helix-turn-helix;1.2e-10
98527_at	44		---	---	---	---
102193_at	43		Sah	SA rat hypertension-associated homolog	IPR000873 // AMP-dependent synthetase and ligase	AMP-binding // AMP-binding enzyme;1.2e-102
93332_at	43		Cd36	CD36 antigen	IPR002159 // CD36 antigen /// IPR005428 // Adhesion molecule CD36	CD36 // CD36 family;1e-208
93528_s_at	43		Klf9	Kruppel-like factor 9	IPR000822 // Zn-finger, C2H2 type	zf-C2H2 // Zinc finger, C2H2 type;2.4e-21

93994_at	43		Sycp3	synaptonemal complex protein 3	---	---
95730_at	43		Tce2	T-complex expressed gene 2	---	---
96676_at	43		1810049H20Rik	RIKEN cDNA 1810049H20 gene	---	---
97512_at	43	21312554	2010107E04Rik	RIKEN cDNA 2010107E04 gene	---	---
101078_at	42		Bsg	basigin	IPR003599 // Immunoglobulin subtype /// IPR003006 // Immunoglobulin/major histocompatibility complex	---
94365_at	42		1190005L05Rik	RIKEN cDNA 1190005L05 gene	IPR001310 // Histidine triad (HIT) protein	---
94485_at	42		Peci	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase	IPR001753 // Enoyl-CoA hydratase/isomerase /// IPR000582 // Acyl-coA-binding protein, ACBP	ECH // Enoyl-CoA hydratase/isomerase family;3.2e-22 /// ACBP // Acyl CoA binding protein;9.2e-41
95056_r_at	42		Tcte1l	t-complex-associated-testis-expressed 1-like	IPR005334 // Tctex-1 family	Tctex-1 // Tctex-1 family;5.5e-55
98966_at	42	6753610	Dbt	dihydrolipoamide branched chain transacylase E2	IPR004167 // E3 binding domain /// IPR001078 // Catalytic domain of components of various dehydrogenase complexes /// IPR003016 // 2-oxo acid dehydrogenase, acyltransferase component, lipoyl-binding /// IPR000089 // Biotin/lipoyl attachment	e3_binding // e3 binding domain;6.3e-18 /// 2-oxoacid_dh // 2-oxo acid dehydrogenases acyltransfera;5.4e-108 /// biotin_lipoyl // Biotin-requiring enzyme;2e-25
100963_at	41		2810403H05Rik	RIKEN cDNA 2810403H05 gene	---	---
102049_at	41	7305375	Pdk4	pyruvate dehydrogenase kinase,	IPR005467 //	HATPase_c //

				isoenzyme 4	Histidine kinase /// IPR004358 // Bacterial sensor protein C-terminal /// IPR003594 // ATP-binding protein, ATPase-like	Histidine kinase-, DNA gyrase B-, and HSP90;5e-19
103319_at	41		Psmd10	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	IPR002110 // Ankyrin	ank // Ankyrin repeat;8.1e-49
93040_at	41		Fxyd1	FXYD domain-containing ion transport regulator 1	IPR000272 // ATP1G1/PLM/MAT8 family	ATP1G1_PLM_MAT8 // ATP1G1/PLM/MAT8 family;4e-35
93948_at	41		Nck2	non-catalytic region of tyrosine kinase adaptor protein 2	IPR001452 // SH3 domain /// IPR000980 // SH2 motif	SH3 // SH3 domain;1.4e-57 /// SH2 // SH2 domain;6e-29
96388_at	41		---	EST	---	---
98924_at	41		4930569O04Rik	RIKEN cDNA 4930569O04 gene	IPR000768 // NAD:arginine ADP-ribosyltransferase, ART	---
100099_at	40		Smpd1	sphingomyelin phosphodiesterase 1, acid lysosomal	IPR000004 // Saposin type B /// IPR004843 // Metallo-phosphoesterase	Metallophos // Calcineurin-like phosphoesterase;6.9e-17
100756_r_at	40		Tyms-ps	thymidylate synthase, pseudogene	---	---
95149_at	40		Copz1	coatomer protein complex, subunit zeta 1	IPR000804 // Clathrin adaptor complex, small chain	Clat_adaptor_s // Clathrin adaptor complex small chain;3.8e-76
95695_at	40		---	---	---	---
95721_at	40		Mapkapk2	MAP kinase-activated protein kinase 2	IPR002290 // Serine/Threonine protein kinase /// IPR000719 // Eukaryotic protein kinase	---
99661_r_at	40	6680991	Cox7c	cytochrome c oxidase, subunit VIIc	IPR004202 // Cytochrome c	COX7C // Cytochrome c oxidase subunit

					oxidase subunit VIIc	VIIc;4e-33
100991_at	39		Itgb1bp1	integrin beta 1 binding protein 1	IPR006020 // Phosphotyrosine interaction domain	---
93786_i_at	39		1010001C05Rik	RIKEN cDNA 1010001C05 gene	---	---
95468_at	39		Egln1	EGL nine homolog 1 (C. elegans)	IPR002893 // Zn-finger, MYND type /// IPR005123 // 2OG-Fe(II) oxygenase superfamily	2OG-FeII_Oxy // 2OG-Fe(II) oxygenase superfamily;3.4e-10
103492_at	38		Cpxm1	carboxypeptidase X 1 (M14 family)	IPR000834 // Zinc carboxypeptidase A metalloprotease (M14) /// IPR000421 // Coagulation factor 5/8 type C domain (FA58C) /// IPR001993 // Mitochondrial substrate carrier	F5_F8_type_C // F5/8 type C domain;3.2e-70 /// Zn_carbOpept // Zinc carboxypeptidase;8.8e-21
95653_at	38		Mrpl37	mitochondrial ribosomal protein L37	---	---
95718_f_at	38	13128954	Usmg5	upregulated during skeletal muscle growth 5	---	---
98545_at	38	6671622	Bcap37	B-cell receptor-associated protein 37	IPR001107 // Band 7 protein /// IPR000163 // Prohibitin	Band_7 // SPFH domain / Band 7 family;6e-56
98616_f_at	38		Myh7	myosin, heavy polypeptide 7, cardiac muscle, beta	IPR004009 // Myosin N-terminal SH3-like domain /// IPR000048 // IQ calmodulin-binding region /// IPR002928 // Myosin tail /// IPR001609 // Myosin head (motor domain)	myosin_head // Myosin head (motor domain);0 /// Myosin_N // Myosin N-terminal SH3-like domain;4.3e-18 /// IQ // IQ calmodulin-binding motif;0.01 /// Myosin_tail // Myosin tail;0
99678_f_at	38	31980744	Atp5l	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit	---	---

				g		
100592_at	37		Ghitm	growth hormone inducible transmembrane protein	IPR002199 // Bax inhibitor 1	---
92845_at	37	18266680	Oxct	3-oxoacid CoA transferase	IPR004165 // Coenzyme A transferase /// IPR004164 // Coenzyme A transferase 2 /// IPR004163 // Coenzyme A transferase 1	CoA_trans // Coenzyme A transferase;2.9e-197
93277_at	37	31981679	Hspd1	heat shock protein 1 (chaperonin)	IPR002423 // Chaperonin Cpn60/TCP-1 /// IPR001844 // Chaperonin Cpn60	cpn60_TCP1 // TCP-1/cpn60 chaperonin family;2.3e-190
93551_at	37		2510029B14Rik	RIKEN cDNA 2510029B14 gene	IPR000268 // RNA polymerases N/8 Kd subunits	---
95076_at	37		1500032L24Rik	RIKEN cDNA 1500032L24 gene	---	---
95426_at	37	29789289	Echs1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	IPR001753 // Enoyl-CoA hydratase/isomerase	---
98561_at	37		Tnni1	troponin I, skeletal, slow 1	IPR001978 // Troponin	Troponin // Troponin;2e-59
99536_at	37		Kip2-pending	kinase interacting protein 2	IPR002048 // Calcium-binding EF-hand	efhand // EF hand;3.4e-06
102145_f_at	36		Esrra	estrogen related receptor, alpha	IPR001628 // Zn-finger, C4-type steroid receptor /// IPR000324 // Vitamin D receptor /// IPR001723 // Steroid hormone receptor /// IPR000536 // Ligand-binding domain of nuclear hormone	zf-C4 // Zinc finger, C4 type (two domains);3.1e-51 /// hormone_rec // Ligand-binding domain of nuclear hormone;4.2e-32

					receptor /// IPR000515 // Binding-protein-dependent transport systems inner membrane component	
93459_s_at	36		Fzd4	frizzled homolog 4 (Drosophila)	IPR000539 // Frizzled protein /// IPR000024 // Frizzled CRD region /// IPR000832 // G-protein coupled receptors family 2 (secretin-like)	Fz // Fz domain;2.2e-65 /// Frizzled // Frizzled/Smoothened family membrane region;1.7e-206
95693_at	36		Idh2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	IPR001804 // Isocitrate/isopropylmalate dehydrogenase /// IPR004790 // Isocitrate dehydrogenase NADP-dependent, eukaryotic	isodh // Isocitrate/isopropylmalate dehydrogenase;4.3e-116 /// isodh // Isocitrate/isopropylmalate dehydrogenase;1.1e-102
97279_at	36	21704140	AI265272	EST AI265272	IPR002204 // 3-hydroxyisobutyrate dehydrogenase /// IPR006115 // 6-phosphogluconate dehydrogenase, NAD binding domain /// IPR006183 // 6-phosphogluconate dehydrogenase	NAD_binding_2 // NAD binding domain of 6-phosphogluconat;0.0053
102378_at	35		Sspn	sarcospan	---	---
93114_at	35	10181184	Atp5j2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	---	---
94375_at	35		Hk2	hexokinase 2	IPR001312 // Hexokinase	hexokinase2 // Hexokinase;0 ///

					hexokinase // Hexokinase;7.2e-290
100574_f_at	34	Gpi1	glucose phosphate isomerase 1	IPR001672 // Phosphoglucose isomerase (PGI)	PGI // Phosphoglucose isomerase;0
93740_at	34	Nsep1	nuclease sensitive element binding protein 1	IPR002059 // Cold-shock DNA-binding domain	CSD // 'Cold-shock' DNA-binding domain;4.7e-36
101347_at	33	Igk-V8	immunoglobulin kappa chain variable 8 (V8)	IPR003600 // Immunoglobulin-like /// IPR003599 // Immunoglobulin subtype /// IPR001865 // Ribosomal protein S2 /// IPR003006 // Immunoglobulin/major histocompatibility complex /// IPR003597 // Immunoglobulin C-type /// IPR003596 // Immunoglobulin V-type	---
101588_at	33	Slc16a1	solute carrier family 16 (monocarboxylic acid transporters), member 1	IPR004743 // Monocarboxylate transporter	---
101991_at	33	Fmo1	flavin containing monooxygenase 1	IPR002253 // Flavin-containing monooxygenase (FMO) 1 /// IPR001327 // FAD-dependent pyridine nucleotide-disulphide oxidoreductase /// IPR000759 // Adrenodoxin reductase /// IPR000960 // Flavin-	FMO-like // Flavin-binding monooxygenase-like;0

					containing monooxygenase FMO /// IPR000566 // Lipocalin-related protein and Bos/Can/Equ allergen	
92646_at	33		Mrpl23	mitochondrial ribosomal protein L23	IPR001014 // Ribosomal L23 protein	---
93325_at	33		Polr2e	polymerase (RNA) II (DNA directed) polypeptide E (25kDa)	---	---
94507_at	33	31560705	Facl2	fatty acid Coenzyme A ligase, long chain 2	IPR000873 // AMP-dependent synthetase and ligase	AMP-binding // AMP-binding enzyme;1.6e-103
96122_at	33		2310016A09Rik	RIKEN cDNA 2310016A09 gene	IPR002925 // Dienelactone hydrolase /// IPR001064 // Beta and gamma crystallin /// IPR000379 // Esterase/lipase/thioesterase, active site	---
96256_at	33	6680690	Prdx3	peroxiredoxin 3	IPR000866 // Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	AhpC-TSA // AhpC/TSA family;3.1e-83
96678_at	33	13507612	D14Ucla2	DNA segment, Chr 14, University of California at Los Angeles 2	IPR001092 // Basic helix-loop-helix dimerization domain bHLH /// IPR002198 // Short-chain dehydrogenase/reductase SDR /// IPR002347 // Glucose/ribitol dehydrogenase	adh_short // short chain dehydrogenase;1.9e-12
100538_at	32		Sod1	superoxide dismutase 1, soluble	IPR001424 //	---

101990_at	32		Ldh2	lactate dehydrogenase 2, B chain	Copper/Zinc superoxide dismutase IPR001236 // Lactate/malate dehydrogenase /// IPR001557 // L-lactate dehydrogenase	ldh // lactate/malate dehydrogenase, NAD binding do;2.6e-81 /// ldh_C // lactate/malate dehydrogenase, alpha/beta C-t;3.3e-85
102302_at	32		Bckdhb	branched chain ketoacid dehydrogenase E1, beta polypeptide	---	---
93589_at	32		Lysal1	lysosomal apyrase-like 1	IPR000407 // GDA1/CD39 family of nucleoside phosphatase	GDA1_CD39 // GDA1/CD39 (nucleoside phosphatase) family;2.2e-93
101541_at	31		---	ESTs, Weakly similar to S50828 hypothetical protein - Escherichia coli [E. coli]	---	---
101580_at	31	13384754	Cox7b	cytochrome c oxidase subunit VIIb	---	---
102128_f_at	31	31981257	Mrps25	mitochondrial ribosomal protein S25	---	---
92333_at	31		Sirt1	sirtuin 1 ((silent mating type information regulation 2, homolog) 1 (S. cerevisiae)	IPR003000 // Silent information regulator protein Sir2	SIR2 // Sir2 family;1.7e-99
94489_at	31		Ptp4a1	protein tyrosine phosphatase 4a1	IPR000387 // Tyrosine specific protein phosphatase and dual specificity protein phosphatase /// IPR000242 // Tyrosine specific protein phosphatase /// IPR001230 // Prenyl group binding site (CAAX box) /// IPR000340 // Dual specificity protein	Y_phosphatase // Protein-tyrosine phosphatase;4.2e-07

					phosphatase	
95016_at	31		Nrp	neuropilin	IPR000998 // MAM domain /// IPR000421 // Coagulation factor 5/8 type C domain (FA58C) /// IPR000859 // CUB domain	F5_F8_type_C // F5/8 type C domain;1.5e-128 /// CUB // CUB domain;9.7e-93 /// MAM // MAM domain;1.6e-69
99009_at	31	31543330	Nnt	nicotinamide nucleotide transhydrogenase	IPR004003 // NAD(P) transhydrogenase beta subunit /// IPR004571 // NAD(P) transhydrogenase, alpha subunit /// IPR004002 // Alanine dehydrogenase and pyridine nucleotide transhydrogenase	PNTB // NAD(P) transhydrogenase beta subunit;0 /// AlaDh_PNT // Alanine dehydrogenase/pyridine nucleotide t;1.1e-74
102402_at	30	6679957	Gbas	glioblastoma amplified sequence	---	---
92371_at	30		Hrc	histidine rich calcium binding protein	IPR000561 // EGF-like domain /// IPR002049 // Laminin-type EGF-like domain	---
93308_s_at	30	6679237	Pcx	pyruvate carboxylase	IPR005482 // Biotin carboxylase, C-terminal /// IPR005930 // Pyruvate carboxylase /// IPR005481 // Carbamoyl-phosphate synthetase large chain, N-terminal /// IPR003379 // Conserved carboxylase region /// IPR001882 // Biotin-requiring enzyme,	HMGL-like // HMGL-like;3.5e-43 /// biotin_lipoyl // Biotin-requiring enzyme;1.7e-26 /// CPSase_L_D2 // Carbamoyl-phosphate synthase L chain,;1.7e-100 /// Biotin_carb_C // Biotin carboxylase C-terminal domain;2.3e-61 /// CPSase_L_chain // Carbamoyl-phosphate

					attachment site /// IPR000089 // Biotin/lipoyl attachment /// IPR005479 // Carbamoyl-phosphate synthase L chain, ATP-binding /// IPR000891 // HMG-CoA lyase-like	synthase L chain,;2.4e-43 /// PYC_OADA // Conserved carboxylase domain;4.4e-121
94668_at	30		---	ESTs	---	---
95067_at	30		Mrpl2	mitochondrial ribosomal protein L2	IPR002171 // Ribosomal protein L2	Ribosomal_L2_C // Ribosomal Proteins L2, C-terminal doma;4.6e-46 /// Ribosomal_L2 // Ribosomal Proteins L2, RNA binding dom;9.2e-29
97410_at	30		D130005A03	hypothetical protein D130005A03	---	---
98610_at	30		1500012D08Rik	RIKEN cDNA 1500012D08 gene	IPR003029 // RNA binding S1	---
99507_at	30		Ucp1	uncoupling protein 1, mitochondrial	IPR002030 // Mitochondrial brown fat uncoupling protein /// IPR002113 // Adenine nucleotide translocator 1 /// IPR001993 // Mitochondrial substrate carrier	mito_carr // Mitochondrial carrier protein;2e-79
AFFX-GapdhMur/M32599_3_at	30	6679937				
100671_at	29		---	---	---	---
102668_at	29		Ppara	peroxisome proliferator activated receptor alpha	IPR001628 // Zn-finger, C4-type steroid receptor /// IPR003074 //	zf-C4 // Zinc finger, C4 type (two domains);1.1e-46 /// hormone_rec //

					Peroxisome proliferator-activated receptor /// IPR001723 // Steroid hormone receptor /// IPR003076 // Peroxisome proliferator-activated receptor, alpha /// IPR000536 // Ligand-binding domain of nuclear hormone receptor	Ligand-binding domain of nuclear hormone;3.1e-38
103881_at	29	22203753	1110013G13Rik	RIKEN cDNA 1110013G13 gene	IPR001596 // Inorganic pyrophosphatase	Pyrophosphatase // Inorganic pyrophosphatase;1.1e-107
104577_at	29		Mlh1	mutL homolog 1 (E. coli)	IPR002099 // DNA mismatch repair protein /// IPR003594 // ATP-binding protein, ATPase-like	DNA_mis_repair // DNA mismatch repair protein, C-termina;1.7e-43 /// HATPase_c // Histidine kinase-, DNA gyrase B-, and;0.00044
92592_at	29		Gpd1	glycerol-3-phosphate dehydrogenase 1 (soluble)	IPR006109 // NAD-dependent glycerol-3-phosphate dehydrogenase domain /// IPR006168 // NAD-dependent glycerol-3-phosphate dehydrogenase	NAD_Gly3P_dh // NAD-dependent glycerol-3-phosphate dehyd;5.8e-204
93050_at	29		Mylpc	myosin light chain, phosphorylatable, cardiac ventricles	IPR002048 // Calcium-binding EF-hand	efhand // EF hand;1.7e-12
93646_at	29		Ptk9	PTK9 protein tyrosine kinase 9	IPR002108 // Actin-binding, cofilin/tropomyosin	cofilin_ADF // Cofilin/tropomyosin-type actin-binding

					type	pr;3.8e-08
94902_at	29		Sod3	superoxide dismutase 3, extracellular	IPR001424 // Copper/Zinc superoxide dismutase	sodcu // Copper/zinc superoxide dismutase (SODC);1e-67
96856_at	29	6680816	C1qbp	complement component 1, q subcomponent binding protein	IPR003428 // Mitochondrial glycoprotein	MAM33 // Mitochondrial glycoprotein;2e-108
98056_at	29		Phlda3	pleckstrin homology-like domain, family A, member 3	IPR001849 // Pleckstrin-like	---
98876_at	29		Mrpl11	mitochondrial ribosomal protein L11	IPR000911 // Ribosomal protein L11	Ribosomal_L11 // Ribosomal protein L11, RNA binding do;3.7e-18 /// Ribosomal_L11_N // Ribosomal protein L11, N-terminal dom;7.1e-25
99604_at	29		1810015H18Rik	RIKEN cDNA 1810015H18 gene	---	---
99667_at	29	6753502	Cox6a2	cytochrome c oxidase, subunit VI a, polypeptide 2	IPR001349 // Cytochrome c oxidase, subunit VIa	COX6A // Cytochrome c oxidase subunit VIa;1.9e-51
AFFX-GapdhMur/M32599_5_st	29	6679937				
AFFX-PyruCarbMur/L09192_MA_at	29	6679237				
101063_at	28		Tncc	troponin C, cardiac/slow skeletal	IPR002048 // Calcium-binding EF-hand /// IPR001125 // Recoverin	efhand // EF hand;1.5e-25
92553_at	28		Es10	esterase 10	IPR000801 // Putative esterase /// IPR000379 // Esterase/lipase/thioesterase, active site	Esterase // Putative esterase;5.5e-107
93514_at	28		---	---	---	---
94166_g_at	28		Ccl1	chemokine (C-C motif) ligand 1	IPR001811 // Small	IL8 // Small cytokines

				chemokine, interleukin-8 like /// IPR000827 // Small chemokine, C-C subfamily	(intecrine/chemokine), inter;2.2e-23
96003_at	28	Mta1l1	metastasis associated 1-like 1	IPR001005 // Myb DNA-binding domain /// IPR000949 // ELM2 domain /// IPR000679 // Zn-finger, GATA type /// IPR000345 // Cytochrome c heme-binding site /// IPR001025 // Bromo adjacent region	myb_DNA-binding // Myb-like DNA-binding domain;3.2e-09 /// ELM2 // ELM2 domain;1.4e-21 /// BAH // BAH domain;5.7e-20 /// GATA // GATA zinc finger;2.9e-14
97265_at	28	1810013D10Rik	RIKEN cDNA 1810013D10 gene	---	---
97319_at	28	Rrad	Ras-related associated with diabetes	IPR003575 // Ras small GTPase /// IPR005225 // Small GTP-binding protein domain /// IPR001806 // Ras GTPase superfamily	ras // Ras family;1.8e-16
97951_s_at	28	Tsc2	tuberous sclerosis 2	IPR003913 // Tuberin /// IPR000331 // Rap/ran-GAP	Tuberin // Tuberin;0 /// Rap_GAP // Rap/ran-GAP;2.4e-84
98039_at	28	2410015M20Rik	RIKEN cDNA 2410015M20 gene	---	---
99532_at	28	Tob1	transducer of ErbB-2.1	---	Anti_proliferat // BTG1 family;3.1e-100
100535_at	27	Eif4g2	eukaryotic translation initiation factor 4, gamma 2	IPR000504 // RNA-binding region RNP-1 (RNA recognition motif) /// IPR003890 // Initiation factor eIF-4 gamma, middle /// IPR003891 // Initiation factor eIF-4 gamma, MA3 ///	W2 // eIF4-gamma/eIF5/eIF2-epsilon;7.1e-33 /// MA3 // MA3 domain;4.5e-33 /// MIF4G // MIF4G domain;2.7e-61

					IPR003307 // eIF4-gamma/eIF5/eIF2-epsilon	---
101028_i_at	27		Actc1	actin, alpha, cardiac	IPR004000 // Actin/actin-like /// IPR004001 // Actin	actin // Actin;1.2e-276
101409_at	27		Lgtn	ligatin	IPR004521 // Uncharacterized domain 2 /// IPR001950 // Translation initiation factor SUI1 /// IPR002478 // PUA domain	---
101946_at	27	6678760	Lypla1	lysophospholipase 1	IPR003140 // Phospholipase/Carboxylesterase /// IPR000379 // Esterase/lipase/thioesterase, active site	abhydrolase_2 // Phospholipase/Carboxylesterase;2.2e-121
102560_at	27		---	---	---	---
103559_at	27		Prkaca	protein kinase, cAMP dependent, catalytic, alpha	IPR000961 // Protein kinase C-terminal domain /// IPR002290 // Serine/Threonine protein kinase /// IPR000719 // Eukaryotic protein kinase	pkinase_C // Protein kinase C terminal domain;0.00063 /// pkinase // Protein kinase domain;1.5e-84
92831_at	27		Sfxn1	sideroflexin 1	IPR004686 // Tricarboxylate/iron carrier	Mtc // Tricarboxylate carrier;2e-200
93196_at	27		D8Ertd531e	DNA segment, Chr 8, ERATO Doi 531, expressed	---	---
94192_at	27		Gdap10	ganglioside-induced differentiation-associated-protein 10	---	---
94381_at	27		Umpk	uridine monophosphate kinase	IPR000764 // Uridine kinase /// IPR006083 //	---

				Phosphoribulokinase/ uridine kinase	
94925_at	27	1810055D05Rik	RIKEN cDNA 1810055D05 gene	IPR001623 // Heat shock protein DnaJ, N-terminal	DnaJ // DnaJ domain;2.3e-05
95469_at	27	Btd	biotinidase	IPR003010 // Nitrilase/cyanide hydratase	CN_hydrolase // Carbon-nitrogen hydrolase;2.4e-05
95587_at	27	---	Mus musculus adult male adrenal gland cDNA, RIKEN full-length enriched library, clone:B330005C17 product:hypothetical Arginine-rich region containing protein, full insert sequence.	---	---
95869_at	27	---	ESTs	---	---
95943_at	27	---	ESTs	---	---
96243_f_at	27	Aldh9a1	aldehyde dehydrogenase 9, subfamily A1	IPR002086 // Aldehyde dehydrogenase	aldedh // Aldehyde dehydrogenase family;3.9e-212
96348_at	27	0610039C21Rik	RIKEN cDNA 0610039C21 gene	IPR002641 // Patatin	Patatin // Patatin-like phospholipase;7.7e-34
96355_at	27	2900055D03Rik	RIKEN cDNA 2900055D03 gene	---	---
97777_at	27	Nkx2-5	NK2 transcription factor related, locus 5 (Drosophila)	IPR001356 // Homeobox	homeobox // Homeobox domain;8.9e-27
99331_at	27	Apeg1	aortic preferentially expressed gene 1	IPR003006 // Immunoglobulin/major histocompatibility complex /// IPR002290 // Serine/Threonine protein kinase /// IPR003599 // Immunoglobulin subtype /// IPR003600 // Immunoglobulin-like /// IPR003961 //	ig // Immunoglobulin domain;0.00073

				Fibronectin, type III /// IPR001245 // Tyrosine protein kinase /// IPR002965 // Proline-rich extensin /// IPR000719 // Eukaryotic protein kinase /// IPR003598 // Immunoglobulin C-2 type	
99994_at	27	Cidea	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	IPR003508 // Caspase-activated nuclease CIDE-N	CIDE-N // CIDE-N domain;7.7e-51
100614_at	26	Mb	myoglobin	---	globin // Globin;1.4e-36
100921_at	26	Tnni3	troponin I, cardiac	IPR001978 // Troponin	Troponin // Troponin;7.3e-59
101015_s_at	26	Ifnar2	interferon (alpha and beta) receptor 2	IPR000282 // Cytokine receptor class 2	---
101490_at	26	1810010A06Rik	RIKEN cDNA 1810010A06 gene	IPR000361 // Protein of unknown function, HesB/YadR/YfhF	HesB-like // HesB-like domain;4e-42
102653_at	26	Ryr2	ryanodine receptor 2, cardiac	IPR005821 // Ion transport protein /// IPR003877 // SPla/RYanodine receptor SPRY /// IPR003608 // MIR domain /// IPR002048 // Calcium-binding EF-hand /// IPR000699 // Intracellular calcium-release channel /// IPR003032 // Ryanodine receptor Ryr /// IPR001215 //	RyR // RyR domain;8.8e-227 /// MIR // MIR domain;3.1e-40 /// SPRY // SPRY domain;6.9e-116 /// RYDR_ITPR // RIH domain;1.4e-179 /// ion_trans // Ion transport protein;2.1e-05 /// efhand // EF hand;0.0053

					Ryanodine receptor /// IPR001682 // Ca2+/Na+ channel, pore region	
103939_at	26		2610509I15Rik	RIKEN cDNA 2610509I15 gene	IPR001753 // Enoyl-CoA hydratase/isomerase	ECH // Enoyl-CoA hydratase/isomerase family;6.2e-20
104325_at	26		1110025G12Rik	RIKEN cDNA 1110025G12 gene	---	---
104743_at	26		Cdh13	cadherin 13	IPR002126 // Cadherin	cadherin // Cadherin domain;1e-114
94554_at	26		4021401A16Rik	RIKEN cDNA 4021401A16 gene	---	TRAPP_Bet3 // Transport protein particle (TRAPP) compone;2.3e-123
96089_at	26		4931406C07Rik	RIKEN cDNA 4931406C07 gene	---	---
96237_at	26		SMAF1	SMAF1	---	---
97248_at	26	6681137	Dbi	diazepam binding inhibitor	IPR000582 // Acyl-coA-binding protein, ACBP	ACBP // Acyl CoA binding protein;1.8e-52
97430_at	26		G6pt1	glucose-6-phosphatase, transport protein 1	IPR000849 // GlpT family of transporters /// IPR005828 // General substrate transporter	sugar_tr // Sugar (and other) transporter;0.00018
98984_f_at	26	31981769	Gpd2	glycerol phosphate dehydrogenase 1, mitochondrial	IPR002048 // Calcium-binding EF-hand /// IPR006076 // FAD dependent oxidoreductase /// IPR000447 // FAD-dependent glycerol-3-phosphate dehydrogenase	efhand // EF hand;9.4e-09 /// DAO // FAD dependent oxidoreductase;3.6e-158
99154_s_at	26		---	Mus musculus, Similar to PTD015 protein, clone MGC:36240 IMAGE:5027461, mRNA, complete cds	---	---
99570_s_at	26		Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	IPR004014 // Cation transporting ATPase,	Cation_ATPase_N // Cation

				N terminal /// IPR001757 // ATPase, E1-E2 type /// IPR006069 // Cation transporting ATPase /// IPR005834 // haloacid dehalogenase-like hydrolase /// IPR006068 // Cation transporting ATPase, C-terminal /// IPR000695 // H+ transporting ATPase, proton pump	transporter/ATPase, N-terminus;2.2e-26 /// E1-E2_ATPase // E1-E2 ATPase;2.5e-123 /// Cation_ATPase_C // Cation transporting ATPase, C-terminu;6.5e-84 /// Hydrolase // haloacid dehalogenase-like hydrolase;6.1e-12
100400_at	25	4921531G14Rik	RIKEN cDNA 4921531G14 gene	IPR001440 // TPR repeat	TPR // TPR Domain;0.005
100726_at	25	Grin2a	glutamate receptor, ionotropic, NMDA2A (epsilon 1)	IPR001311 // Solute-binding protein/glutamate receptor /// IPR001508 // NMDA receptor /// IPR001320 // Ionotropic glutamate receptor	lig_chan // Ligand-gated ion channel;4.4e-107
101071_at	25	Myhca	myosin heavy chain, cardiac muscle, adult	IPR004009 // Myosin N-terminal SH3-like domain /// IPR000048 // IQ calmodulin-binding region /// IPR002928 // Myosin tail /// IPR000533 // Tropomyosin /// IPR001609 // Myosin head (motor domain)	myosin_head // Myosin head (motor domain);0 /// Myosin_N // Myosin N-terminal SH3-like domain;2.5e-17 /// IQ // IQ calmodulin-binding motif;0.0029 /// Myosin_tail // Myosin tail;0
101082_at	25	Mod1	malic enzyme, supernatant	IPR001891 // Malic oxidoreductase	malic_N // Malic enzyme, NAD binding

					domain;8.6e-126 /// malic // Malic enzyme, N-terminal domain;1.1e-123
101605_at	25	---	ESTs	---	---
101844_at	25	Pso	peroxisomal sarcosine oxidase	---	---
102314_at	25	Slc2a4	solute carrier family 2 (facilitated glucose transporter), member 4	IPR003663 // Sugar transporter /// IPR005829 // Sugar transporter superfamily /// IPR005828 // General substrate transporter /// IPR000803 // Facilitated glucose transporter family /// IPR002441 // Glucose transporter, type 4 (GLUT4)	sugar_tr // Sugar (and other) transporter;1.9e-185
103084_at	25	Csrp3	cysteine-rich protein 3	IPR001781 // Zn-binding protein, LIM	LIM // LIM domain;1.4e-32
103422_at	25	Cd1d1	CD1d1 antigen	IPR003006 // Immunoglobulin/major histocompatibility complex /// IPR003597 // Immunoglobulin C-type	---
103495_at	25	---	ESTs	---	---
104725_at	25	Tc10-pending	ras-like protein	IPR003577 // Ras small GTPase, Ras type /// IPR003578 // Ras small GTPase, Rho type /// IPR001230 // Prenyl group binding site (CAAX box) /// IPR003579 // Ras small GTPase, Rab	ras // Ras family;1.8e-79

					type /// IPR001806 // Ras GTPase superfamily	
92241_at	25		1500041O16Rik	RIKEN cDNA 1500041O16 gene	---	---
95908_at	25		Klra1	killer cell lectin-like receptor, subfamily A, member 1	IPR001304 // C-type lectin	lectin_c // Lectin C-type domain;1.5e-09
96803_at	25		Gbe1	glucan (1,4-alpha-), branching enzyme 1	IPR004193 // Glycoside hydrolase, family 13, N-terminal /// IPR006047 // Alpha amylase, catalytic domain	isoamylase_N // Isoamylase N-terminal domain;1e-27 /// alpha-amylase // Alpha amylase, catalytic domain;4.3e-07
97207_f_at	25	6678760	Lypla1	lysophospholipase 1	IPR003140 // Phospholipase/Carboxylesterase /// IPR000379 // Esterase/lipase/thioesterase, active site	abhydrolase_2 // Phospholipase/Carboxylesterase;2.2e-121
97302_at	25		Nd1-pending	Nd1	IPR000210 // BTB/POZ domain /// IPR001798 // Kelch repeat	Kelch // Kelch motif;2.1e-98 /// BTB // BTB/POZ domain;6.8e-28
98497_at	25		Eps15-rs	epidermal growth factor receptor pathway substrate 15, related sequence	IPR002048 // Calcium-binding EF-hand /// IPR000261 // EPS15 homology (EH) /// IPR005613 // Actin interacting protein 3 /// IPR003903 // Ubiquitin interacting motif	efhand // EF hand;5.6e-15
99108_s_at	25		---	---	---	---
99631_f_at	25	6680988	Cox6a1	cytochrome c oxidase, subunit VI a, polypeptide 1	IPR001349 // Cytochrome c oxidase, subunit VIa	COX6A // Cytochrome c oxidase subunit VIa;1.9e-53
AFFX-GapdhMur/M32	25	6679937				

599_M_at						
100136_at	24		Lamp2	lysosomal membrane glycoprotein 2	IPR002000 // Lysosome-associated membrane glycoprotein (Lamp)/CD68 /// IPR001412 // Aminoacyl-tRNA synthetase, class I	Lamp // Lysosome-associated membrane glycoprotein (L;7.6e-241
100403_at	24		Mylc2a	myosin light chain, regulatory A	---	efhand // EF hand;1.8e-08
100593_at	24		Tnnt2	troponin T2, cardiac	IPR001978 // Troponin	Troponin // Troponin;1.7e-38
101214_f_at	24	6679937	Gapd	glyceraldehyde-3-phosphate dehydrogenase	IPR000173 // Glyceraldehyde 3-phosphate dehydrogenase	gpdh // Glyceraldehyde 3-phosphate dehydrogenase, NA;2.5e-102 /// gpdh_C // Glyceraldehyde 3-phosphate dehydrogenase, C-;1.3e-123
101532_g_at	24		Aldo2	aldolase 2, B isoform	IPR000741 // Fructose-bisphosphate aldolase, class-I	glycolytic_enzy // Fructose-bisphosphate aldolase class-;3.7e-243
101538_i_at	24		Ces3	carboxylesterase 3	IPR002018 // Carboxylesterase, type B /// IPR000379 // Esterase/lipase/thioesterase, active site	COesterase // Carboxylesterase;2.5e-206
101676_at	24		Gpx3	glutathione peroxidase 3	IPR000889 // Glutathione peroxidase	GSHPx // Glutathione peroxidase;7.9e-68
102048_at	24		Crap	cardiac responsive adriamycin protein	IPR002110 // Ankyrin	ank // Ankyrin repeat;2e-35
103255_at	24		Traf5	Tnf receptor-associated factor 5	IPR003007 // Meprin	zf-TRAF // TRAF-type

				A, C-terminal TRAF /// IPR001293 // Zn-finger, TRAF type /// IPR001841 // Zn-finger, RING /// IPR000345 // Cytochrome c heme-binding site /// IPR002083 // Meprin/TRAF-like MATH	zinc finger;1.1e-45 /// MATH // MATH domain;2.7e-36
103442_at	24	LOC216820	similar to DKFZP566O084 protein	IPR001986 // EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase) /// IPR002198 // Short-chain dehydrogenase/reductase SDR /// IPR002347 // Glucose/ribitol dehydrogenase	adh_short // short chain dehydrogenase;1e-52
103719_at	24	Msh5	mutS homolog 5 (E. coli)	IPR002863 // DNA mismatch repair protein MutS , N-terminal /// IPR000432 // DNA mismatch repair protein MutS, C-terminal	MutS_N // MutS family, N-terminal putative DNA binding;0.00025 /// MutS_C // DNA mismatch repair proteins, mutS family;5.6e-55
103782_at	24	Clcnk1	chloride channel K1	IPR000644 // CBS domain /// IPR002250 // Chloride channel CLC-K /// IPR001807 // Cl- channel, voltage gated	voltage_CLC // Voltage gated chloride channel;5e-155 /// CBS // CBS domain;4.3e-10
104161_at	24	Cpsf2	cleavage and polyadenylation specific factor 2	---	---
104338_r_at	24	1200008D14Rik	RIKEN cDNA 1200008D14 gene	IPR000225 //	Armadillo_seg //

					Armadillo repeat	Armadillo/beta-catenin-like repeat;6.6e-36
104648_at	24		Pacs1	phosphofurin acidic cluster sorting protein 1	---	---
92637_at	24		Pfkl	phosphofructokinase, liver, B-type	IPR000023 // Phosphofructokinase	PFK // Phosphofructokinase; 8.2e-274
93143_at	24		1190005I06Rik	RIKEN cDNA 1190005I06 gene	---	---
93304_at	24		Slc3a1	solute carrier family 3, member 1	IPR006047 // Alpha amylase, catalytic domain	alpha-amylase // Alpha amylase, catalytic domain;2.1e-64
96048_at	24	6680277	Hrsp12	heat-responsive protein 12	IPR006056 // YjgF-like protein /// IPR006175 // Endoribonuclease L-PSP	ribonuc_L-PSP // Endoribonuclease L-PSP;6.6e-65
96956_at	24		0610038D11Rik	RIKEN cDNA 0610038D11 gene	IPR005651 // Protein of unknown function DUF343 /// IPR000866 // Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	DUF343 // Protein of unknown function (DUF343);5.7e-63 /// AhpC-TSA // AhpC/TSA family;3.5e-08
97316_at	24	31541815	1300002P22Rik	RIKEN cDNA 1300002P22 gene	IPR006180 // 3-hydroxyacyl-CoA dehydrogenase /// IPR006109 // NAD-dependent glycerol-3-phosphate dehydrogenase domain /// IPR001101 // Plectin repeat /// IPR001753 // Enoyl-CoA hydratase/isomerase /// IPR006108 // 3-	3HCDH // 3-hydroxyacyl-CoA dehydrogenase, C-terminal;2.2e-42

					hydroxyacyl-CoA dehydrogenase, C-terminal domain /// IPR006176 // 3-hydroxyacyl-CoA dehydrogenase, NAD binding domain /// IPR001993 // Mitochondrial substrate carrier	
98353_at	24		Cyp4a10	cytochrome P450, 4a10	IPR001230 // Prenyl group binding site (CAAX box) /// IPR002402 // E-class P450, group II /// IPR001128 // Cytochrome P450 /// IPR002401 // E-class P450, group I	---
99581_at	24		Hint	histidine triad nucleotide binding protein	IPR001310 // Histidine triad (HIT) protein	---
99894_at	24		Ptgfrn	prostaglandin F2 receptor negative regulator	IPR003600 // Immunoglobulin-like /// IPR003006 // Immunoglobulin/major histocompatibility complex /// IPR003596 // Immunoglobulin V-type	ig // Immunoglobulin domain;3e-33
AFFX-GapdhMur/M32599_M_st	24	6679937				
100828_at	23		Myla	myosin light chain, alkali, cardiac atria	IPR002048 // Calcium-binding EF-hand	---
100967_at	23	6755548	Slc27a2	solute carrier family 27 (fatty acid transporter), member 2	IPR000873 // AMP-dependent	AMP-binding // AMP-binding enzyme;2.3e-

					synthetase and ligase	54
101006_at	23		Tcp1-rs1	t-complex protein 1, related sequence 1	IPR002155 // Thiolase	---
101531_at	23		Aldo2	aldolase 2, B isoform	IPR000741 // Fructose-bisphosphate aldolase, class-I	glycolytic_enzy // Fructose-bisphosphate aldolase class-;3.7e-243
101758_at	23		Cktsf1b1	cysteine knot superfamily 1, BMP antagonist 1	IPR000359 // Cystine-knot domain /// IPR004133 // DAN domain	DAN // DAN domain;6.7e-79
102035_at	23		Tpmt	thiopurine methyltransferase	---	---
102636_at	23		Klc2	kinesin light chain 2	IPR001440 // TPR repeat /// IPR002151 // Kinesin light chain	TPR // TPR Domain;5.2e-20
102944_at	23		---	Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030073N12 product:unknown EST, full insert sequence.	---	---
103333_at	23		G6pc	glucose-6-phosphatase, catalytic	IPR000326 // PA-phosphatase related phosphoesterase	PAP2 // PAP2 superfamily;8.4e-31
103618_at	23		Ckmt2	creatine kinase, mitochondrial 2	---	---
103703_f_at	23		C730048C13Rik	RIKEN cDNA C730048C13 gene	---	---
104255_at	23		---	ESTs, Weakly similar to DIA3_MOUSE Diaphanous protein homolog 3 (Diaphanous-related formin 3) (DRF3) (mDIA2) (p134mDIA2) [M.musculus]	---	---
92826_at	23		Gdap3	ganglioside-induced differentiation-associated-protein 3	---	---
92835_at	23		Cml1	camello-like 1	IPR000182 // GCN5-related N-acetyltransferase	Acetyltransf // Acetyltransferase (GNAT) family;6.1e-16
93820_at	23	31981830	Cox7a2	cytochrome c oxidase, subunit VIIa 2	IPR003177 // Cytochrome c oxidase, subunit VIIa	COX7a // Cytochrome c oxidase subunit VIIa;3.6e-52

94549_at	23		1200003O06Rik	RIKEN cDNA 1200003O06 gene	IPR005828 // General substrate transporter	sugar_tr // Sugar (and other) transporter;0.0036
95588_at	23	6678766	Amacr	alpha-methylacyl-CoA racemase	IPR003673 // L-carnitine dehydratase/bile acid-inducible protein F	CAIB-BAIF // CAIB/BAIF family;6.6e-99
96072_at	23		Ldh1	lactate dehydrogenase 1, A chain	IPR001236 // Lactate/malate dehydrogenase /// IPR001557 // L-lactate dehydrogenase	ldh // lactate/malate dehydrogenase, NAD binding do;6.4e-82 /// ldh_C // lactate/malate dehydrogenase, alpha/beta C-t;2.4e-87
96090_g_at	23		4931406C07Rik	RIKEN cDNA 4931406C07 gene	---	---
96629_at	23	14861848	D7Rp2e	DNA segment, Chr 7, Roswell Park 2 complex, expressed	IPR000086 // NUDIX hydrolase	NUDIX // NUDIX domain;1.9e-14
97204_s_at	23		1110003P16Rik	RIKEN cDNA 1110003P16 gene	IPR001623 // Heat shock protein DnaJ, N-terminal	DnaJ // DnaJ domain;4.8e-05
98457_at	23		Slc4a4	solute carrier family 4 (anion exchanger), member 4	IPR003020 // HCO3- transporter /// IPR003024 // Na+/HCO3- co-transporter /// IPR001717 // Anion exchange protein	HCO3_cotransp // HCO3- transporter family;0
98904_at	23		1110066C01Rik	RIKEN cDNA 1110066C01 gene	IPR001706 // Ribosomal protein L35	---
100916_at	22		Slc22a1	solute carrier family 22 (organic cation transporter), member 1	IPR005829 // Sugar transporter superfamily /// IPR005828 // General substrate transporter /// IPR004749 // Organic cation transport protein	sugar_tr // Sugar (and other) transporter;3.9e-10
101897_g_at	22		Cd1d2	CD1d2 antigen	IPR003006 //	ig // Immunoglobulin

					Immunoglobulin/major histocompatibility complex /// IPR003597 // Immunoglobulin C-type	domain;1.2e-05
101964_at	22		Tkt	transketolase	IPR005476 // Transketolase, C terminal /// IPR005475 // Transketolase, central region /// IPR005474 // Transketolase, N terminal	transketolase_C // Transketolase, C-terminal domain;2.4e-34 /// transket_pyr // Transketolase, pyridine binding domai;3.4e-55 /// transketolase // Transketolase, thiamine diphosphate b;3.2e-154
102861_at	22		Slc22a1l	solute carrier family 22 (organic cation transporter), member 1-like	IPR001958 // Tetracycline resistance protein /// IPR001226 // Flavodoxin	---
102947_at	22		Slc22a2	solute carrier family 22 (organic cation transporter), member 2	IPR005829 // Sugar transporter superfamily /// IPR005828 // General substrate transporter /// IPR004749 // Organic cation transport protein	sugar_tr // Sugar (and other) transporter;7.3e-13
103389_at	22	31980703	Aass	aminoadipate-semialdehyde synthase	IPR005097 // Saccharopine dehydrogenase /// IPR004002 // Alanine dehydrogenase and pyridine nucleotide transhydrogenase /// IPR002016 // Haem peroxidase	AlaDh_PNT // Alanine dehydrogenase/pyridine nucleotid;1.9e-215 /// Saccharop_dh // Saccharopine dehydrogenase;0

103580_at	22		LOC215751	similar to hypothetical protein BC014320	IPR001950 // Translation initiation factor SUI1	---
104583_at	22		2400007G07Rik	RIKEN cDNA 2400007G07 gene	IPR001452 // SH3 domain /// IPR001594 // Zn-finger, DHHC type	zf-DHHC // DHHC zinc finger domain;2.5e-27
104584_f_at	22		---	Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730439B18 product:hypothetical protein, full insert sequence.	---	---
93045_at	22		Abcd3	ATP-binding cassette, sub-family D (ALD), member 3	IPR003439 // ABC transporter /// IPR003593 // AAA ATPase /// IPR005283 // Peroxysomal long chain fatty acyl transporter	ABC_tran // ABC transporter;6.1e-27
93048_at	22	8393156	Clpp	caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli)	IPR001907 // Clp protease	CLP_protease // Clp protease;2.3e-98
93084_at	22		Slc25a4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	IPR002030 // Mitochondrial brown fat uncoupling protein /// IPR002113 // Adenine nucleotide translocator 1 /// IPR001993 // Mitochondrial substrate carrier /// IPR002067 // Mitochondrial carrier protein	---
93431_at	22		Dm15	dystrophia myotonica kinase, B15	---	pkinase // Protein kinase domain;4.1e-57
93570_at	22		Slc12a3	solute carrier family 12, member 3	IPR002948 //	---

				Thiazide-sensitive Na/Cl co-transporter /// IPR004842 // K-Cl cotransporter superfamily /// IPR002293 // Amino acid/polyamine transporter, family I	
93736_at	22	Tcn2	transcobalamin 2	IPR002157 // Eukaryotic cobalamin-binding protein	Cobalamin_bind // Eukaryotic cobalamin-binding protein;2.1e-289
93775_at	22	D12Ertd647e	DNA segment, Chr 12, ERATO Doi 647, expressed	---	---
93826_at	22	2310028N02Rik	RIKEN cDNA 2310028N02 gene	IPR002554 // Protein phosphatase 2A, regulatory B subunit (B56 family)	B56 // Protein phosphatase 2A regulatory B subunit;8.7e-15
93832_at	22	5730443G10	hypothetical protein 5730443G10	---	R3H // R3H domain;1.5e-15
93833_s_at	22	Hist1h2bc	histone 1, H2bc	IPR000558 // Histone H2B /// IPR004822 // Histone-fold/TFIID-TAF/NF-Y domain	---
93851_at	22	Rabggta	Rab geranylgeranyl transferase, a subunit	IPR002088 // Protein prenyltransferase, alpha subunit /// IPR001611 // Leucine-rich repeat	PPTA // Protein prenyltransferase alpha subunit repe;6.3e-56 /// LRR // Leucine Rich Repeat;2.5e-07
94419_at	22	Slc19a1	solute carrier family 19 (sodium/hydrogen exchanger), member 1	IPR002666 // Reduced folate carrier	Folate_carrier // Reduced folate carrier;1.8e-290
95119_at	22	1110038D17Rik	RIKEN cDNA 1110038D17 gene	---	---
95478_at	22	Deb1	differentially expressed in B16F10 1	---	---
95620_at	22	2310016E22Rik	RIKEN cDNA 2310016E22 gene	IPR002198 // Short-chain dehydrogenase/reduc	adh_short // short chain dehydrogenase;3.5e-

					tase SDR /// IPR002347 // Glucose/ribitol dehydrogenase	45
95725_at	22		0610006H10Rik	RIKEN cDNA 0610006H10 gene	---	---
96231_at	22	21624609	2010012D11Rik	RIKEN cDNA 2010012D11 gene	IPR000073 // Alpha/beta hydrolase fold /// IPR003089 // Alpha/beta hydrolase /// IPR000734 // Lipase /// IPR000379 // Esterase/lipase/thioesterase, active site	abhydrolase // alpha/beta hydrolase fold;1.3e-19
97525_at	22	6680139	Gyk	glycerol kinase	IPR005999 // Glycerol kinase /// IPR000577 // Carbohydrate kinase, FGGY	FGGY_C // FGGY family of carbohydrate kinases, C-termi;3.5e-110 /// FGGY // FGGY family of carbohydrate kinases, N-termi;6.5e-135
97533_at	22		Fcgrt	Fc receptor, IgG, alpha chain transporter	IPR001220 // Legume lectin, beta domain /// IPR001039 // Major histocompatibility complex protein, class I /// IPR003006 // Immunoglobulin/major histocompatibility complex /// IPR003597 // Immunoglobulin C-type	MHC_I // Class I Histocompatibility antigen, domains;2.7e-72
98124_at	22		0610011F06Rik	RIKEN cDNA 0610011F06 gene	---	---
98482_at	22		Pthr1	parathyroid hormone receptor 1	IPR002170 // Parathyroid hormone receptor ///	7tm_2 // 7 transmembrane receptor (Secretin

					IPR001879 // Hormone receptor, extracellular /// IPR000832 // G-protein coupled receptors family 2 (secretin-like)	family);2.8e-129 /// HRM // Hormone receptor domain;9.1e-26
99112_at	22	7305501	Slc25a10	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	IPR002030 // Mitochondrial brown fat uncoupling protein /// IPR001993 // Mitochondrial substrate carrier	mito_carr // Mitochondrial carrier protein;4.3e-70
99115_at	22	21539599	2610041P16Rik	RIKEN cDNA 2610041P16 gene	IPR003422 // Ubiquinol-cytochrome C reductase hinge protein	UCR_hinge // Ubiquinol-cytochrome C reductase hinge prot;2.6e-42
99959_at	22	6753022	Ak4	adenylate kinase 4	IPR000850 // Adenylate kinase	adenylatekinase // Adenylate kinase;2.3e-102
99974_at	22		Kcnj15	potassium inwardly-rectifying channel, subfamily J, member 15	IPR001622 // K+ channel, pore region /// IPR001838 // K+ channel, inward rectifier /// IPR003270 // Kir1.3 inward rectifier K+ channel	IRK // Inward rectifier potassium channel;2.2e-221
AFFX-PyruCarbMur/L09192_3_at	22	6679237				
100567_at	21		Fabp4	fatty acid binding protein 4, adipocyte	IPR000463 // Cytosolic fatty-acid binding protein /// IPR000566 // Lipocalin-related protein and Bos/Can/Equ allergen	lipocalin // Lipocalin / cytosolic fatty-acid binding pr;3e-39

100986_at	21	Fhl2	four and a half LIM domains 2	IPR001781 // Zn-binding protein, LIM	LIM // LIM domain;1.2e-34
101029_f_at	21	Actc1	actin, alpha, cardiac	IPR004000 // Actin/actin-like /// IPR004001 // Actin	actin // Actin;1.2e-276
101299_at	21	---	---	---	---
101394_at	21	Sgcg	sarcoglycan, gamma (35kD dystrophin-associated glycoprotein)	---	---
101872_at	21	Gsta2	glutathione S-transferase, alpha 2 (Yc2)	IPR004045 // Glutathione S-transferase, N-terminal /// IPR003080 // Glutathione S-transferase, alpha class /// IPR004046 // Glutathione S-transferase, C-terminal	GST_N // Glutathione S-transferase, N-terminal domain;2.4e-25 /// GST_C // Glutathione S-transferase, C-terminal domain;3.3e-30
102114_f_at	21	Angptl4	angiopoietin-like 4	IPR002181 // Fibrinogen, beta/gamma chain, C-terminal globular	fibrinogen_C // Fibrinogen beta and gamma chains, C-term;4.8e-58
102886_at	21	Gpc4	glypican 4	IPR001863 // Glypican	Glypican // Glypican;0
103602_at	21	Dao1	D-amino acid oxidase	IPR006181 // D-amino acid oxidase /// IPR006076 // FAD dependent oxidoreductase /// IPR001412 // Aminoacyl-tRNA synthetase, class I	DAO // FAD dependent oxidoreductase;1.7e-133
103879_at	21	LOC235169	hypothetical protein LOC235169	IPR006076 // FAD dependent oxidoreductase	DAO // FAD dependent oxidoreductase;0.0011
103955_at	21	Cryl1	crystallin, lamda 1	IPR006180 // 3-hydroxyacyl-CoA	3HCDH // 3-hydroxyacyl-CoA

					dehydrogenase /// IPR006109 // NAD-dependent glycerol-3-phosphate dehydrogenase domain /// IPR000205 // NAD binding site /// IPR006108 // 3-hydroxyacyl-CoA dehydrogenase, C-terminal domain /// IPR006176 // 3-hydroxyacyl-CoA dehydrogenase, NAD binding domain	dehydrogenase, C-terminal;3.5e-22 /// 3HCDH_N // 3-hydroxyacyl-CoA dehydrogenase, NAD binding;1.2e-86
104258_at	21		Acyp2	acylphosphatase 2, muscle type	IPR002048 // Calcium-binding EF-hand /// IPR001792 // Acylphosphatase	Acylphosphatase // Acylphosphatase;2.9e-59
104387_at	21		Slc23a2	solute carrier family 23 (nucleobase transporters), member 2	IPR006043 // Xanthine/uracil/vitamin C permease family	xan_ur_permease // Permease family;9.2e-94
104706_at	21		Pex7	peroxisome biogenesis factor 7	IPR001680 // G-protein beta WD-40 repeat	WD40 // WD domain, G-beta repeat;3.9e-49
92814_at	21		Cyp2j5	cytochrome P450, 2j5	IPR001128 // Cytochrome P450 /// IPR002401 // E-class P450, group I	p450 // Cytochrome P450;1.5e-165
92869_at	21	6680291	Hsd3b4	hydroxysteroid dehydrogenase-4, delta<5>-3-beta	IPR002225 // 3-beta hydroxysteroid dehydrogenase/isomerase	3Beta_HSD // 3-beta hydroxysteroid dehydrogenase/isomera;1.8e-203
93221_at	21		4921540P06Rik	RIKEN cDNA 4921540P06 gene	IPR001356 // Homeobox /// IPR001827 // Homeobox protein, antennapedia type	---
93542_at	21		Pter	phosphotriesterase related	IPR001559 //	PTE //

93629_s_at	21		Folh1	folate hydrolase	Aryldialkylphosphatase IPR003137 // Protease-associated PA	Phosphotriesterase family;8.9e-239 PA // PA domain;8.6e-21 /// TFR_dimer // Transferring receptor-like dimerisation dom;3.8e-65
93696_at	21		Nr1i2	nuclear receptor subfamily 1, group I, member 2	IPR001628 // Zn-finger, C4-type steroid receptor /// IPR000324 // Vitamin D receptor /// IPR001723 // Steroid hormone receptor /// IPR000536 // Ligand-binding domain of nuclear hormone receptor	---
93781_at	21		Aldrl6	aldehyde reductase (aldose reductase)-like 6	IPR001395 // Aldo/keto reductase	---
94199_at	21		Kap	kidney androgen regulated protein	---	---
94241_at	21		1300003G02Rik	RIKEN cDNA 1300003G02 gene	IPR001977 // Dephospho-CoA kinase	CoaE // Dephospho-CoA kinase;3.1e-87 /// CTP_transf_2 // Cytidylyltransferase;2.3e-08
94435_at	21		D10Ertd438e	DNA segment, Chr 10, ERATO Doi 438, expressed	---	---
95028_r_at	21		---	---	---	---
95074_at	21		Pxf	peroxisomal farnesylated protein	IPR001230 // Prenyl group binding site (CAAX box)	---
95539_at	21		Gtpat12	gene trap PAT 12	---	---
96069_at	21	27659728	Afar	aflatoxin B1 aldehyde reductase	IPR001395 // Aldo/keto reductase	aldo_ket_red // Aldo/keto reductase family;3e-14
96078_g_at	21		Slc17a1	solute carrier family 17 vesicular glutamate transporter), member 1	IPR005828 // General substrate transporter /// IPR004745 //	---

					Na(+)-dependent inorganic phosphate cotransporter	
96888_at	21		Akr1a4	aldo-keto reductase family 1, member A4 (aldehyde reductase)	IPR001395 // Aldo/keto reductase	aldo_ket_red // Aldo/keto reductase family;1.1e-147
97001_r_at	21		Olfr37c	olfactory receptor 37c	---	7tm_1 // 7 transmembrane receptor (rhodopsin family);2.2e-38
97089_at	21		Folh1	folate hydrolase	IPR003137 // Protease-associated PA	PA // PA domain;8.6e-21 /// TFR_dimer // Transferring receptor-like dimerisation dom;3.8e-65
97287_at	21		4933412D19Rik	RIKEN cDNA 4933412D19 gene	---	---
97342_at	21	13384894	Mrps14	mitochondrial ribosomal protein S14	IPR001209 // Ribosomal protein S14	Ribosomal_S14 // Ribosomal protein S14p/S29e;1.6e-18
97514_at	21		1810063B05Rik	RIKEN cDNA 1810063B05 gene	---	---
98131_at	21		Cryz	crystallin, zeta	IPR002085 // Zinc-containing alcohol dehydrogenase superfamily /// IPR002364 // Quinone oxidoreductase/zeta-crystallin	---
99107_at	21		Ghr	growth hormone receptor	IPR002996 // Cytokine receptor, common beta/gamma chain /// IPR003528 // Long hematopoietin receptor, single chain	---
99402_at	21		Art2b	ADP-ribosyltransferase 2b	IPR000768 // NAD:arginine ADP-ribosyltransferase, ART	ART // NAD:arginine ADP-ribosyltransferase;1.3e-147
100085_at	20		Ggtp	gamma-glutamyl transpeptidase	IPR000101 //	G_glu_transpept //

100909_at	20	Prss8	protease, serine, 8 (prostasin)	Gamma-glutamyltranspeptidase IPR001314 // Chymotrypsin serine protease, family S1 /// IPR001254 // Serine protease, trypsin family	Gamma-glutamyltranspeptidase;3.1e-273 trypsin // Trypsin;4.6e-90
100913_at	20	Thea	thioesterase, adipose associated	IPR002590 // Acyl-CoA thioester hydrolase, cytosolic long chain /// IPR002913 // Lipid-binding START	START // START domain;6.4e-25 /// Acyl-CoA_hydro // Cytosolic long-chain acyl-CoA thioeste;1.4e-34
100956_at	20	Kl	klotho	IPR001360 // Glycoside hydrolase, family 1	Glyco_hydro_1 // Glycosyl hydrolase family 1;1e-203
101539_f_at	20	Ces3	carboxylesterase 3	IPR002018 // Carboxylesterase, type B /// IPR000379 // Esterase/lipase/thioesterase, active site	COesterase // Carboxylesterase;2.5e-206
101659_at	20	Hsd3b2	hydroxysteroid dehydrogenase-2, delta<5>-3-beta	IPR002225 // 3-beta hydroxysteroid dehydrogenase/isomerase	3Beta_HSD // 3-beta hydroxysteroid dehydrogenase/isomera;2.3e-209
101907_s_at	20	Ceacam2	CEA-related cell adhesion molecule 2	IPR003599 // Immunoglobulin subtype /// IPR003598 // Immunoglobulin C-2 type /// IPR003006 // Immunoglobulin/major histocompatibility complex	ig // Immunoglobulin domain;6.6e-05
101972_at	20	Kdap	kidney-derived aspartic protease-like protein	IPR001969 // Eukaryotic/viral	asp // Eukaryotic aspartyl

					aspartic protease, active site /// IPR001461 // Aspartic protease A1, pepsin	protease;7.6e-147
102192_r_at	20	31982720	Sah	SA rat hypertension-associated homolog	IPR000873 // AMP-dependent synthetase and ligase	AMP-binding // AMP-binding enzyme;1.2e-102
102429_at	20		Slc22al2	solute carrier family 22 (organic cation transporter)-like 2	IPR005828 // General substrate transporter	sugar_tr // Sugar (and other) transporter;8.2e-08
103353_f_at	20		Cyp4b1	cytochrome P450, subfamily IV B, polypeptide 1	IPR001128 // Cytochrome P450 /// IPR002401 // E-class P450, group I	p450 // Cytochrome P450;2.9e-144
103377_at	20		Lrp2	low density lipoprotein receptor-related protein 2	IPR000033 // Low-density lipoprotein receptor, YWTD repeat	---
103570_at	20		Cors-pending	collagenous repeat-containing sequence	IPR000087 // Collagen triple helix repeat /// IPR001073 // Complement C1q protein	Collagen // Collagen triple helix repeat (20 copies);1e-10 /// C1q // C1q domain;7.7e-18
103973_at	20		Kcnj1	potassium inwardly-rectifying channel, subfamily J, member 1	IPR001622 // K+ channel, pore region /// IPR001838 // K+ channel, inward rectifier /// IPR003268 // Kir1.1 inward rectifier K+ channel	IRK // Inward rectifier potassium channel;1.4e-231
103984_at	20		---	Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630026G14 product:hypothetical protein, full insert sequence.	---	---
104164_at	20		1300019N10Rik	RIKEN cDNA 1300019N10 gene	IPR000126 // Serine	---

				proteases, V8 family /// IPR001254 // Serine protease, trypsin family	
104381_at	20	Nr1h3	nuclear receptor subfamily 1, group H, member 3	IPR001628 // Zn-finger, C4-type steroid receptor /// IPR003069 // Ecdysteroid receptor /// IPR001723 // Steroid hormone receptor /// IPR000536 // Ligand-binding domain of nuclear hormone receptor /// IPR000923 // Blue (type 1) copper domain	zf-C4 // Zinc finger, C4 type (two domains);5.5e-38 /// hormone_rec // Ligand-binding domain of nuclear hormone;4.8e-52
104565_at	20	Ap4s1	adaptor-related protein complex AP-4, sigma 1	IPR000804 // Clathrin adaptor complex, small chain	Clat_adaptor_s // Clathrin adaptor complex small chain;1.7e-49
92375_at	20	1810015P09Rik	RIKEN cDNA 1810015P09 gene	IPR004088 // KH domain, type 1 /// IPR004087 // KH domain	---
92561_at	20	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	IPR000407 // GDA1/CD39 family of nucleoside phosphatase	GDA1_CD39 // GDA1/CD39 (nucleoside phosphatase) family;7.3e-44
93515_at	20	Cdh16	cadherin 16	IPR002126 // Cadherin /// IPR001412 // Aminoacyl-tRNA synthetase, class I	cadherin // Cadherin domain;2.3e-54
94126_at	20	Wnt2b	wingless related MMTV integration site 2b	IPR005817 // Wnt superfamily ///	wnt // wnt family;4.8e-194

				IPR005816 // Secreted growth factor Wnt protein	
94337_at	20	Gas2	growth arrest specific 2	IPR003108 // Growth-arrest-specific protein 2 /// IPR001715 // Calponin-like actin-binding	GAS2 // Growth-Arrest-Specific Protein 2 Domain;3.5e-53 /// CH // Calponin homology (CH) domain;9.4e-08
94338_g_at	20	Gas2	growth arrest specific 2	IPR003108 // Growth-arrest-specific protein 2 /// IPR001715 // Calponin-like actin-binding	GAS2 // Growth-Arrest-Specific Protein 2 Domain;3.5e-53 /// CH // Calponin homology (CH) domain;9.4e-08
94424_at	20	Scd1	stearoyl-Coenzyme A desaturase 1	IPR001522 // Fatty acid desaturase, type 1 /// IPR005804 // Fatty acid desaturase family	FA_desaturase // Fatty acid desaturase;5.2e-80
94518_at	20	0610033H09Rik	RIKEN cDNA 0610033H09 gene	---	---
94827_at	20	Fxyd2	FXYD domain-containing ion transport regulator 2	---	ATP1G1_PLM_MAT8 // ATP1G1/PLM/MAT8 family;2.9e-33
95594_at	20	6330416C07Rik	RIKEN cDNA 6330416C07 gene	---	---
96605_at	20	0610011I04Rik	RIKEN cDNA 0610011I04 gene	---	---
96684_at	20	D5Wsu31e	DNA segment, Chr 5, Wayne State University 31, expressed	---	---
96790_f_at	20	A530057M15Rik	RIKEN cDNA A530057M15 gene	---	---
96935_at	20	Map17-pending	membrane-associated protein 17	---	---
97288_at	20	Pdzk1	PDZ domain containing 1	IPR001478 // PDZ/DHR/GLGF domain	PDZ // PDZ domain (Also known as DHR or GLGF);8.8e-50
97886_at	20	Spr	sepiapterin reductase	IPR002198 // Short-chain dehydrogenase/reductase SDR /// IPR002347 // Glucose/ribitol	adh_short // short chain dehydrogenase;1e-07

					dehydrogenase	
98123_at	20	6754408	Kat2	kynurenine aminotransferase II	---	---
98575_at	20		Fasn	fatty acid synthase	IPR001031 // Thioesterase /// IPR000051 // SAM (and some other nucleotide) binding motif /// IPR002085 // Zinc-containing alcohol dehydrogenase superfamily /// IPR000794 // Beta-ketoacyl synthase /// IPR006162 // Phosphopantetheine attachment site /// IPR001227 // Acyl transferase /// IPR006163 // Phosphopantetheine-binding domain	---
99019_at	20		Por	P450 (cytochrome) oxidoreductase	IPR001094 // Flavodoxin-like domain /// IPR003097 // FAD-binding /// IPR001433 // Oxidoreductase FAD/NAD(P)-binding /// IPR001709 // Flavoprotein pyridine nucleotide cytochrome reductase /// IPR001226 // Flavodoxin	NAD_binding_1 // Oxidoreductase NAD-binding domain;7.8e-44 /// FAD_binding_1 // FAD binding domain;5e-121 /// flavodoxin // Flavodoxin;1e-55
99070_at	20		Chuk	conserved helix-loop-helix ubiquitous kinase	IPR001245 // Tyrosine protein kinase /// IPR002290.	pkinase // Protein kinase domain;1.3e-48

					// Serine/Threonine protein kinase /// IPR000719 // Eukaryotic protein kinase	
99094_at	20		Slc12a1	solute carrier family 12, member 1	IPR004841 // Domain found in permeases /// IPR002443 // Na-K-Cl co-transporter /// IPR002445 // Na-K-Cl co-transporter 2 /// IPR004842 // K-Cl cotransporter superfamily /// IPR002293 // Amino acid/polyamine transporter, family I	aa_permeases // Amino acid permease;0.56
99521_at	20	6753022	Ak4	adenylate kinase 4	IPR000850 // Adenylate kinase	adenylatekinase // Adenylate kinase;2.3e-102
99525_at	20		Slc8a1	solute carrier family 8 (sodium/calcium exchanger), member 1	IPR004836 // Sodium/calcium exchanger protein /// IPR002987 // Sodium/calcium exchanger, isoform 1 /// IPR001623 // Heat shock protein DnaJ, N-terminal /// IPR003644 // Na-Ca exchanger/integrin-beta4 /// IPR004837 // Sodium/calcium exchanger membrane region	Na_Ca_Ex // Sodium/calcium exchanger protein;4.8e-70 /// Calx-beta // Calx-beta domain;2.2e-84
99966_at	20		---	Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430007C20 product:weakly	---	---

				similar to ACTIN INTERACTING PROTEIN [Arabidopsis thaliana], full insert sequence.		
AFFX-GapdhMur/M32599_5_at	20	6679937				
AFFX-PyruCarbMur/L09192_MB_at	20	6679237				
100040_at	19		Mrpl17	mitochondrial ribosomal protein L17	IPR000456 // Ribosomal protein L17	Ribosomal_L17 // Ribosomal protein L17;5.3e-20
100491_at	19		Slc16a2	solute carrier family 16 (monocarboxylic acid transporters), member 2	---	---
100542_at	19		Mep1a	meprin 1 alpha	IPR001506 // Astacin /// IPR000998 // MAM domain /// IPR003007 // Meprin A, C-terminal TRAF /// IPR006025 // Neutral zinc metallopeptidases, zinc-binding region /// IPR000561 // EGF-like domain /// IPR006026 // Neutral zinc metallopeptidase /// IPR003006 // Immunoglobulin/major histocompatibility complex /// IPR002083 // Meprin/TRAF-like MATH	Astacin // Astacin (Peptidase family M12A);8.1e-93 /// MAM // MAM domain;1.4e-62 /// EGF // EGF-like domain;1.3e-10 /// MATH // MATH domain;6.4e-24
101086_f_at	19		Cnbp	cellular nucleic acid binding protein	IPR001878 // Zn-finger, CCHC type	zf-CCHC // Zinc knuckle;1.4e-51
101396_at	19		Tcf2	transcription factor 2	IPR001356 // Homeobox	---

101552_at	19	Slc34a1	solute carrier family 34 (sodium phosphate), member 1	IPR003841 // Na+/Pi-cotransporter	Na_Pi_cotrans // Na+/Pi-cotransporter;5.4e-209
102053_at	19	Plscr2	phospholipid scramblase 2	IPR005552 // Scramblase	Scramblase // Scramblase;4.7e-130
103083_at	19	Lipe	lipase, hormone sensitive	IPR002168 // Lipolytic enzyme /// IPR000379 // Esterase/lipase/thioesterase, active site	---
103972_at	19	Kcnj1	potassium inwardly-rectifying channel, subfamily J, member 1	IPR001622 // K+ channel, pore region /// IPR001838 // K+ channel, inward rectifier /// IPR003268 // Kir1.1 inward rectifier K+ channel	IRK // Inward rectifier potassium channel;1.4e-231
104060_at	19	2700088M22Rik	RIKEN cDNA 2700088M22 gene	IPR000504 // RNA-binding region RNP-1 (RNA recognition motif) /// IPR001878 // Zn-finger, CCHC type	zf-CCHC // Zinc knuckle;0.00063 /// rrm // RNA recognition motif. (a.k.a. RRM, RBD, or;8.6e-22
104076_at	19	1190017O12Rik	RIKEN cDNA 1190017O12 gene	---	---
104138_at	19	2310074E22Rik	RIKEN cDNA 2310074E22 gene	---	---
104603_at	19	Gstt2	glutathione S-transferase, theta 2	IPR004045 // Glutathione S-transferase, N-terminal /// IPR004046 // Glutathione S-transferase, C-terminal	GST_N // Glutathione S-transferase, N-terminal domain;3.7e-11 /// GST_C // Glutathione S-transferase, C-terminal domain;1.3e-24
92382_at	19	Myo6	myosin VI	IPR000048 // IQ calmodulin-binding region /// IPR001609 // Myosin head (motor domain)	myosin_head // Myosin head (motor domain);6.4e-249

92605_at	19		Umod	uromodulin	IPR001881 // EGF-like calcium-binding /// IPR000152 // Aspartic acid and asparagine hydroxylation site /// IPR001507 // Endoglin/CD105 antigen /// IPR000561 // EGF-like domain /// IPR000345 // Cytochrome c heme-binding site	zona_pellucida // Zona pellucida-like domain;3.4e-93 /// EGF // EGF-like domain;2.5e-12
93053_at	19		Casq2	calsequestrin 2	IPR001393 // Calsequestrin	Calsequestrin // Calsequestrin;1.6e-267
93320_at	19	27804309	Cpt1a	carnitine palmitoyltransferase 1, liver	IPR000542 // Acyltransferase ChoActase/COT/CPT	---
93365_s_at	19		2410174K12Rik	RIKEN cDNA 2410174K12 gene	IPR001440 // TPR repeat	TPR // TPR Domain;3.2e-10
93435_at	19	6753572	Cyp24	cytochrome P450, 24	IPR001128 // Cytochrome P450 /// IPR002401 // E-class P450, group I	p450 // Cytochrome P450;3.2e-102
93595_at	19	6753448	Cln2	ceroid-lipofuscinosis, neuronal 2	---	---
93671_at	19		Erf	Est2 repressor factor	---	Ets // Ets-domain;1.1e-54
93760_at	19		Cript-pending	postsynaptic protein Cript	---	---
94418_at	19		Lce-pending	long chain fatty acyl elongase	IPR002076 // GNS1/SUR4 membrane protein	GNS1_SUR4 // GNS1/SUR4 family;3.7e-48
94807_at	19	23943838	Slc25a1	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	---	mito_carr // Mitochondrial carrier protein;1.6e-83
94906_at	19		Adh1	alcohol dehydrogenase 1 (class I)	IPR002085 // Zinc-containing alcohol dehydrogenase superfamily ///	adh_zinc // Zinc-binding dehydrogenase;2.6e-143

96910_at	19	22122743	MGC37245	hypothetical protein MGC37245	IPR002328 // Zinc-containing alcohol dehydrogenase IPR000873 // AMP-dependent synthetase and ligase	AMP-binding // AMP-binding enzyme;7.1e-95
96938_at	19	19482166	Keg1	kidney expressed gene 1	---	---
97257_at	19	21703764	Cgi-83-pending	CGI-83 protein	IPR001279 // Beta-lactamase-like	lactamase_B // Metallo-beta-lactamase superfamily;1.9e-23
97258_at	19	21703764	Cgi-83-pending	CGI-83 protein	IPR001279 // Beta-lactamase-like	lactamase_B // Metallo-beta-lactamase superfamily;1.9e-23
97431_at	19		Slc22a6	solute carrier family 22 (organic anion transporter), member 6	IPR005828 // General substrate transporter /// IPR004749 // Organic cation transport protein	sugar_tr // Sugar (and other) transporter;1.8e-16
97707_at	19		---	ESTs, Weakly similar to RIKEN cDNA 5730493B19 [Mus musculus] [M.musculus]	---	---
AFFX-PyruCarbMur/L09192_5_at	19	6679237				
100285_at	18		Col4a3	procollagen, type IV, alpha 3	IPR000504 // RNA-binding region RNP-1 (RNA recognition motif) /// IPR000087 // Collagen triple helix repeat /// IPR001442 // Type 4 procollagen, C-terminal repeat	Collagen // Collagen triple helix repeat (20 copies);2e-176 /// C4 // C-terminal tandem repeated domain in type 4;3.4e-146
101666_at	18		Nr5a1	nuclear receptor subfamily 5, group A, member 1	IPR001628 // Zn-finger, C4-type steroid receptor /// IPR000324 // Vitamin D receptor ///	hormone_rec // Ligand-binding domain of nuclear hormone;2.7e-48 /// hormone_rec //

					IPR001723 // Steroid hormone receptor /// IPR000536 // Ligand-binding domain of nuclear hormone receptor	Ligand-binding domain of nuclear hormone;2.4e-48 /// zf-C4 // Zinc finger, C4 type (two domains);3.3e-52
101757_at	18		Nfe2l1	nuclear factor, erythroid derived 2,-like 1	IPR004827 // Basic-leucine zipper (bZIP) transcription factor	---
102329_at	18		Cideb	cell death-inducing DNA fragmentation factor, alpha subunit-like effector B	IPR003508 // Caspase-activated nuclease CIDE-N	CIDE-N // CIDE-N domain;9.6e-46
103647_at	18		Glb1	galactosidase, beta 1	IPR001944 // Glycoside hydrolase, family 35	Glyco_hydro_35 // Glycosyl hydrolases family 35;0
104184_at	18		Nppb	natriuretic peptide precursor type B	---	ANP // Atrial natriuretic peptide;3.9e-29
104605_at	18		1110001I14Rik	RIKEN cDNA 1110001I14 gene	---	---
104748_s_at	18	6678001	Slc1a1	solute carrier family 1, member 1	IPR001991 // Sodium:dicarboxylate symporter	SDF // Sodium:dicarboxylate symporter family;2.7e-248
92407_at	18		Myom1	myomesin 1	IPR003600 // Immunoglobulin-like /// IPR000097 // AP endonuclease, family 1 /// IPR003961 // Fibronectin, type III /// IPR003962 // Fibronectin, type III repeat /// IPR003598 // Immunoglobulin C-2 type /// IPR003006 // Immunoglobulin/major histocompatibility complex	ig // Immunoglobulin domain;1.2e-22 /// fn3 // Fibronectin type III domain;3e-100
92600_f_at	18		Cyp4a10	cytochrome P450, 4a10	IPR001230 // Prenyl group binding site	---

				(CAAX box) /// IPR002402 // E-class P450, group II /// IPR001128 // Cytochrome P450 /// IPR002401 // E-class P450, group I	
93500_at	18	Alas1	aminolevulinic acid synthase 1	IPR001917 // Aminotransferase, class-II /// IPR003408 // Aminolevulinic acid synthase /// IPR004839 // Aminotransferase, class I and II	aminotran_1_2 // Aminotransferase class I and II;6.3e-59 /// ALA_synthase // Aminolevulinic acid synthase domain;1.3e-45
93603_at	18	Mrpl40	mitochondrial ribosomal protein L40	---	---
93776_at	18	1500001L15Rik	RIKEN cDNA 1500001L15 gene	---	---
93868_at	18	Nsdhl	NAD(P) dependent steroid dehydrogenase-like	IPR002225 // 3-beta hydroxysteroid dehydrogenase/isomerase	3Beta_HSD // 3-beta hydroxysteroid dehydrogenase/isomera;4.4e-95
93933_at	18	Ppp1r3c	protein phosphatase 1, regulatory (inhibitor) subunit 3C	IPR005036 // Putative phosphatase regulatory subunit	---
94330_at	18	Npl	N-acetylneuraminate pyruvate lyase	IPR002220 // Dihydrodipicolinate synthetase	DHDPS // Dihydrodipicolinate synthetase family;4.5e-30
95000_g_at	18	Cubn	cubilin (intrinsic factor-cobalamin receptor)	IPR001412 // Aminoacyl-tRNA synthetase, class I /// IPR000859 // CUB domain	---
95066_at	18	Taldo1	transaldolase 1	IPR004730 // Transaldolase AB /// IPR001585 // Transaldolase	---
96077_at	18	Slc17a1	solute carrier family 17 vesicular	IPR005828 // General	---

				glutamate transporter), member 1	substrate transporter /// IPR004745 // Na(+)-dependent inorganic phosphate cotransporter	
97172_s_at	18		Abcc9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	IPR003439 // ABC transporter /// IPR000388 // Sulphonylurea receptor /// IPR003593 // AAA ATPase /// IPR001140 // ABC transporter, transmembrane region /// IPR001475 // Sulphonylurea receptor, type 2	ABC_tran // ABC transporter;9.5e-87 /// ABC_membrane // ABC transporter transmembrane region;2.7e-68 /// ABC_tran // ABC transporter;2.1e-87 /// ABC_tran // ABC transporter;1.4e-89
97281_at	18		AA420407	expressed sequence AA420407	IPR002618 // UTP--glucose-1-phosphate uridylyltransferase	UDPGP // UTP--glucose-1-phosphate uridylyltransferase;1.3 e-234
97477_at	18	7305579	Timm8b	translocase of inner mitochondrial membrane 8 homolog b (yeast)	IPR004217 // Zn-finger, Tim10/DDP type	zf-Tim10_DDP // Tim10/DDP family zinc finger;3.2e-28
97521_at	18		Ass1	argininosuccinate synthetase 1	IPR001518 // Argininosuccinate synthase	Arginosuc_synth // Arginosuccinate synthase;2.3e-262
97751_f_at	18		---	ESTs, Moderately similar to G3P_MOUSE Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) [M.musculus]	---	---
98626_at	18		1810017G16Rik	RIKEN cDNA 1810017G16 gene	---	---
99184_at	18		Csad	cysteine sulfinic acid decarboxylase	---	pyridoxal_deC // Pyridoxal-dependent decarboxylase conse;1.4e-125
99580_s_at	18		Ugt1a1	UDP-glucuronosyltransferase 1 family, member 1	IPR002213 // UDP-glucoronosyl/UDP-	---

					glucosyl transferase	
100573_f_at	17		Gpi1	glucose phosphate isomerase 1	IPR001672 // Phosphoglucose isomerase (PGI)	PGI // Phosphoglucose isomerase;0
101695_at	17		Eif3s6	eukaryotic translation initiation factor 3, subunit 6	IPR000717 // Domain in components of the proteasome, COP9-complex and eIF3 (PCI)	---
101822_at	17		Mc3r	melanocortin 3 receptor	---	7tm_1 // 7 transmembrane receptor (rhodopsin family);2.4e-54
103484_at	17		Pop3-pending	popeye 3	---	---
103702_i_at	17		C730048C13Rik	RIKEN cDNA C730048C13 gene	---	---
103833_at	17		Hipk2	homeodomain interacting protein kinase 2	IPR001245 // Tyrosine protein kinase /// IPR002290 // Serine/Threonine protein kinase /// IPR000719 // Eukaryotic protein kinase	pkinase // Protein kinase domain;1.3e-49
103899_at	17		4930558F19Rik	RIKEN cDNA 4930558F19 gene	---	---
104438_at	17		Zfp30	zinc finger protein 30	IPR001909 // KRAB box /// IPR000822 // Zn-finger, C2H2 type	zf-C2H2 // Zinc finger, C2H2 type;8e-80 /// KRAB // KRAB box;5.6e-23
92650_at	17		Man1b	mannosidase 1, beta	IPR001382 // Glycoside hydrolase, family 47	Glyco_hydro_47 // Glycosyl hydrolase family 47;6.8e-286
92829_at	17	6680309	Hspe1	heat shock protein 1 (chaperonin 10)	IPR001476 // Chaperonin Cpn10	cpn10 // Chaperonin 10 Kd subunit;2.8e-46
93798_at	17		Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	IPR004014 // Cation transporting ATPase, N terminal /// IPR001757 // ATPase, E1-E2 type /// IPR006069 //	Cation_ATPase_N // Cation transporter/ATPase, N-terminus;1.1e-37 /// Hydrolase // haloacid dehalogenase-like

					Cation transporting ATPase /// IPR005834 // haloacid dehalogenase-like hydrolase /// IPR005775 // Na+/K+ ATPase, alpha subunit /// IPR006068 // Cation transporting ATPase, C-terminal	hydrolase;4.2e-15 /// E1-E2_ATPase // E1-E2 ATPase;1.3e-113 /// Cation_ATPase_C // Cation transporting ATPase, C-terminu;1.3e-68
94262_at	17		B230333E16Rik	RIKEN cDNA B230333E16 gene	---	---
96336_at	17	13385454	Gatm	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	IPR003198 // Amidinotransferase /// IPR000531 // TonB-dependent receptor protein	Amidinotransf // Amidinotransferase;3.6e-06
96918_at	17		Fbp1	fructose bisphosphatase 1	IPR000146 // Inositol phosphatase/fructose-1,6-bisphosphatase	FBPase // Fructose-1-6-bisphosphatase;4.4e-197
97515_at	17	31982273	Hsd17b4	hydroxysteroid (17-beta) dehydrogenase 4	IPR002539 // MaoC-like dehydratase /// IPR002198 // Short-chain dehydrogenase/reductase SDR /// IPR003033 // Sterol-binding /// IPR002347 // Glucose/ribitol dehydrogenase	SCP2 // SCP-2 sterol transfer family;7.9e-48 /// MaoC_dehydratas // MaoC like domain;1.3e-50 /// adh_short // short chain dehydrogenase;2.4e-65
97758_at	17		Prdx1	peroxiredoxin 1	IPR000866 // Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen	AhpC-TSA // AhpC/TSA family;8e-89
97926_s_at	17		Pparg	peroxisome proliferator activated receptor gamma	IPR001628 // Zn-finger, C4-type steroid receptor ///	hormone_rec // Ligand-binding domain of nuclear

				IPR003077 // Peroxisome proliferator-activated receptor, gamma /// IPR003074 // Peroxisome proliferator-activated receptor /// IPR001723 // Steroid hormone receptor /// IPR000536 // Ligand-binding domain of nuclear hormone receptor	hormone;7.7e-40 /// zf-C4 // Zinc finger, C4 type (two domains);2.3e-45
98322_at	17	Slc22a5	solute carrier family 22 (organic cation transporter), member 5	IPR005829 // Sugar transporter superfamily /// IPR005828 // General substrate transporter /// IPR004749 // Organic cation transport protein	sugar_tr // Sugar (and other) transporter;1.4e-07
98496_at	17	Gys3	glycogen synthase 3, brain	---	---
98552_at	17	2600009M07Rik	RIKEN cDNA 2600009M07 gene	---	---
99587_at	17	Rab7	RAB7, member RAS oncogene family	IPR002078 // Sigma-54 factor interaction domain /// IPR005225 // Small GTP-binding protein domain /// IPR003579 // Ras small GTPase, Rab type /// IPR001806 // Ras GTPase superfamily	ras // Ras family;6.3e-94
99872_s_at	17	Ftl1	ferritin light chain 1	IPR001519 // Ferritin	ferritin // Ferritin-like domain;2.2e-53
99973_s_at	17	Kcnj15	potassium inwardly-rectifying channel, subfamily J, member 15	IPR001622 // K+ channel, pore region /// IPR001838 // K+	IRK // Inward rectifier potassium channel;2.2e-221

				channel, inward rectifier /// IPR003270 // Kir1.3 inward rectifier K+ channel	
100041_at	16	3010027G13Rik	RIKEN cDNA 3010027G13 gene	IPR001993 // Mitochondrial substrate carrier	mito_carr // Mitochondrial carrier protein;1.3e-65
101013_at	16	Oaz1	ornithine decarboxylase antizyme	IPR002993 // Ornithine decarboxylase antizyme	ODC_AZ // Ornithine decarboxylase antizyme;1.6e-158
101913_at	16	---	ESTs, Highly similar to CLC5_MOUSE Chloride channel protein 5 (ClC-5) [M.musculus]	---	---
102899_at	16	Siat7c	sialyltransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) C	IPR001675 // Glycosyl transferase, family 29	Glyco_transf_29 // Glycosyltransferase family 29 (sialyl;1.2e-104
104014_at	16	Hfe	hemochromatosis	IPR001039 // Major histocompatibility complex protein, class I /// IPR003006 // Immunoglobulin/major histocompatibility complex /// IPR003597 // Immunoglobulin C-type	ig // Immunoglobulin domain;8.8e-05 /// MHC_I // Class I Histocompatibility antigen, domains;5.4e-49
104101_at	16	1200006P13Rik	RIKEN cDNA 1200006P13 gene	IPR004709 // Sodium/hydrogen exchanger subfamily /// IPR006153 // Sodium/hydrogen exchanger	Na_H_Exchanger // Sodium/hydrogen exchanger family;1.5e-103
104745_at	16	Arl6ip2	ADP-ribosylation-like factor 6 interacting protein 2	---	---

93051_at	16	Ephx2	epoxide hydrolase 2, cytoplasmic	IPR005833 // Haloacid dehalogenase/epoxide hydrolase /// IPR000073 // Alpha/beta hydrolase fold /// IPR003089 // Alpha/beta hydrolase /// IPR005834 // haloacid dehalogenase-like hydrolase /// IPR000639 // Epoxide hydrolase /// IPR000379 // Esterase/lipase/thioesterase, active site	abhydrolase // alpha/beta hydrolase fold;8.2e-50 /// Hydrolase // haloacid dehalogenase-like hydrolase;2.3e-16
94042_f_at	16	Gng5	guanine nucleotide binding protein (G protein), gamma 5 subunit	IPR001770 // G-protein, gamma subunit	---
94057_g_at	16	Scd1	stearoyl-Coenzyme A desaturase 1	IPR001522 // Fatty acid desaturase, type 1 /// IPR005804 // Fatty acid desaturase family	FA_desaturase // Fatty acid desaturase;5.2e-80
94276_at	16	Hsd17b12	hydroxysteroid (17-beta) dehydrogenase 12	IPR002198 // Short-chain dehydrogenase/reductase SDR /// IPR002347 // Glucose/ribitol dehydrogenase	adh_short // short chain dehydrogenase;1.7e-37
95518_at	16	1810015C04Rik	RIKEN cDNA 1810015C04 gene	---	---
96068_at	16	1500034J20Rik	RIKEN cDNA 1500034J20 gene	IPR000508 // Signal peptidase /// IPR000223 // Bacterial signal peptidase S26A	Peptidase_S26 // Signal peptidase I;7.7e-06
96346_at	16	Cdo1	cysteine dioxygenase 1, cytosolic	---	---

97402_at	16		Temt	thioether S-methyltransferase	IPR000940 // Methyltransferase, NNMT/PNMT/TEMT family /// IPR001601 // Generic methyltransferase	NNMT_PNMT_TEMT // NNMT/PNMT/TEMT family;2.6e-176
97450_s_at	16	20070418	Aldh7a1	aldehyde dehydrogenase family 7, member A1	IPR002086 // Aldehyde dehydrogenase	aldedh // Aldehyde dehydrogenase family;9.5e-166
97800_at	16		Fastk	Fas-activated serine/threonine kinase	---	---
100424_at	15		Ercc1	excision repair cross-complementing rodent repair deficiency, complementation group 1	IPR000445 // Helix-hairpin-helix motif /// IPR003583 // Helix-hairpin-helix DNA-binding, class 1 /// IPR004579 // DNA repair protein rad10	HHH // Helix-hairpin-helix motif;1.5e-09 /// Rad10 // DNA repair protein rad10;3.5e-47
100597_at	15		Gyg1	glycogenin 1	IPR002495 // Glycosyl transferase, family 8	Glyco_transf_8 // Glycosyl transferase family 8;0.00077
100959_at	15		S100a13	S100 calcium binding protein A13	IPR002048 // Calcium-binding EF-hand /// IPR001751 // Calcium-binding protein, S-100/ICaBP type	S_100 // S-100/ICaBP type calcium binding domain;2.7e-13
102041_at	15		Myom2	myomesin 2	IPR003600 // Immunoglobulin-like /// IPR003961 // Fibronectin, type III /// IPR003962 // Fibronectin, type III repeat /// IPR003598 // Immunoglobulin C-2 type /// IPR003006 // Immunoglobulin/major histocompatibility	fn3 // Fibronectin type III domain;1.7e-105 /// ig // Immunoglobulin domain;4e-21

					complex	
102671_at	15		Creb1	cAMP responsive element binding protein 1	IPR004827 // Basic-leucine zipper (bZIP) transcription factor /// IPR001630 // cAMP response element binding (CREB) protein /// IPR003102 // Coactivator CBP, pKID	pKID // pKID domain;4.7e-24 /// bZIP // bZIP transcription factor;6.4e-20 /// bZIP // bZIP transcription factor;7.2e-21
103845_at	15		Slc31a1	solute carrier family 31, member 1	---	---
92726_at	15		Sox6	SRY-box containing gene 6	IPR000910 // HMG1/2 (high mobility group) box	HMG_box // HMG (high mobility group) box;9e-27
92775_at	15		Pabpc4	poly(A) binding protein, cytoplasmic 4 (inducible form)	IPR002004 // Poly-adenylate-binding protein/HECT-associated /// IPR000504 // RNA-binding region RNP-1 (RNA recognition motif)	rrm // RNA recognition motif. (a.k.a. RRM, RBD, or;3.5e-111 /// PABP // Poly-adenylate binding protein, unique domai;2.3e-45
94012_at	15	7305575	Timm13a	translocase of inner mitochondrial membrane 13 homolog a (yeast)	IPR004217 // Zn-finger, Tim10/DDP type	zf-Tim10_DDP // Tim10/DDP family zinc finger;2.7e-25
94056_at	15		Scd1	stearoyl-Coenzyme A desaturase 1	IPR001522 // Fatty acid desaturase, type 1 /// IPR005804 // Fatty acid desaturase family	FA_desaturase // Fatty acid desaturase;5.2e-80
94922_i_at	15		4930431L18Rik	RIKEN cDNA 4930431L18 gene	---	---
95026_at	15		0610039N19Rik	RIKEN cDNA 0610039N19 gene	---	---
95407_at	15		Pah	phenylalanine hydroxylase	IPR002912 // Amino acid-binding ACT /// IPR001273 // Aromatic amino acid hydroxylase /// IPR005961 // Phenylalanine-4-	biopterin_H // Biopterin-dependent aromatic amino acid h;3.7e-294 /// ACT // ACT domain;5.5e-11

				hydroxylase, tetrameric form	
96934_at	15	1110002M09Rik	RIKEN cDNA 1110002M09 gene	---	---
97334_at	15	Hes6	hairy and enhancer of split 6, (Drosophila)	IPR003650 // Orange /// IPR001092 // Basic helix-loop-helix dimerization domain bHLH	HLH // Helix-loop-helix DNA-binding domain;8.3e-09
97449_at	15	Aldh7a1	aldehyde dehydrogenase family 7, member A1	IPR002086 // Aldehyde dehydrogenase	aldedh // Aldehyde dehydrogenase family;9.5e-166
98447_at	15	Cebpa	CCAAT/enhancer binding protein (C/EBP), alpha	IPR004827 // Basic-leucine zipper (bZIP) transcription factor	---
98871_at	15	Oa1	mouse homolog of human ocular albinism 1 (Nettleship-Falls)	IPR001414 // Ocular albinism protein, type 1	Ocular_alb // Ocular albinism type 1 protein;0
99056_at	15	Pcbd	6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1)	IPR001533 // Transcriptional coactivator/pterin dehydratase	Pterin_4a // Pterin 4 alpha carbinolamine dehydratase;6.4e-61
99164_at	15	Mapbpip-pending	mitogen activated protein binding protein interacting protein	IPR004942 // Roadblock/LC7 family	Robl_LC7 // Roadblock/LC7 domain;2e-25
99988_at	15	4933427L07Rik	RIKEN cDNA 4933427L07 gene	---	---

Table 8 shows motifs associated with differential expression on days 1, 2, and 3.

Day	Motif	Frequency	Nominal *P*-value	Adjusted *P*-value	Annotation	Reference
1	TGACCTTG	0.07	3.15E-11	2.06E-06	Errα	(22)
	TGACCTTGA	0.02	4.59E-10	1.20E-04	Errα	
2	TGACCTTG	0.07	4.44E-14	2.91E-09	Errα	(22)
	TGACCTT	0.16	3.62E-12	5.93E-08	Errα	
	TGACCT	0.45	1.46E-11	5.97E-08	NR half-site	(35)
	GACCTTG	0.16	7.92E-11	1.30E-06	Errα	
	GACCTT	0.41	1.42E-09	5.81E-06	Errα	
	TTGACC	0.27	2.42E-07	9.92E-04	Errα	
3	CTTCCG	0.33	2.19E-12	8.97E-09	Gabpa	(36)
	TGACCTTG	0.07	1.17E-11	7.66E-07	Errα	(22)
	TGACCTT	0.16	1.23E-10	2.02E-06	Errα	
	CCCGCC	0.54	2.04E-08	8.36E-05		
	GCGGCG	0.43	3.78E-08	1.55E-04		
	AGGTCA	0.42	3.90E-08	1.60E-04	NR half-site	(35)
	CTTCCGG	0.16	1.95E-08	3.19E-04	Gabpa	
	TTCCGG	0.31	1.09E-07	4.46E-04	Gabpa	
	GGGGCG	0.54	1.24E-07	5.08E-04		
	TTCCGCT	0.07	3.30E-08	5.41E-04	Gabpa	
	GCCGGC	0.42	1.57E-07	6.44E-04		
	ACTTCCG	0.09	5.11E-08	8.38E-04	Gabpa	

motifADE was performed using the mouse promoter database on each of days 1, 2, and 3. All motifs achieving a Bonferroni-corrected *P*-value < 1 x 10^{-3} are shown. Annotations of the motif and the literature references, when available, are indicated.

Table 9 motifs discovered using the mouse promoter database achieving $P<0.05$

Day	Motif	Frequency	P-value	Adjusted P-value
1	TGACCTTG	0.07	3.15E-11	2.06E-06
	TGACCTTGA	0.02	4.59E-10	1.20E-04
	GACCTTGA	0.05	5.76E-08	3.77E-03
	GACCTTG	0.16	1.54E-06	2.53E-02
	GTCACG	0.18	8.04E-06	3.29E-02
2	TGACCTTG	0.07	4.44E-14	2.91E-09
	TGACCTT	0.16	3.62E-12	5.93E-08
	TGACCT	0.45	1.46E-11	5.97E-08
	GACCTTG	0.16	7.92E-11	1.30E-06
	GACCTT	0.41	1.42E-09	5.81E-06
	TTGACC	0.27	2.42E-07	9.92E-04
	GTGACCTT	0.05	3.86E-08	2.53E-03
	GTGACCT	0.15	3.91E-07	6.41E-03
	GTGACCTTG	0.02	3.97E-08	1.04E-02
	TGACCTTGA	0.02	4.63E-08	1.21E-02
	AGGTCA	0.42	3.46E-06	1.42E-02
	CGCTGAGG	0.04	3.06E-07	2.01E-02
	GACCTTGA	0.05	3.33E-07	2.19E-02
	AGGTCAC	0.13	1.99E-06	3.26E-02
	GTGACC	0.40	8.80E-06	3.61E-02
3	CTTCCG	0.33	2.19E-12	8.97E-09
	TGACCTTG	0.07	1.17E-11	7.66E-07
	TGACCTT	0.16	1.23E-10	2.02E-06
	CCCGCC	0.54	2.04E-08	8.36E-05
	GCGGCG	0.43	3.78E-08	1.55E-04
	AGGTCA	0.42	3.90E-08	1.60E-04
	CTTCCGG	0.16	1.95E-08	3.19E-04
	TTCCGG	0.31	1.09E-07	4.46E-04
	GGGGCG	0.54	1.24E-07	5.08E-04
	TTCCGCT	0.07	3.30E-08	5.41E-04
	GCCGGC	0.42	1.57E-07	6.44E-04
	ACTTCCG	0.09	5.11E-08	8.38E-04
	GACCTT	0.41	2.72E-07	1.11E-03
	CGGGGC	0.51	4.86E-07	1.99E-03
	ATGGCGGC	0.05	4.76E-08	3.12E-03
	GACCTTG	0.16	1.90E-07	3.12E-03
	CTTCCGGC	0.05	7.34E-08	4.81E-03
	ATGGCGG	0.11	3.24E-07	5.31E-03
	AAGATGGCG	0.03	2.07E-08	5.43E-03
	CCGGGG	0.47	1.43E-06	5.85E-03

GCGGAC	0.24	1.52E-06	6.23E-03
GGCGGC	0.48	1.55E-06	6.35E-03
TCACGG	0.19	1.79E-06	7.31E-03
GTGACCTT	0.05	1.23E-07	8.07E-03
CCGGCT	0.39	2.23E-06	9.13E-03
GGCCGG	0.47	2.24E-06	9.16E-03
TCACCG	0.21	2.79E-06	1.14E-02
GCCGGG	0.49	2.81E-06	1.15E-02
CGCCTT	0.30	2.93E-06	1.20E-02
CGGACC	0.24	3.33E-06	1.36E-02
TTCCGC	0.23	3.42E-06	1.40E-02
CGCTGA	0.26	3.44E-06	1.41E-02
CCCCGC	0.51	3.55E-06	1.46E-02
CGCGAG	0.24	3.71E-06	1.52E-02
GTCACG	0.18	4.14E-06	1.69E-02
CGTCCT	0.25	4.15E-06	1.70E-02
AAGGTCA	0.15	1.28E-06	2.10E-02
GCCCGG	0.49	5.14E-06	2.11E-02
CCGCCG	0.36	5.25E-06	2.15E-02
TCCGGG	0.42	5.75E-06	2.35E-02
AAGATGGC	0.08	3.93E-07	2.57E-02
GGCGGA	0.40	6.56E-06	2.69E-02
GGGCGG	0.58	7.63E-06	3.12E-02
CGGGCG	0.38	7.77E-06	3.18E-02
ACCCCG	0.31	8.07E-06	3.30E-02
CGCGCC	0.37	8.13E-06	3.33E-02
CGCCTC	0.41	9.12E-06	3.74E-02
TTCCCG	0.34	9.44E-06	3.86E-02
GGGTCGTGG	0.01	1.56E-07	4.09E-02
CGGCGG	0.40	1.01E-05	4.15E-02
CCGGAA	0.30	1.14E-05	4.68E-02
CGTCGC	0.16	1.15E-05	4.73E-02

motifADE was performed using the mouse promoter database on each of days 1, 2, and 3. Motifs achieving a Bonferroni corrected *P*value < 0.05 are shown. MotifADE was performed using the mouse promoter database on each of days 1, 2, and 3. Motifs achieving a Bonferroni corrected *P*

Table 10 shows motifs discovered using the masked promoter database achieving P<0.05.

Day	Motif	Frequency	P-value	Adjusted P-value
1	TGACCTTG	0.04	7.30E-11	4.78E-06
	TGACCTT	0.09	2.65E-07	4.34E-03
	AAGGTC	0.20	7.83E-06	3.21E-02
	CTTCCGG	0.12	2.56E-06	4.20E-02
2	TGACCT	0.26	1.43E-13	5.84E-10
	TGACCTT	0.09	1.74E-12	2.85E-08
	TGACCTTG	0.04	2.59E-09	1.70E-04
	GACCTT	0.23	4.88E-08	2.00E-04
	GTGACCTT	0.03	3.23E-09	2.12E-04
	GTGACCT	0.09	1.58E-08	2.59E-04
	AGGTCA	0.25	2.04E-07	8.37E-04
	GACCTTG	0.08	7.65E-08	1.25E-03
	GTGACCTTG	0.02	3.02E-08	7.93E-03
	GGTCAC	0.24	2.00E-06	8.17E-03
	ACCTTG	0.22	2.05E-06	8.38E-03
	AGGTCAC	0.08	8.57E-07	1.40E-02
	TTTTCGT	0.02	1.96E-06	3.22E-02
3	TGACCTT	0.09	7.77E-16	1.27E-11
	CTTCCG	0.25	7.59E-14	3.11E-10
	TGACCTTG	0.04	8.68E-13	5.69E-08
	GTGACCTT	0.03	8.75E-13	5.74E-08
	CTTCCGG	0.12	6.12E-12	1.00E-07
	GTGACCT	0.09	3.96E-11	6.48E-07
	GACCTT	0.23	1.39E-09	5.71E-06
	ATGGCGGC	0.05	2.59E-10	1.70E-05
	GACCTTG	0.08	1.23E-09	2.01E-05
	TTCCGG	0.24	1.79E-08	7.34E-05
	CTTCCGGC	0.04	1.66E-09	1.09E-04
	TGACCT	0.26	3.58E-08	1.47E-04
	CCTTCCG	0.08	1.67E-08	2.74E-04
	AAGATGGCG	0.03	1.17E-09	3.07E-04
	ATGGCGGCG	0.03	1.28E-09	3.37E-04
	CCGGGG	0.38	1.03E-07	4.23E-04
	GGCGGG	0.52	1.33E-07	5.47E-04
	GTGACCTTG	0.02	4.87E-09	1.28E-03
	ACTTCCG	0.08	9.04E-08	1.48E-03
	AGATGGCG	0.04	3.79E-08	2.48E-03
	ATGGCGG	0.10	1.66E-07	2.72E-03
	AGATGGCGG	0.02	1.11E-08	2.90E-03
	AGGTCA	0.25	1.04E-06	4.25E-03
	CCCGCC	0.47	1.29E-06	5.30E-03
	CGGTGA	0.20	1.38E-06	5.66E-03
	GGCGGC	0.43	1.55E-06	6.34E-03
	GCGGCG	0.39	1.83E-06	7.51E-03

TTCCGCT	0.05	4.87E-07	7.98E-03
GCGTCA	0.11	2.30E-06	9.41E-03
ACTTCCGG	0.04	1.89E-07	1.24E-02
TTCCGC	0.18	3.93E-06	1.61E-02
CGTCCT	0.17	4.00E-06	1.64E-02
CTGCGG	0.35	4.81E-06	1.97E-02
CGGGGC	0.43	4.86E-06	1.99E-02
GCCGGC	0.33	6.24E-06	2.56E-02
CCGGCT	0.27	6.34E-06	2.60E-02
GACCTTCC	0.03	4.71E-07	3.09E-02
GGGCGG	0.51	8.43E-06	3.45E-02
CCGGCTT	0.07	2.15E-06	3.52E-02
CGGAAGT	0.08	2.22E-06	3.63E-02
TGGCGGC	0.15	2.52E-06	4.13E-02
AAGATGGC	0.05	6.97E-07	4.57E-02

motifADE was performed using the masked promoter database, consisting of regions of the promoters aligned and conserved between mouse and human. Motifs achieving a Bonferroni-corrected *P*-value < 0.05 are shown.

Table 11: Genes having an Errα binding site motif

1: NM_000065 , "Homo sapiens complement component 6 (C6), mRNA", gi|4559405|ref|NM_000065.1|[4559405]; 2: NM_000067 , "Homo sapiens carbonic anhydrase II (CA2), mRNA", gi|4557394|ref|NM_000067.1|[4557394]; 3: NM_000152 , "Homo sapiens glucosidase, alpha; acid (Pompe disease, glycogen storage disease", "type II) (GAA), mRNA", gi|11496988|ref|NM_000152.2|[11496988]; 4: NM_000155 , "Homo sapiens galactose-1-phosphate uridylyltransferase (GALT), transcript", "variant 1, mRNA", gi|22165415|ref|NM_000155.2|[22165415]; 5: NM_000164 , "Homo sapiens gastric inhibitory polypeptide receptor (GIPR), mRNA", gi|4503998|ref|NM_000164.1|[4503998]; 6: NM_000183 , Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A, "thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit", "(HADHB), mRNA", gi|4504326|ref|NM_000183.1|[4504326]; 7: NM_000186 , "Homo sapiens H factor 1 (complement) (HF1), mRNA", gi|4504374|ref|NM_000186.1|[4504374]; 8: NM_000196 , "Homo sapiens hydroxysteroid (11-beta) dehydrogenase 2 (HSD11B2), mRNA", gi|31542940|ref|NM_000196.2|[31542940]; 9: NM_000219 , "Homo sapiens potassium voltage-gated channel, Isk-related family, member 1", "(KCNE1), mRNA", gi|4557686|ref|NM_000219.1|[4557686]; 10: NM_000226 , "Homo sapiens keratin 9 (epidermolytic palmoplantar keratoderma) (KRT9), mRNA", gi|4557704|ref|NM_000226.1|[4557704]; 11: NM_000236 , "Homo sapiens lipase, hepatic (LIPC), mRNA", gi|4557722|ref|NM_000236.1|[4557722]; 12: NM_000249 , "Homo sapiens mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli) (MLH1),", mRNA, gi|28559089|ref|NM_000249.2|[28559089]; 13: NM_000274 , "Homo sapiens ornithine aminotransferase (gyrate atrophy) (OAT), nuclear gene", "encoding mitochondrial protein, mRNA", gi|4557808|ref|NM_000274.1|[4557808]; 14: NM_000297 , "Homo sapiens polycystic kidney disease 2 (autosomal dominant) (PKD2), mRNA",

gi|33286447|ref|NM_000297.2|[33286447]; 15: NM_000343 , "Homo sapiens solute carrier family 5 (sodium/glucose cotransporter), member 1", "(SLC5A1), mRNA", gi|4507030|ref|NM_000343.1|[4507030]; 16: NM_000347 , "Homo sapiens spectrin, beta, erythrocytic (includes spherocytosis, clinical type", "I) (SPTB), mRNA", gi|22507315|ref|NM_000347.3|[22507315]; 17: NM_000349 , "Homo sapiens steroidogenic acute regulatory protein (STAR), mRNA", gi|4507250|ref|NM_000349.1|[4507250]; 18: NM_000364 , "Homo sapiens troponin T2, cardiac (TNNT2), mRNA", gi|4507626|ref|NM_000364.1|[4507626]; 19: NM_000372 , "Homo sapiens tyrosinase (oculocutaneous albinism IA) (TYR), mRNA", gi|24475623|ref|NM_000372.2|[24475623]; 20: NM_000403 , "Homo sapiens galactose-4-epimerase, UDP (GALE), mRNA", gi|9945333|ref|NM_000403.2|[9945333]; 21: NM_000433 , "Homo sapiens neutrophil cytosolic factor 2 (65kDa, chronic granulomatous", "disease, autosomal 2) (NCF2), mRNA", gi|4557786|ref|NM_000433.1|[4557786]; 22: NM_000474 , Homo sapiens twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome), "(Drosophila) (TWIST1), mRNA", gi|17978464|ref|NM_000474.2|[17978464]; 23: NM_000478 , "Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA", gi|13787192|ref|NM_000478.2|[13787192]; 24: NM_000481 , , ref|NM_000481.2|[44662837]; 25: NM_000483 , "Homo sapiens apolipoprotein C-II (APOC2), mRNA", gi|32130517|ref|NM_000483.3|[32130517]; 26: NM_000499 , "Homo sapiens cytochrome P450, family 1, subfamily A, polypeptide 1 (CYP1A1),", mRNA, gi|13325053|ref|NM_000499.2|[13325053]; 27: NM_000526 , "Homo sapiens keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)", "(KRT14), mRNA", gi|15431309|ref|NM_000526.3|[15431309]; 28: NM_000532 , "Homo sapiens propionyl Coenzyme A carboxylase, beta polypeptide (PCCB), mRNA", gi|24475879|ref|NM_000532.2|[24475879]; 29: NM_000536 , "Homo sapiens recombination activating gene 2 (RAG2), mRNA", gi|28629867|ref|NM_000536.1|[28629867]; 30: NM_000593 , "Homo sapiens transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) (TAP1),", mRNA, gi|24797159|ref|NM_000593.4|[24797159]; 31: NM_000603 , "Homo sapiens nitric oxide synthase 3 (endothelial cell) (NOS3), mRNA", gi|40254421|ref|NM_000603.2|[40254421]; 32: NM_000614 , "Homo sapiens ciliary neurotrophic factor (CNTF), mRNA", gi|25952136|ref|NM_000614.2|[25952136]; 33: NM_000616 , "Homo sapiens CD4 antigen (p55) (CD4), mRNA", gi|21314613|ref|NM_000616.2|[21314613]; 34: NM_000628 , "Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA", gi|24430214|ref|NM_000628.3|[24430214]; 35: NM_000634 , "Homo sapiens interleukin 8 receptor, alpha (IL8RA), mRNA", gi|29171679|ref|NM_000634.2|[29171679]; 36: NM_000666 , "Homo sapiens aminoacylase 1 (ACY1), mRNA", gi|4501900|ref|NM_000666.1|[4501900]; 37: NM_000688 , "Homo sapiens aminolevulinate, delta-, synthase 1 (ALAS1), transcript variant 1,", mRNA, gi|40316942|ref|NM_000688.4|[40316942]; 38: NM_000711 , , ref|NM_000711.1|BGLAP[4502400], This record was replaced or removed. See revision history for details., , 39: NM_000735 , "Homo sapiens glycoprotein hormones, alpha polypeptide (CGA), mRNA", gi|10800407|ref|NM_000735.2|[10800407]; 40: NM_000741 , "Homo sapiens cholinergic receptor, muscarinic 4 (CHRM4), mRNA", gi|4502820|ref|NM_000741.1|[4502820]; 41: NM_000742 , "Homo sapiens cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal)", "(CHRNA2), mRNA", gi|4502822|ref|NM_000742.1|[4502822]; 42: NM_000747 , "Homo sapiens cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)", "(CHRNB1), mRNA", gi|41327725|ref|NM_000747.2|[41327725]; 43: NM_000759 , "Homo sapiens colony

stimulating factor 3 (granulocyte) (CSF3), transcript", "variant 1, mRNA", gi|27437047|ref|NM_000759.2|[27437047]; 44: NM_000781 , "Homo sapiens cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1),", "nuclear gene encoding mitochondrial protein, mRNA", gi|4503188|ref|NM_000781.1|[4503188]; 45: NM_000783 , "Homo sapiens cytochrome P450, family 26, subfamily A, polypeptide 1 (CYP26A1),", "transcript variant 1, mRNA", gi|16933529|ref|NM_000783.2|[16933529]; 46: NM_000806 , "Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 1 (GABRA1), mRNA", gi|38327553|ref|NM_000806.3|[38327553]; 47: NM_000808 , "Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 3 (GABRA3), mRNA", gi|34734069|ref|NM_000808.2|[34734069]; 48: NM_000813 , "Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 2 (GABRB2),", "transcript variant 2, mRNA", gi|4503864|ref|NM_000813.1|[4503864]; 49: NM_000835 , "Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2C (GRIN2C),", mRNA, gi|6006004|ref|NM_000835.2|[6006004]; 50: NM_000884 , "Homo sapiens IMP (inosine monophosphate) dehydrogenase 2 (IMPDH2), mRNA", gi|4504688|ref|NM_000884.1|[4504688]; 51: NM_000887 , "Homo sapiens integrin, alpha X (antigen CD11C (p150), alpha polypeptide)", "(ITGAX), mRNA", gi|34452172|ref|NM_000887.3|[34452172]; 52: NM_000909 , "Homo sapiens neuropeptide Y receptor Y1 (NPY1R), mRNA", gi|41350310|ref|NM_000909.4|[41350310]; 53: NM_000911 , "Homo sapiens opioid receptor, delta 1 (OPRD1), mRNA", gi|27734716|ref|NM_000911.2|[27734716]; 54: NM_000915 , "Homo sapiens oxytocin, prepro-(neurophysin I) (OXT), mRNA", gi|12707574|ref|NM_000915.2|[12707574]; 55: NM_000916 , "Homo sapiens oxytocin receptor (OXTR), mRNA", gi|32307151|ref|NM_000916.3|[32307151]; 56: NM_000920 , "Homo sapiens pyruvate carboxylase (PC), nuclear gene encoding mitochondrial", "protein, transcript variant A, mRNA", gi|11761622|ref|NM_000920.2|[11761622]; 57: NM_000928 , "Homo sapiens phospholipase A2, group IB (pancreas) (PLA2G1B), mRNA", gi|38016927|ref|NM_000928.2|[38016927]; 58: NM_000932 , "Homo sapiens phospholipase C, beta 3 (phosphatidylinositol-specific) (PLCB3),", mRNA, gi|11386138|ref|NM_000932.1|[11386138]; 59: NM_000960 , "Homo sapiens prostaglandin I2 (prostacyclin) receptor (IP) (PTGIR), mRNA", gi|39995095|ref|NM_000960.3|[39995095]; 60: NM_001040 , "Homo sapiens sex hormone-binding globulin (SHBG), mRNA", gi|7382459|ref|NM_001040.2|[7382459]; 61: NM_001041 , "Homo sapiens sucrase-isomaltase (SI), mRNA", gi|4506944|ref|NM_001041.1|[4506944]; 62: NM_001087 , "Homo sapiens angio-associated, migratory cell protein (AAMP), mRNA", gi|4557228|ref|NM_001087.1|[4557228]; 63: NM_001094 , "Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1),", "transcript variant 2, mRNA", gi|34452696|ref|NM_001094.4|[34452696]; 64: NM_001099 , "Homo sapiens acid phosphatase, prostate (ACPP), mRNA", gi|6382063|ref|NM_001099.2|[6382063]; 65: NM_001104 , "Homo sapiens actinin, alpha 3 (ACTN3), mRNA", gi|4557240|ref|NM_001104.1|[4557240]; 66: NM_001118 , Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) receptor, "type I (ADCYAP1R1), mRNA", gi|34398688|ref|NM_001118.3|[34398688]; 67: NM_001152 , Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide, "translocator), member 5 (SLC25A5), mRNA", gi|4502098|ref|NM_001152.1|[4502098]; 68: NM_001158 , "Homo sapiens amine oxidase, copper containing 2 (retina-specific) (AOC2),", "transcript variant 1, mRNA", gi|6806880|ref|NM_001158.2|[6806880]; 69: NM_001164 , "Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 1", "(Fe65) (APBB1), transcript

variant 1, mRNA", gi|22035552|ref|NM_001164.2|[22035552]; 70: NM_001165 , "Homo sapiens baculoviral IAP repeat-containing 3 (BIRC3), transcript variant 1,", mRNA, gi|33946283|ref|NM_001165.3|[33946283]; 71: NM_001188 , "Homo sapiens BCL2-antagonist/killer 1 (BAK1), mRNA", gi|33457353|ref|NM_001188.2|[33457353]; 72: NM_001215 , "Homo sapiens carbonic anhydrase VI (CA6), mRNA", gi|4557396|ref|NM_001215.1|[4557396]; 73: NM_001257 , "Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA", gi|16507956|ref|NM_001257.2|[16507956]; 74: NM_001261 , "Homo sapiens cyclin-dependent kinase 9 (CDC2-related kinase) (CDK9), mRNA", gi|17017983|ref|NM_001261.2|[17017983]; 75: NM_001346 , "Homo sapiens diacylglycerol kinase, gamma 90kDa (DGKG), mRNA", gi|4503314|ref|NM_001346.1|[4503314]; 76: NM_001405 , "Homo sapiens ephrin-A2 (EFNA2), mRNA", gi|27894380|ref|NM_001405.2|[27894380]; 77: NM_001425 , "Homo sapiens epithelial membrane protein 3 (EMP3), mRNA", gi|4503562|ref|NM_001425.1|[4503562]; 78: NM_001501 , "Homo sapiens gonadotropin-releasing hormone 2 (GNRH2), transcript variant 1,", mRNA, gi|4504056|ref|NM_001501.1|[4504056]; 79: NM_001507 , "Homo sapiens G protein-coupled receptor 38 (GPR38), mRNA", gi|4504094|ref|NM_001507.1|[4504094]; 80: NM_001525 , "Homo sapiens hypocretin (orexin) receptor 1 (HCRTR1), mRNA", gi|4557636|ref|NM_001525.1|[4557636]; 81: NM_001542 , "Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA", gi|4504626|ref|NM_001542.1|[4504626]; 82: NM_001662 , "Homo sapiens ADP-ribosylation factor 5 (ARF5), mRNA", gi|6995999|ref|NM_001662.2|[6995999]; 83: NM_001665 , "Homo sapiens ras homolog gene family, member G (rho G) (ARHG), mRNA", gi|4502218|ref|NM_001665.1|[4502218]; 84: NM_001666 , "Homo sapiens Rho GTPase activating protein 4 (ARHGAP4), mRNA", gi|41327157|ref|NM_001666.2|[41327157]; 85: NM_001702 , "Homo sapiens brain-specific angiogenesis inhibitor 1 (BAI1), mRNA", gi|4502354|ref|NM_001702.1|[4502354]; 86: NM_001722 , "Homo sapiens polymerase (RNA) III (DNA directed) polypeptide D, 44kDa (POLR3D),", mRNA, gi|4502436|ref|NM_001722.1|[4502436]; 87: NM_001766 , "Homo sapiens CD1D antigen, d polypeptide (CD1D), mRNA", gi|34419629|ref|NM_001766.2|[34419629]; 88: NM_001795 , "Homo sapiens cadherin 5, type 2, VE-cadherin (vascular epithelium) (CDH5), mRNA", gi|14589894|ref|NM_001795.2|[14589894]; 89: NM_001805 , "Homo sapiens CCAAT/enhancer binding protein (C/EBP), epsilon (CEBPE), mRNA", gi|28872799|ref|NM_001805.2|[28872799]; 90: NM_001807 , "Homo sapiens carboxyl ester lipase (bile salt-stimulated lipase) (CEL), mRNA", gi|27894374|ref|NM_001807.2|[27894374]; 91: NM_001823 , "Homo sapiens creatine kinase, brain (CKB), mRNA", gi|34335231|ref|NM_001823.3|[34335231]; 92: NM_001859 , "Homo sapiens solute carrier family 31 (copper transporters), member 1 (SLC31A1),", mRNA, gi|40254457|ref|NM_001859.2|[40254457]; 93: NM_001864 , "Homo sapiens cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1),", mRNA, gi|18105034|ref|NM_001864.2|[18105034]; 94: NM_001887 , "Homo sapiens crystallin, beta B1 (CRYBB1), mRNA", gi|21536279|ref|NM_001887.3|[21536279]; 95: NM_001888 , "Homo sapiens crystallin, mu (CRYM), mRNA", gi|4503064|ref|NM_001888.1|[4503064]; 96: NM_001893 , "Homo sapiens casein kinase 1, delta (CSNK1D), transcript variant 1, mRNA", gi|20544143|ref|NM_001893.3|[20544143]; 97: NM_001895 , "Homo sapiens casein kinase 2, alpha 1 polypeptide (CSNK2A1), transcript variant", "2, mRNA", gi|29570794|ref|NM_001895.2|[29570794]; 98: NM_001923 , "Homo sapiens damage-specific

DNA binding protein 1, 127kDa (DDB1), mRNA", gi|13435358|ref|NM_001923.2|[13435358]; 99: NM_001958 , "Homo sapiens eukaryotic translation elongation factor 1 alpha 2 (EEF1A2), mRNA", gi|25453470|ref|NM_001958.2|[25453470]; 100: NM_001982 , Homo sapiens v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian), "(ERBB3), mRNA", gi|4503596|ref|NM_001982.1|[4503596]; 101: NM_001998 , "Homo sapiens fibulin 2 (FBLN2), mRNA", gi|4503664|ref|NM_001998.1|[4503664]; 102: NM_002010 , "Homo sapiens fibroblast growth factor 9 (glia-activating factor) (FGF9), mRNA", gi|4503706|ref|NM_002010.1|[4503706]; 103: NM_002012 , "Homo sapiens fragile histidine triad gene (FHIT), mRNA", gi|4503718|ref|NM_002012.1|[4503718]; 104: NM_002036 , , ref|NM_002036.2|[42822886]; 105: NM_002054 , "Homo sapiens glucagon (GCG), mRNA", gi|20302161|ref|NM_002054.2|[20302161]; 106: NM_002073 , "Homo sapiens guanine nucleotide binding protein (G protein), alpha z polypeptide", "(GNAZ), mRNA", gi|4504050|ref|NM_002073.1|[4504050]; 107: NM_002083 , "Homo sapiens glutathione peroxidase 2 (gastrointestinal) (GPX2), mRNA", gi|32967606|ref|NM_002083.2|[32967606]; 108: NM_002139 , "Homo sapiens RNA binding motif protein, X-linked (RBMX), mRNA", gi|4504450|ref|NM_002139.1|[4504450]; 109: NM_002151 , "Homo sapiens hepsin (transmembrane protease, serine 1) (HPN), transcript variant", "2, mRNA", gi|4504480|ref|NM_002151.1|[4504480]; 110: NM_002157 , "Homo sapiens heat shock 10kDa protein 1 (chaperonin 10) (HSPE1), mRNA", gi|4504522|ref|NM_002157.1|[4504522]; 111: NM_002193 , "Homo sapiens inhibin, beta B (activin AB beta polypeptide) (INHBB), mRNA", gi|9257224|ref|NM_002193.1|[9257224]; 112: NM_002208 , "Homo sapiens integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen", "1; alpha polypeptide) (ITGAE), mRNA", gi|6007850|ref|NM_002208.3|[6007850]; 113: NM_002217 , "Homo sapiens pre-alpha (globulin) inhibitor, H3 polypeptide (ITIH3), mRNA", gi|10092578|ref|NM_002217.1|[10092578]; 114: NM_002220 , "Homo sapiens inositol 1,4,5-trisphosphate 3-kinase A (ITPKA), mRNA", gi|4504788|ref|NM_002220.1|[4504788]; 115: NM_002236 , "Homo sapiens potassium voltage-gated channel, subfamily F, member 1 (KCNF1),", mRNA, gi|27436998|ref|NM_002236.4|[27436998]; 116: NM_002238 , "Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member", "1 (KCNH1), transcript variant 2, mRNA", gi|27436999|ref|NM_002238.2|[27436999]; 117: NM_002246 , "Homo sapiens potassium channel, subfamily K, member 3 (KCNK3), mRNA", gi|4504848|ref|NM_002246.1|[4504848]; 118: NM_002257 , "Homo sapiens kallikrein 1, renal/pancreas/salivary (KLK1), mRNA", gi|22027643|ref|NM_002257.2|[22027643]; 119: NM_002274 , "Homo sapiens keratin 13 (KRT13), transcript variant 2, mRNA", gi|24234693|ref|NM_002274.2|[24234693]; 120: NM_002279 , "Homo sapiens keratin, hair, acidic, 3B (KRTHA3B), mRNA", gi|15022816|ref|NM_002279.3|[15022816]; 121: NM_002280 , "Homo sapiens keratin, hair, acidic, 5 (KRTHA5), mRNA", gi|15431313|ref|NM_002280.3|[15431313]; 122: NM_002343 , "Homo sapiens lactotransferrin (LTF), mRNA", gi|4505042|ref|NM_002343.1|[4505042]; 123: NM_002374 , "Homo sapiens microtubule-associated protein 2 (MAP2), transcript variant 1, mRNA", gi|14195623|ref|NM_002374.2|[14195623]; 124: NM_002378 , "Homo sapiens megakaryocyte-associated tyrosine kinase (MATK), transcript variant", "2, mRNA", gi|21450841|ref|NM_002378.2|[21450841]; 125: NM_002380 , "Homo sapiens matrilin 2 (MATN2), transcript variant 1, mRNA", gi|13518036|ref|NM_002380.2|[13518036]; 126: NM_002418 , "Homo sapiens motilin (MLN), mRNA", gi|4557033|ref|NM_002418.1|[4557033]; 127: NM_002419 , "Homo sapiens mitogen-activated

protein kinase kinase kinase 11 (MAP3K11), mRNA", gi|21735553|ref|NM_002419.2|[21735553]; 128: NM_002437 , "Homo sapiens MpV17 transgene, murine homolog, glomerulosclerosis (MPV17), mRNA", gi|37059781|ref|NM_002437.3|[37059781]; 129: NM_002469 , "Homo sapiens myogenic factor 6 (herculin) (MYF6), mRNA", gi|4505298|ref|NM_002469.1|[4505298]; 130: NM_002479 , "Homo sapiens myogenin (myogenic factor 4) (MYOG), mRNA", gi|18765726|ref|NM_002479.2|[18765726]; 131: NM_002492 , "Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa", "(NDUFB5), nuclear gene encoding mitochondrial protein, mRNA", gi|33519467|ref|NM_002492.2|[33519467]; 132: NM_002506 , "Homo sapiens nerve growth factor, beta polypeptide (NGFB), mRNA", gi|4505390|ref|NM_002506.1|[4505390]; 133: NM_002527 , "Homo sapiens neurotrophin 3 (NTF3), mRNA", gi|9845503|ref|NM_002527.2|[9845503]; 134: NM_002558 , "Homo sapiens purinergic receptor P2X, ligand-gated ion channel, 1 (P2RX1), mRNA", gi|27894283|ref|NM_002558.2|[27894283]; 135: NM_002590 , "Homo sapiens protocadherin 8 (PCDH8), transcript variant 1, mRNA", gi|6631101|ref|NM_002590.2|[6631101]; 136: NM_002599 , "Homo sapiens phosphodiesterase 2A, cGMP-stimulated (PDE2A), mRNA", gi|4505656|ref|NM_002599.1|[4505656]; 137: NM_002621 , "Homo sapiens properdin P factor, complement (PFC), mRNA", gi|4505736|ref|NM_002621.1|[4505736]; 138: NM_002630 , "Homo sapiens progastricsin (pepsinogen C) (PGC), mRNA", gi|4505756|ref|NM_002630.1|[4505756]; 139: NM_002644 , "Homo sapiens polymeric immunoglobulin receptor (PIGR), mRNA", gi|31377805|ref|NM_002644.2|[31377805]; 140: NM_002646 , "Homo sapiens phosphoinositide-3-kinase, class 2, beta polypeptide (PIK3C2B),", mRNA, gi|15451925|ref|NM_002646.2|[15451925]; 141: NM_002788 , "Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 3 (PSMA3),", "transcript variant 1, mRNA", gi|23110937|ref|NM_002788.2|[23110937]; 142: NM_002831 , "Homo sapiens protein tyrosine phosphatase, non-receptor type 6 (PTPN6),", "transcript variant 1, mRNA", gi|34328900|ref|NM_002831.3|[34328900]; 143: NM_002832 , "Homo sapiens protein tyrosine phosphatase, non-receptor type 7 (PTPN7),", "transcript variant 1, mRNA", gi|18375657|ref|NM_002832.2|[18375657]; 144: NM_002894 , "Homo sapiens retinoblastoma binding protein 8 (RBBP8), transcript variant 1,", mRNA, gi|42718012|ref|NM_002894.2|[42718012]; 145: NM_002904 , "Homo sapiens RD RNA binding protein (RDBP), mRNA", gi|20631983|ref|NM_002904.4|[20631983]; 146: NM_002912 , "Homo sapiens REV3-like, catalytic subunit of DNA polymerase zeta (yeast)", "(REV3L), mRNA", gi|4506482|ref|NM_002912.1|[4506482]; 147: NM_002930 , "Homo sapiens Ras-like without CAAX 2 (RIT2), mRNA", gi|4506532|ref|NM_002930.1|[4506532]; 148: NM_002938 , "Homo sapiens ring finger protein 4 (RNF4), mRNA", gi|34305289|ref|NM_002938.2|[34305289]; 149: NM_002965 , "Homo sapiens S100 calcium binding protein A9 (calgranulin B) (S100A9), mRNA", gi|9845520|ref|NM_002965.2|[9845520]; 150: NM_002981 , "Homo sapiens chemokine (C-C motif) ligand 1 (CCL1), mRNA", gi|4506832|ref|NM_002981.1|[4506832]; 151: NM_003002 , "Homo sapiens succinate dehydrogenase complex, subunit D, integral membrane", "protein (SDHD), nuclear gene encoding mitochondrial protein, mRNA", gi|4506864|ref|NM_003002.1|[4506864]; 152: NM_003015 , "Homo sapiens secreted frizzled-related protein 5 (SFRP5), mRNA", gi|8400734|ref|NM_003015.2|[8400734]; 153: NM_003021 , "Homo sapiens small glutamine-rich tetratricopeptide repeat (TPR)-containing,", "alpha (SGTA), mRNA", gi|38788107|ref|NM_003021.3|[38788107]; 154: NM_003042 , "Homo sapiens solute carrier

family 6 (neurotransmitter transporter, GABA),", "member 1 (SLC6A1), mRNA", gi|40254466|ref|NM_003042.2|[40254466]; 155: NM_003047 , "Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 1", "(antiporter, Na+/H+, amiloride sensitive) (SLC9A1), mRNA", gi|27777631|ref|NM_003047.2|[27777631]; 156: NM_003055 , "Homo sapiens solute carrier family 18 (vesicular acetylcholine), member 3", "(SLC18A3), mRNA", gi|4506990|ref|NM_003055.1|[4506990]; 157: NM_003059 , "Homo sapiens solute carrier family 22 (organic cation transporter), member 4", "(SLC22A4), mRNA", gi|24497489|ref|NM_003059.2|[24497489]; 158: NM_003063 , "Homo sapiens sarcolipin (SLN), mRNA", gi|4507062|ref|NM_003063.1|[4507062]; 159: NM_003085 , "Homo sapiens synuclein, beta (SNCB), mRNA", gi|6466453|ref|NM_003085.2|[6466453]; 160: NM_003097 , "Homo sapiens small nuclear ribonucleoprotein polypeptide N (SNRPN), transcript", "variant 1, mRNA", gi|29540556|ref|NM_003097.3|[29540556]; 161: NM_003105 , "Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing", "(SORL1), mRNA", gi|18379347|ref|NM_003105.3|[18379347]; 162: NM_003115 , "Homo sapiens UDP-N-acteylglucosamine pyrophosphorylase 1 (UAP1), mRNA", gi|34147515|ref|NM_003115.3|[34147515]; 163: NM_003159 , "Homo sapiens cyclin-dependent kinase-like 5 (CDKL5), mRNA", gi|4507280|ref|NM_003159.1|[4507280]; 164: NM_003212 , "Homo sapiens teratocarcinoma-derived growth factor 1 (TDGF1), mRNA", gi|4507424|ref|NM_003212.1|[4507424]; 165: NM_003216 , "Homo sapiens thyrotrophic embryonic factor (TEF), mRNA", gi|34486096|ref|NM_003216.2|[34486096]; 166: NM_003239 , "Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA", gi|4507464|ref|NM_003239.1|[4507464]; 167: NM_003240 , "Homo sapiens endometrial bleeding associated factor (left-right determination,", "factor A; transforming growth factor beta superfamily) (EBAF), mRNA", gi|27436880|ref|NM_003240.2|[27436880]; 168: NM_003249 , "Homo sapiens thimet oligopeptidase 1 (THOP1), mRNA", gi|34222291|ref|NM_003249.3|[34222291]; 169: NM_003259 , "Homo sapiens intercellular adhesion molecule 5, telencephalin (ICAM5), mRNA", gi|12545403|ref|NM_003259.2|[12545403]; 170: NM_003279 , "Homo sapiens troponin C2, fast (TNNC2), mRNA", gi|40807466|ref|NM_003279.2|[40807466]; 171: NM_003325 , Homo sapiens HIR histone cell cycle regulation defective homolog A (S., "cerevisiae) (HIRA), mRNA", gi|21536484|ref|NM_003325.3|[21536484]; 172: NM_003334 , Homo sapiens ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature, "sensitivity complementing) (UBE1), transcript variant 1, mRNA", gi|23510337|ref|NM_003334.2|[23510337]; 173: NM_003341 , "Homo sapiens ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)", "(UBE2E1), transcript variant 1, mRNA", gi|33359692|ref|NM_003341.3|[33359692]; 174: NM_003361 , "Homo sapiens uromodulin (uromucoid, Tamm-Horsfall glycoprotein) (UMOD), mRNA", gi|4507832|ref|NM_003361.1|[4507832]; 175: NM_003364 , "Homo sapiens uridine phosphorylase 1 (UPP1), transcript variant 1, mRNA", gi|31742506|ref|NM_003364.2|[31742506]; 176: NM_003374 , "Homo sapiens voltage-dependent anion channel 1 (VDAC1), mRNA", gi|4507878|ref|NM_003374.1|[4507878]; 177: NM_003384 , "Homo sapiens vaccinia related kinase 1 (VRK1), mRNA", gi|4507902|ref|NM_003384.1|[4507902]; 178: NM_003418 , Homo sapiens zinc finger protein 9 (a cellular retroviral nucleic acid binding, "protein) (ZNF9), mRNA", gi|4827070|ref|NM_003418.1|[4827070]; 179: NM_003458 , "Homo sapiens bassoon (presynaptic cytomatrix protein) (BSN), mRNA", gi|4508018|ref|NM_003458.1|[4508018]; 180: NM_003459 , "Homo sapiens solute carrier family 30 (zinc transporter), member 3

(SLC30A3),", mRNA, gi|34222155|ref|NM_003459.3|[34222155]; 181: NM_003485 , "Homo sapiens G protein-coupled receptor 68 (GPR68), mRNA", gi|40217828|ref|NM_003485.2|[40217828]; 182: NM_003490 , "Homo sapiens synapsin III (SYN3), transcript variant IIIa, mRNA", gi|19924104|ref|NM_003490.2|[19924104]; 183: NM_003492 , "Homo sapiens chromosome X open reading frame 12 (CXorf12), mRNA", gi|4504738|ref|NM_003492.1|[4504738]; 184: NM_003524 , "Homo sapiens histone 1, H2bh (HIST1H2BH), mRNA", gi|21166386|ref|NM_003524.2|[21166386]; 185: NM_003526 , "Homo sapiens histone 1, H2bc (HIST1H2BC), mRNA", gi|21166388|ref|NM_003526.2|[21166388]; 186: NM_003531 , "Homo sapiens histone 1, H3c (HIST1H3C), mRNA", gi|21071022|ref|NM_003531.2|[21071022]; 187: NM_003549 , "Homo sapiens hyaluronoglucosaminidase 3 (HYAL3), mRNA", gi|15208650|ref|NM_003549.2|[15208650]; 188: NM_003554 , "Homo sapiens olfactory receptor, family 1, subfamily E, member 2 (OR1E2), mRNA", gi|11386152|ref|NM_003554.1|[11386152]; 189: NM_003571 , "Homo sapiens beaded filament structural protein 2, phakinin (BFSP2), mRNA", gi|21536442|ref|NM_003571.2|[21536442]; 190: NM_003594 , "Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA", gi|40807470|ref|NM_003594.3|[40807470]; 191: NM_003602 , "Homo sapiens FK506 binding protein 6, 36kDa (FKBP6), mRNA", gi|17149848|ref|NM_003602.2|[17149848]; 192: NM_003627 , "Homo sapiens solute carrier family 43, member 1 (SLC43A1), mRNA", gi|42476323|ref|NM_003627.4|[42476323]; 193: NM_003632 , "Homo sapiens contactin associated protein 1 (CNTNAP1), mRNA", gi|4505462|ref|NM_003632.1|[4505462]; 194: NM_003691 , "Homo sapiens serine/threonine kinase 16 (STK16), mRNA", gi|4505836|ref|NM_003691.1|[4505836]; 195: NM_003860 , "Homo sapiens barrier to autointegration factor 1 (BANF1), mRNA", gi|11038645|ref|NM_003860.2|[11038645]; 196: NM_003897 , "Homo sapiens immediate early response 3 (IER3), transcript variant short, mRNA", gi|16554595|ref|NM_003897.2|[16554595]; 197: NM_003915 , "Homo sapiens copine I (CPNE1), transcript variant 3, mRNA", gi|23397694|ref|NM_003915.2|[23397694]; 198: NM_003922 , Homo sapiens hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and, "RCC1 (CHC1)-like domain (RLD) 1 (HERC1), mRNA", gi|4557025|ref|NM_003922.1|[4557025]; 199: NM_003947 , "Homo sapiens huntingtin-associated protein interacting protein (duo) (HAPIP),", mRNA, gi|4504334|ref|NM_003947.1|[4504334]; 200: NM_003954 , "Homo sapiens mitogen-activated protein kinase kinase kinase 14 (MAP3K14), mRNA", gi|4505396|ref|NM_003954.1|[4505396]; 201: NM_003957 , "Homo sapiens serine/threonine kinase 29 (STK29), mRNA", gi|27501463|ref|NM_003957.1|[27501463]; 202: NM_003961 , "Homo sapiens rhomboid, veinlet-like 1 (Drosophila) (RHBDL1), mRNA", gi|4506524|ref|NM_003961.1|[4506524]; 203: NM_003974 , "Homo sapiens docking protein 2, 56kDa (DOK2), transcript variant 1, mRNA", gi|41406049|ref|NM_003974.2|[41406049]; 204: NM_004051 , , ref|NM_004051.3|[44680134]; 205: NM_004056 , "Homo sapiens carbonic anhydrase VIII (CA8), mRNA", gi|22027499|ref|NM_004056.3|[22027499]; 206: NM_004062 , "Homo sapiens cadherin 16, KSP-cadherin (CDH16), mRNA", gi|16507958|ref|NM_004062.2|[16507958]; 207: NM_004074 , "Homo sapiens cytochrome c oxidase subunit VIII (COX8), mRNA", gi|4758043|ref|NM_004074.1|[4758043]; 208: NM_004077 , "Homo sapiens citrate synthase (CS), nuclear gene encoding mitochondrial protein,", "transcript variant 1, mRNA", gi|38327624|ref|NM_004077.2|[38327624]; 209: NM_004078 , "Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), mRNA", gi|4758085|ref|NM_004078.1|[4758085]; 210:

NM_004088 , "Homo sapiens deoxynucleotidyltransferase, terminal (DNTT), mRNA", gi|29788761|ref|NM_004088.2|[29788761]; 211: NM_004091 , "Homo sapiens E2F transcription factor 2 (E2F2), mRNA", gi|34485718|ref|NM_004091.2|[34485718]; 212: NM_004100 , "Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript variant 1,", mRNA, gi|26667248|ref|NM_004100.2|[26667248]; 213: NM_004106 , "Homo sapiens Fc fragment of IgE, high affinity I, receptor for; gamma", "polypeptide (FCER1G), mRNA", gi|4758343|ref|NM_004106.1|[4758343]; 214: NM_004174 , "Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 3", "(SLC9A3), mRNA", gi|6806920|ref|NM_004174.1|[6806920]; 215: NM_004176 , "Homo sapiens sterol regulatory element binding transcription factor 1 (SREBF1),", mRNA, gi|22547194|ref|NM_004176.2|[22547194]; 216: NM_004178 , "Homo sapiens TAR (HIV) RNA binding protein 2 (TARBP2), transcript variant 3,", mRNA, gi|19743837|ref|NM_004178.3|[19743837]; 217: NM_004260 , "Homo sapiens RecQ protein-like 4 (RECQL4), mRNA", gi|4759029|ref|NM_004260.1|[4759029]; 218: NM_004267 , "Homo sapiens carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 (CHST2),", mRNA, gi|27369496|ref|NM_004267.2|[27369496]; 219: NM_004271 , "Homo sapiens lymphocyte antigen 86 (LY86), mRNA", gi|4758707|ref|NM_004271.1|[4758707]; 220: NM_004294 , "Homo sapiens mitochondrial translational release factor 1 (MTRF1), nuclear gene", "encoding mitochondrial protein, mRNA", gi|34577119|ref|NM_004294.2|[34577119]; 221: NM_004333 , "Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF), mRNA", gi|33188458|ref|NM_004333.2|[33188458]; 222: NM_004344 , "Homo sapiens centrin, EF-hand protein, 2 (CETN2), mRNA", gi|4757901|ref|NM_004344.1|[4757901]; 223: NM_004358 , "Homo sapiens cell division cycle 25B (CDC25B), transcript variant 1, mRNA", gi|11641416|ref|NM_004358.2|[11641416]; 224: NM_004374 , "Homo sapiens cytochrome c oxidase subunit VIc (COX6C), mRNA", gi|17999531|ref|NM_004374.2|[17999531]; 225: NM_004427 , "Homo sapiens polyhomeotic-like 2 (Drosophila) (PHC2), transcript variant 2, mRNA", gi|37595529|ref|NM_004427.2|[37595529]; 226: NM_004455 , "Homo sapiens exostoses (multiple)-like 1 (EXTL1), mRNA", gi|4758317|ref|NM_004455.1|[4758317]; 227: NM_004470 , "Homo sapiens FK506 binding protein 2, 13kDa (FKBP2), transcript variant 1, mRNA", gi|17149841|ref|NM_004470.2|[17149841]; 228: NM_004484 , "Homo sapiens glypican 3 (GPC3), mRNA", gi|5360213|ref|NM_004484.2|[5360213]; 229: NM_004514 , "Homo sapiens interleukin enhancer binding factor 1 (ILF1), transcript variant 1,", mRNA, gi|31563337|ref|NM_004514.2|[31563337]; 230: NM_004528 , "Homo sapiens microsomal glutathione S-transferase 3 (MGST3), mRNA", gi|22035640|ref|NM_004528.2|[22035640]; 231: NM_004550 , "Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa", "(NADH-coenzyme Q reductase) (NDUFS2), mRNA", gi|34147556|ref|NM_004550.3|[34147556]; 232: NM_004590 , "Homo sapiens chemokine (C-C motif) ligand 16 (CCL16), mRNA", gi|22538800|ref|NM_004590.2|[22538800]; 233: NM_004604 , "Homo sapiens syntaxin 4A (placental) (STX4A), mRNA", gi|34147603|ref|NM_004604.3|[34147603]; 234: NM_004616 , "Homo sapiens transmembrane 4 superfamily member 3 (TM4SF3), mRNA", gi|21265107|ref|NM_004616.2|[21265107]; 235: NM_004647 , "Homo sapiens D4, zinc and double PHD fingers family 1 (DPF1), mRNA", gi|4758797|ref|NM_004647.1|[4758797]; 236: NM_004656 , Homo sapiens BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase), "(BAP1), mRNA", gi|19718752|ref|NM_004656.2|[19718752]; 237: NM_004672 , "Homo sapiens mitogen-activated protein kinase kinase kinase 6 (MAP3K6),", "transcript variant 1, mRNA",

gi|24497521|ref|NM_004672.2|[24497521]; 238: NM_004704 , "Homo sapiens RNA, U3 small nucleolar interacting protein 2 (RNU3IP2), mRNA", gi|31543556|ref|NM_004704.2|[31543556]; 239: NM_004753 , "Homo sapiens dehydrogenase/reductase (SDR family) member 3 (DHRS3), mRNA", gi|34222303|ref|NM_004753.3|[34222303]; 240: NM_004794 , "Homo sapiens RAB33A, member RAS oncogene family (RAB33A), mRNA", gi|34485717|ref|NM_004794.2|[34485717]; 241: NM_004798 , "Homo sapiens kinesin family member 3B (KIF3B), mRNA", gi|31742486|ref|NM_004798.2|[31742486]; 242: NM_004810 , "Homo sapiens GRB2-related adaptor protein 2 (GRAP2), mRNA", gi|19913386|ref|NM_004810.2|[19913386]; 243: NM_004840 , "Homo sapiens Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 (ARHGEF6),", mRNA, gi|22027524|ref|NM_004840.1|[22027524]; 244: NM_004858 , "Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 8", "(SLC4A8), mRNA", gi|4759133|ref|NM_004858.1|[4759133]; 245: NM_004861 , Homo sapiens cerebroside (3'-phosphoadenylylsulfate:galactosylceramide 3'), "sulfotransferase (CST), mRNA", gi|4758087|ref|NM_004861.1|[4758087]; 246: NM_004870 , "Homo sapiens mannose-P-dolichol utilization defect 1 (MPDU1), mRNA", gi|4759109|ref|NM_004870.1|[4759109]; 247: NM_004904 , "Homo sapiens cAMP responsive element binding protein 5 (CREB5), mRNA", gi|4758499|ref|NM_004904.1|[4758499]; 248: NM_004913 , "Homo sapiens chromosome 16 open reading frame 7 (C16orf7), mRNA", gi|4757805|ref|NM_004913.1|[4757805]; 249: NM_004927 , "Homo sapiens mitochondrial ribosomal protein L49 (MRPL49), nuclear gene encoding", "mitochondrial protein, mRNA", gi|27436906|ref|NM_004927.2|[27436906]; 250: NM_004941 , "Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 8 (DHX8), mRNA", gi|4826689|ref|NM_004941.1|[4826689]; 251: NM_004959 , "Homo sapiens nuclear receptor subfamily 5, group A, member 1 (NR5A1), mRNA", gi|24432033|ref|NM_004959.3|[24432033]; 252: NM_004964 , "Homo sapiens histone deacetylase 1 (HDAC1), mRNA", gi|13128859|ref|NM_004964.2|[13128859]; 253: NM_004987 , "Homo sapiens LIM and senescent cell antigen-like domains 1 (LIMS1), mRNA", gi|13518025|ref|NM_004987.2|[13518025]; 254: NM_004994 , "Homo sapiens matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa", "type IV collagenase) (MMP9), mRNA", gi|4826835|ref|NM_004994.1|[4826835]; 255: NM_004997 , "Homo sapiens myosin binding protein H (MYBPH), mRNA", gi|4826841|ref|NM_004997.1|[4826841]; 256: NM_005006 , "Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa", "(NADH-coenzyme Q reductase) (NDUFS1), nuclear gene encoding mitochondrial", "protein, mRNA", gi|33519474|ref|NM_005006.5|[33519474]; 257: NM_005023 , "Homo sapiens protein geranylgeranyltransferase type I, beta subunit (PGGT1B),", mRNA, gi|27597101|ref|NM_005023.2|[27597101]; 258: NM_005027 , "Homo sapiens phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85", "beta) (PIK3R2), mRNA", gi|4826907|ref|NM_005027.1|[4826907]; 259: NM_005055 , "Homo sapiens receptor-associated protein of the synapse, 43kD (RAPSN),", "transcript variant 1, mRNA", gi|38045929|ref|NM_005055.3|[38045929]; 260: NM_005070 , "Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA", gi|4827015|ref|NM_005070.1|[4827015]; 261: NM_005124 , "Homo sapiens nucleoporin 153kDa (NUP153), mRNA", gi|24430145|ref|NM_005124.2|[24430145]; 262: NM_005125 , "Homo sapiens copper chaperone for superoxide dismutase (CCS), mRNA", gi|4826664|ref|NM_005125.1|[4826664]; 263: NM_005154 , "Homo sapiens ubiquitin specific protease 8 (USP8), mRNA", gi|41281375|ref|NM_005154.2|[41281375]; 264: NM_005161 ,

"Homo sapiens angiotensin II receptor-like 1 (AGTRL1), mRNA", gi|34577064|ref|NM_005161.2|[34577064]; 265: NM_005163 , "Homo sapiens v-akt murine thymoma viral oncogene homolog 1 (AKT1), mRNA", gi|4885060|ref|NM_005163.1|[4885060]; 266: NM_005165 , "Homo sapiens aldolase C, fructose-bisphosphate (ALDOC), mRNA", gi|4885062|ref|NM_005165.1|[4885062]; 267: NM_005182 , "Homo sapiens carbonic anhydrase VII (CA7), mRNA", gi|4885100|ref|NM_005182.1|[4885100]; 268: NM_005186 , "Homo sapiens calpain 1, (mu/I) large subunit (CAPN1), mRNA", gi|12408655|ref|NM_005186.2|[12408655]; 269: NM_005194 , "Homo sapiens CCAAT/enhancer binding protein (C/EBP), beta (CEBPB), mRNA", gi|28872795|ref|NM_005194.2|[28872795]; 270: NM_005210 , "Homo sapiens crystallin, gamma B (CRYGB), mRNA", gi|13376999|ref|NM_005210.2|[13376999]; 271: NM_005223 , "Homo sapiens deoxyribonuclease I (DNASE1), mRNA", gi|21361253|ref|NM_005223.2|[21361253]; 272: NM_005260 , "Homo sapiens growth differentiation factor 9 (GDF9), mRNA", gi|6715598|ref|NM_005260.2|[6715598]; 273: NM_005261 , "Homo sapiens GTP binding protein overexpressed in skeletal muscle (GEM),", "transcript variant 1, mRNA", gi|32483372|ref|NM_005261.2|[32483372]; 274: NM_005286 , "Homo sapiens G protein-coupled receptor 8 (GPR8), mRNA", gi|30581163|ref|NM_005286.2|[30581163]; 275: NM_005288 , "Homo sapiens G protein-coupled receptor 12 (GPR12), mRNA", gi|4885294|ref|NM_005288.1|[4885294]; 276: NM_005301 , "Homo sapiens G protein-coupled receptor 35 (GPR35), mRNA", gi|33695096|ref|NM_005301.2|[33695096]; 277: NM_005302 , Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like), "(GPR37), mRNA", gi|31377788|ref|NM_005302.2|[31377788]; 278: NM_005306 , "Homo sapiens G protein-coupled receptor 43 (GPR43), mRNA", gi|4885332|ref|NM_005306.1|[4885332]; 279: NM_005326 , "Homo sapiens hydroxyacylglutathione hydrolase (HAGH), mRNA", gi|38327035|ref|NM_005326.3|[38327035]; 280: NM_005335 , "Homo sapiens hematopoietic cell-specific Lyn substrate 1 (HCLS1), mRNA", gi|37059786|ref|NM_005335.3|[37059786]; 281: NM_005341 , "Homo sapiens GLI-Kruppel family member HKR3 (HKR3), mRNA", gi|4885418|ref|NM_005341.1|[4885418]; 282: NM_005393 , "Homo sapiens plexin B3 (PLXNB3), mRNA", gi|10864080|ref|NM_005393.1|[10864080]; 283: NM_005398 , "Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3C (PPP1R3C),", mRNA, gi|42476161|ref|NM_005398.3|[42476161]; 284: NM_005410 , "Homo sapiens selenoprotein P, plasma, 1 (SEPP1), mRNA", gi|4885590|ref|NM_005410.1|[4885590]; 285: NM_005418 , "Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 1, mRNA", gi|21264611|ref|NM_005418.2|[21264611]; 286: NM_005453 , "Homo sapiens zinc finger protein 297 (ZNF297), mRNA", gi|20070223|ref|NM_005453.3|[20070223]; 287: NM_005468 , "Homo sapiens N-acetylated alpha-linked acidic dipeptidase-like 1 (NAALADL1),", mRNA, gi|4885506|ref|NM_005468.1|[4885506]; 288: NM_005475 , "Homo sapiens lymphocyte adaptor protein (LNK), mRNA", gi|4885454|ref|NM_005475.1|[4885454]; 289: NM_005485 , Homo sapiens ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)-like 3, "(ADPRTL3), mRNA", gi|11496992|ref|NM_005485.2|[11496992]; 290: NM_005550 , "Homo sapiens kinesin family member C3 (KIFC3), mRNA", gi|19923320|ref|NM_005550.2|[19923320]; 291: NM_005557 , Homo sapiens keratin 16 (focal non-epidermolytic palmoplantar keratoderma), "(KRT16), mRNA", gi|24430191|ref|NM_005557.2|[24430191]; 292: NM_005560 , "Homo sapiens laminin, alpha 5 (LAMA5), mRNA", gi|21264601|ref|NM_005560.3|[21264601]; 293: NM_005563 , "Homo sapiens stathmin 1/oncoprotein 18 (STMN1), mRNA",

gi|13518023|ref|NM_005563.2|[13518023]; 294: NM_005593 , "Homo sapiens myogenic factor 5 (MYF5), mRNA", gi|5031928|ref|NM_005593.1|[5031928]; 295: NM_005598 , "Homo sapiens nescient helix loop helix 1 (NHLH1), mRNA", gi|19923328|ref|NM_005598.2|[19923328]; 296: NM_005606 , "Homo sapiens legumain (LGMN), mRNA", gi|21914880|ref|NM_005606.3|[21914880]; 297: NM_005626 , "Homo sapiens splicing factor, arginine/serine-rich 4 (SFRS4), mRNA", gi|34147660|ref|NM_005626.3|[34147660]; 298: NM_005630 , "Homo sapiens solute carrier organic anion transporter family, member 2A1", "(SLCO2A1), mRNA", gi|5032094|ref|NM_005630.1|[5032094]; 299: NM_005634 , "Homo sapiens SRY (sex determining region Y)-box 3 (SOX3), mRNA", gi|30061555|ref|NM_005634.2|[30061555]; 300: NM_005684 , "Homo sapiens G protein-coupled receptor 52 (GPR52), mRNA", gi|5031720|ref|NM_005684.1|[5031720]; 301: NM_005698 , "Homo sapiens secretory carrier membrane protein 3 (SCAMP3), transcript variant", "1, mRNA", gi|16445418|ref|NM_005698.2|[16445418]; 302: NM_005716 , Homo sapiens regulator of G-protein signalling 19 interacting protein 1, "(RGS19IP1), transcript variant 1, mRNA", gi|42544147|ref|NM_005716.2|[42544147]; 303: NM_005726 , "Homo sapiens Ts translation elongation factor, mitochondrial (TSFM), mRNA", gi|21361279|ref|NM_005726.2|[21361279]; 304: NM_005727 , "Homo sapiens tetraspan 1 (TSPAN-1), mRNA", gi|21264577|ref|NM_005727.2|[21264577]; 305: NM_005747 , "Homo sapiens elastase 3A, pancreatic (protease E) (ELA3A), mRNA", gi|21361297|ref|NM_005747.2|[21361297]; 306: NM_005777 , "Homo sapiens RNA binding motif protein 6 (RBM6), mRNA", gi|5032032|ref|NM_005777.1|[5032032]; 307: NM_005822 , "Homo sapiens Down syndrome critical region gene 1-like 1 (DSCR1L1), mRNA", gi|5032234|ref|NM_005822.1|[5032234]; 308: NM_005845 , "Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4),", mRNA, gi|34452699|ref|NM_005845.2|[34452699]; 309: NM_005860 , "Homo sapiens follistatin-like 3 (secreted glycoprotein) (FSTL3), mRNA", gi|5031700|ref|NM_005860.1|[5031700]; 310: NM_005892 , "Homo sapiens formin-like 1 (FMNL1), mRNA", gi|33356147|ref|NM_005892.3|[33356147]; 311: NM_005893 , "Homo sapiens calicin (CCIN), mRNA", gi|17738311|ref|NM_005893.1|[17738311]; 312: NM_005909 , "Homo sapiens microtubule-associated protein 1B (MAP1B), transcript variant 1,", mRNA, gi|14165457|ref|NM_005909.2|[14165457]; 313: NM_005959 , "Homo sapiens melatonin receptor 1B (MTNR1B), mRNA", gi|14141172|ref|NM_005959.2|[14141172]; 314: NM_005965 , "Homo sapiens myosin, light polypeptide kinase (MYLK), transcript variant 6, mRNA", gi|16950600|ref|NM_005965.2|[16950600]; 315: NM_005972 , "Homo sapiens pancreatic polypeptide receptor 1 (PPYR1), mRNA", gi|40254824|ref|NM_005972.2|[40254824]; 316: NM_005984 , Homo sapiens solute carrier family 25 (mitochondrial carrier; citrate, "transporter), member 1 (SLC25A1), mRNA", gi|21389314|ref|NM_005984.1|[21389314]; 317: NM_006017 , "Homo sapiens prominin 1 (PROM1), mRNA", gi|5174386|ref|NM_006017.1|[5174386]; 318: NM_006019 , "Homo sapiens T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0", "protein a isoform 3 (TCIRG1), transcript variant 1, mRNA", gi|19924144|ref|NM_006019.2|[19924144]; 319: NM_006067 , "Homo sapiens neighbor of COX4 (NOC4), mRNA", gi|34147520|ref|NM_006067.3|[34147520]; 320: NM_006090 , "Homo sapiens choline/ethanolaminephosphotransferase (CEPT1), mRNA", gi|21735567|ref|NM_006090.2|[21735567]; 321: NM_006091 , "Homo sapiens coronin, actin binding protein, 2B (CORO2B), mRNA", gi|24307902|ref|NM_006091.1|[24307902]; 322: NM_006114 , Homo sapiens translocase of outer mitochondrial membrane 40 homolog (yeast),

"(TOMM40), mRNA", gi|5174722|ref|NM_006114.1|[5174722]; 323: NM_006120 , "Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA),", mRNA, gi|18765714|ref|NM_006120.2|[18765714]; 324: NM_006157 , "Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA", gi|5453763|ref|NM_006157.1|[5453763]; 325: NM_006163 , "Homo sapiens nuclear factor (erythroid-derived 2), 45kDa (NFE2), mRNA", gi|5453773|ref|NM_006163.1|[5453773]; 326: NM_006170 , "Homo sapiens nucleolar protein 1, 120kDa (NOL1), mRNA", gi|5453791|ref|NM_006170.1|[5453791]; 327: NM_006172 , "Homo sapiens natriuretic peptide precursor A (NPPA), mRNA", gi|23510318|ref|NM_006172.1|[23510318]; 328: NM_006174 , "Homo sapiens neuropeptide Y receptor Y5 (NPY5R), mRNA", gi|31377784|ref|NM_006174.2|[31377784]; 329: NM_006196 , "Homo sapiens poly(rC) binding protein 1 (PCBP1), mRNA", gi|14141164|ref|NM_006196.2|[14141164]; 330: NM_006198 , "Homo sapiens Purkinje cell protein 4 (PCP4), mRNA", gi|5453857|ref|NM_006198.1|[5453857]; 331: NM_006205 , "Homo sapiens phosphodiesterase 6H, cGMP-specific, cone, gamma (PDE6H), mRNA", gi|5453867|ref|NM_006205.1|[5453867]; 332: NM_006215 , "Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1", "antiproteinase, antitrypsin), member 4 (SERPINA4), mRNA", gi|21361301|ref|NM_006215.2|[21361301]; 333: NM_006228 , "Homo sapiens prepronociceptin (PNOC), mRNA", gi|11079650|ref|NM_006228.2|[11079650]; 334: NM_006252 , "Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2),", mRNA, gi|5453965|ref|NM_006252.1|[5453965]; 335: NM_006261 , "Homo sapiens prophet of Pit1, paired-like homeodomain transcription factor", "(PROP1), mRNA", gi|40254838|ref|NM_006261.2|[40254838]; 336: NM_006274 , "Homo sapiens chemokine (C-C motif) ligand 19 (CCL19), mRNA", gi|22165424|ref|NM_006274.2|[22165424]; 337: NM_006289 , "Homo sapiens talin 1 (TLN1), mRNA", gi|16753232|ref|NM_006289.2|[16753232]; 338: NM_006365 , "Homo sapiens transcriptional activator of the c-fos promoter (CROC4), mRNA", gi|5453624|ref|NM_006365.1|[5453624]; 339: NM_006368 , "Homo sapiens cAMP responsive element binding protein 3 (CREB3), mRNA", gi|38327637|ref|NM_006368.4|[38327637]; 340: NM_006399 , "Homo sapiens basic leucine zipper transcription factor, ATF-like (BATF), mRNA", gi|18375640|ref|NM_006399.2|[18375640]; 341: NM_006442 , "Homo sapiens DR1-associated protein 1 (negative cofactor 2 alpha) (DRAP1), mRNA", gi|18426972|ref|NM_006442.2|[18426972]; 342: NM_006466 , "Homo sapiens polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa (POLR3F),", mRNA, gi|33598951|ref|NM_006466.2|[33598951]; 343: NM_006477 , "Homo sapiens RAS-related on chromosome 22 (RRP22), mRNA", gi|42476128|ref|NM_006477.2|[42476128]; 344: NM_006565 , "Homo sapiens CCCTC-binding factor (zinc finger protein) (CTCF), mRNA", gi|5729789|ref|NM_006565.1|[5729789]; 345: NM_006614 , Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1), "(CHL1), mRNA", gi|27894375|ref|NM_006614.2|[27894375]; 346: NM_006637 , "Homo sapiens olfactory receptor, family 5, subfamily I, member 1 (OR5I1), mRNA", gi|5729959|ref|NM_006637.1|[5729959]; 347: NM_006650 , "Homo sapiens complexin 2 (CPLX2), mRNA", gi|17738306|ref|NM_006650.2|[17738306]; 348: NM_006698 , "Homo sapiens bladder cancer associated protein (BLCAP), mRNA", gi|5729737|ref|NM_006698.1|[5729737]; 349: NM_006703 , Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 3, "(NUDT3), mRNA", gi|37622350|ref|NM_006703.2|[37622350]; 350: NM_006747 , "Homo sapiens signal-induced

proliferation-associated gene 1 (SIPA1), transcript", "variant 2, mRNA", gi|24497626|ref|NM_006747.2|[24497626]; 351: NM_006764 , "Homo sapiens interferon-related developmental regulator 2 (IFRD2), mRNA", gi|21361365|ref|NM_006764.2|[21361365]; 352: NM_006794 , "Homo sapiens G protein-coupled receptor 75 (GPR75), mRNA", gi|5803024|ref|NM_006794.1|[5803024]; 353: NM_006810 , "Homo sapiens for protein disulfide isomerase-related (PDIR), mRNA", gi|5803120|ref|NM_006810.1|[5803120]; 354: NM_006813 , "Homo sapiens proline-rich nuclear receptor coactivator 1 (PNRC1), mRNA", gi|5802981|ref|NM_006813.1|[5802981]; 355: NM_006823 , "Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibitor alpha (PKIA),", "transcript variant 1, mRNA", gi|32483387|ref|NM_006823.2|[32483387]; 356: NM_006841 , "Homo sapiens solute carrier family 38, member 3 (SLC38A3), mRNA", gi|40795668|ref|NM_006841.3|[40795668]; 357: NM_006876 , "Homo sapiens UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6", "(B3GNT6), mRNA", gi|5802983|ref|NM_006876.1|[5802983]; 358: NM_006917 , "Homo sapiens retinoid X receptor, gamma (RXRG), mRNA", gi|21361386|ref|NM_006917.2|[21361386]; 359: NM_006923 , "Homo sapiens stromal cell-derived factor 2 (SDF2), mRNA", gi|14141194|ref|NM_006923.2|[14141194]; 360: NM_006946 , "Homo sapiens spectrin, beta, non-erythrocytic 2 (SPTBN2), mRNA", gi|5902121|ref|NM_006946.1|[5902121]; 361: NM_006982 , "Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA", gi|5901917|ref|NM_006982.1|[5901917]; 362: NM_006998 , "Homo sapiens secretagogin, EF-hand calcium binding protein (SCGN), mRNA", gi|15055536|ref|NM_006998.2|[15055536]; 363: NM_007000 , "Homo sapiens uroplakin 1A (UPK1A), mRNA", gi|21264372|ref|NM_007000.2|[21264372]; 364: NM_007022 , "Homo sapiens putative tumor suppressor 101F6 (101F6), mRNA", gi|31541779|ref|NM_007022.3|[31541779]; 365: NM_007023 , "Homo sapiens cAMP-regulated guanine nucleotide exchange factor II (CGEF2), mRNA", gi|5901913|ref|NM_007023.1|[5901913]; 366: NM_007046 , "Homo sapiens elastin microfibril interfacer 1 (EMILIN1), mRNA", gi|5901943|ref|NM_007046.1|[5901943]; 367: NM_007076 , , ref|NM_007076.2|[42794619]; 368: NM_007112 , "Homo sapiens thrombospondin 3 (THBS3), mRNA", gi|40317629|ref|NM_007112.3|[40317629]; 369: NM_007149 , "Homo sapiens zinc finger protein 184 (Kruppel-like) (ZNF184), mRNA", gi|24307934|ref|NM_007149.1|[24307934]; 370: NM_007182 , "Homo sapiens Ras association (RalGDS/AF-6) domain family 1 (RASSF1), transcript", "variant A, mRNA", gi|25777678|ref|NM_007182.4|[25777678]; 371: NM_007194 , "Homo sapiens CHK2 checkpoint homolog (S. pombe) (CHEK2), transcript variant 1,", mRNA, gi|22209010|ref|NM_007194.2|[22209010]; 372: NM_007238 , "Homo sapiens peroxisomal membrane protein 4, 24kDa (PXMP4), transcript variant", "1, mRNA", gi|34452733|ref|NM_007238.3|[34452733]; 373: NM_007272 , "Homo sapiens chymotrypsin C (caldecrin) (CTRC), mRNA", gi|11321627|ref|NM_007272.1|[11321627]; 374: NM_007312 , "Homo sapiens hyaluronoglucosaminidase 1 (HYAL1), transcript variant 1, mRNA", gi|24497560|ref|NM_007312.3|[24497560]; 375: NM_007357 , "Homo sapiens component of oligomeric golgi complex 2 (COG2), mRNA", gi|6678675|ref|NM_007357.1|[6678675]; 376: NM_012093 , "Homo sapiens adenylate kinase 5 (AK5), transcript variant 2, mRNA", gi|28144898|ref|NM_012093.2|[28144898]; 377: NM_012105 , "Homo sapiens beta-site APP-cleaving enzyme 2 (BACE2), transcript variant a, mRNA", gi|21040358|ref|NM_012105.3|[21040358]; 378: NM_012109 , "Homo sapiens chromosome 19 open reading frame 4 (C19orf4), mRNA", gi|6912273|ref|NM_012109.1|[6912273]; 379:

NM_012164 , "Homo sapiens F-box and WD-40 domain protein 2 (FBXW2), mRNA", gi|7549806|ref|NM_012164.2|[7549806]; 380: NM_012168 , "Homo sapiens F-box only protein 2 (FBXO2), mRNA", gi|15812197|ref|NM_012168.2|[15812197]; 381: NM_012191 , "Homo sapiens putative tumor suppressor (FUS2), mRNA", gi|6912379|ref|NM_012191.1|[6912379]; 382: NM_012193 , "Homo sapiens frizzled homolog 4 (Drosophila) (FZD4), mRNA", gi|22547160|ref|NM_012193.2|[22547160]; 383: NM_012204 , "Homo sapiens general transcription factor IIIC, polypeptide 4, 90kDa (GTF3C4),", mRNA, gi|6912399|ref|NM_012204.1|[6912399]; 384: NM_012225 , "Homo sapiens nucleotide binding protein 2 (MinD homolog, E. coli) (NUBP2), mRNA", gi|6912539|ref|NM_012225.1|[6912539]; 385: NM_012236 , "Homo sapiens sex comb on midleg homolog 1 (Drosophila) (SCMH1), mRNA", gi|6912641|ref|NM_012236.1|[6912641]; 386: NM_012285 , "Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member", "4 (KCNH4), mRNA", gi|6912445|ref|NM_012285.1|[6912445]; 387: NM_012311 , "Homo sapiens KIN, antigenic determinant of recA protein homolog (mouse) (KIN),", mRNA, gi|40068516|ref|NM_012311.2|[40068516]; 388: NM_012409 , "Homo sapiens prion protein 2 (dublet) (PRND), mRNA", gi|34335267|ref|NM_012409.2|[34335267]; 389: NM_012430 , "Homo sapiens SEC22 vesicle trafficking protein-like 2 (S. cerevisiae) (SEC22L2),", mRNA, gi|14591918|ref|NM_012430.2|[14591918]; 390: NM_012459 , Homo sapiens translocase of inner mitochondrial membrane 8 homolog B (yeast), "(TIMM8B), mRNA", gi|6912711|ref|NM_012459.1|[6912711]; 391: NM_012460 , Homo sapiens translocase of inner mitochondrial membrane 9 homolog (yeast), "(TIMM9), mRNA", gi|21359892|ref|NM_012460.2|[21359892]; 392: NM_012482 , "Homo sapiens zinc finger protein 281 (ZNF281), mRNA", gi|40255235|ref|NM_012482.3|[40255235]; 393: NM_013235 , "Homo sapiens nuclear RNase III Drosha (RNASE3L), mRNA", gi|21359821|ref|NM_013235.2|[21359821]; 394: NM_013246 , "Homo sapiens cardiotrophin-like cytokine (CLC), mRNA", gi|7019350|ref|NM_013246.1|[7019350]; 395: NM_013314 , "Homo sapiens B-cell linker (BLNK), mRNA", gi|40353774|ref|NM_013314.2|[40353774]; 396: NM_013333 , "Homo sapiens epsin 1 (EPN1), mRNA", gi|41350200|ref|NM_013333.2|[41350200]; 397: NM_013335 , "Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA), mRNA", gi|31881778|ref|NM_013335.2|[31881778]; 398: NM_013343 , "Homo sapiens loss of heterozygosity, 3, chromosomal region 2, gene A (LOH3CR2A),", mRNA, gi|7106370|ref|NM_013343.1|[7106370]; 399: NM_013387 , "Homo sapiens ubiquinol-cytochrome c reductase complex (7.2 kD) (HSPC051), mRNA", gi|41281884|ref|NM_013387.2|[41281884]; 400: NM_013403 , "Homo sapiens striatin, calmodulin binding protein 4 (STRN4), mRNA", gi|7019572|ref|NM_013403.1|[7019572]; 401: NM_013441 , "Homo sapiens Down syndrome critical region gene 1-like 2 (DSCR1L2), mRNA", gi|38455419|ref|NM_013441.2|[38455419]; 402: NM_013450 , "Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA", gi|7304922|ref|NM_013450.1|[7304922]; 403: NM_014015 , "Homo sapiens dexamethasone-induced transcript (DEXI), mRNA", gi|33620720|ref|NM_014015.3|[33620720]; 404: NM_014099 , , ref|NM_014099.1|[7662610], This record was temporarily removed by RefSeq staff for additional review., , 405: NM_014123 , , ref|NM_014123.1|[7662539], This record was temporarily removed by RefSeq staff for additional review., , 406: NM_014124 , , ref|NM_014124.1|[7662541], This record was temporarily removed by RefSeq staff for additional review., , 407: NM_014165 , "Homo sapiens chromosome 6 open reading frame 66 (C6orf66), mRNA", gi|7661785|ref|NM_014165.1|[7661785]; 408: NM_014222 , "Homo

sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa", "(NDUFA8), nuclear gene encoding mitochondrial protein, mRNA", gi|33519464|ref|NM_014222.2|[33519464]; 409: NM_014236 , "Homo sapiens glyceronephosphate O-acyltransferase (GNPAT), mRNA", gi|7657133|ref|NM_014236.1|[7657133]; 410: NM_014301 , "Homo sapiens nitrogen fixation cluster-like (NIFU), mRNA", gi|24307952|ref|NM_014301.1|[24307952]; 411: NM_014332 , "Homo sapiens small muscle protein, X-linked (SMPX), mRNA", gi|10047089|ref|NM_014332.1|[10047089]; 412: NM_014342 , "Homo sapiens mitochondrial carrier homolog 2 (C. elegans) (MTCH2), nuclear gene", "encoding mitochondrial protein, mRNA", gi|40254847|ref|NM_014342.2|[40254847]; 413: NM_014348 , "Homo sapiens POM121 membrane glycoprotein-like 1 (rat) (POM121L1), mRNA", gi|7657468|ref|NM_014348.1|[7657468]; 414: NM_014393 , "Homo sapiens staufen, RNA binding protein, homolog 2 (Drosophila) (STAU2), mRNA", gi|7657624|ref|NM_014393.1|[7657624]; 415: NM_014433 , "Homo sapiens rhabdoid tumor deletion region gene 1 (RTDR1), mRNA", gi|22209005|ref|NM_014433.2|[22209005]; 416: NM_014453 , "Homo sapiens putative breast adenocarcinoma marker (32kD) (BC-2), transcript", "variant 1, mRNA", gi|38372936|ref|NM_014453.2|[38372936]; 417: NM_014548 , "Homo sapiens tropomodulin 2 (neuronal) (TMOD2), mRNA", gi|40789262|ref|NM_014548.2|[40789262]; 418: NM_014576 , "Homo sapiens apobec-1 complementation factor (ACF), transcript variant 1, mRNA", gi|20357571|ref|NM_014576.2|[20357571]; 419: NM_014606 , , ref|NM_014606.1|[7657151], This record was temporarily removed by RefSeq staff for additional review., , 420: NM_014617 , "Homo sapiens crystallin, gamma A (CRYGA), mRNA", gi|13376998|ref|NM_014617.2|[13376998]; 421: NM_014662 , , ref|NM_014662.1|[7662221], This record was temporarily removed by RefSeq staff for additional review., , 422: NM_014674 , , ref|NM_014674.1|[7662001], This record was temporarily removed by RefSeq staff for additional review., , 423: NM_014685 , "Homo sapiens homocysteine-inducible, endoplasmic reticulum stress-inducible,", "ubiquitin-like domain member 1 (HERPUD1), mRNA", gi|7661869|ref|NM_014685.1|[7661869]; 424: NM_014702 , , ref|NM_014702.1|[7662095], This record was temporarily removed by RefSeq staff for additional review., , 425: NM_014731 , "Homo sapiens ProSAPiP1 protein (ProSAPiP1), mRNA", gi|35493938|ref|NM_014731.2|[35493938]; 426: NM_014745 , "Homo sapiens KIAA0233 gene product (KIAA0233), mRNA", gi|7662013|ref|NM_014745.1|[7662013]; 427: NM_014748 , "Homo sapiens sorting nexin 17 (SNX17), mRNA", gi|23238249|ref|NM_014748.2|[23238249]; 428: NM_014766 , "Homo sapiens secernin 1 (SCRN1), mRNA", gi|28461170|ref|NM_014766.2|[28461170]; 429: NM_014786 , "Homo sapiens Rho guanine nucleotide exchange factor (GEF) 17 (ARHGEF17), mRNA", gi|21361457|ref|NM_014786.2|[21361457]; 430: NM_014813 , , ref|NM_014813.1|[7662319], This record was temporarily removed by RefSeq staff for additional review., , 431: NM_014814 , "Homo sapiens proteasome regulatory particle subunit p44S10 (p44S10), mRNA", gi|7661913|ref|NM_014814.1|[7661913]; 432: NM_014849 , "Homo sapiens synaptic vesicle glycoprotein 2A (SV2A), mRNA", gi|41281523|ref|NM_014849.2|[41281523]; 433: NM_014901 , "Homo sapiens ring finger protein 44 (RNF44), mRNA", gi|42718018|ref|NM_014901.4|[42718018]; 434: NM_014907 , "Homo sapiens FERM and PDZ domain containing 1 (FRMPD1), mRNA", gi|7662415|ref|NM_014907.1|[7662415]; 435: NM_014912 , "Homo sapiens cytoplasmic polyadenylation element binding protein 3 (CPEB3),

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NM_016388 , "Homo sapiens T-cell receptor interacting molecule (TRIM), mRNA", gi|7706744|ref|NM_016388.1|[7706744]; 467: NM_016649 , "Homo sapiens chromosome 20 open reading frame 6 (C20orf6), mRNA", gi|22507381|ref|NM_016649.3|[22507381]; 468: NM_017409 , "Homo sapiens homeo box C10 (HOXC10), mRNA", gi|24497532|ref|NM_017409.2|[24497532]; 469: NM_017410 , "Homo sapiens homeo box C13 (HOXC13), mRNA", gi|24497535|ref|NM_017410.2|[24497535]; 470: NM_017418 , "Homo sapiens deleted in esophageal cancer 1 (DEC1), mRNA", gi|8393249|ref|NM_017418.1|[8393249]; 471: NM_017509 , "Homo sapiens kallikrein 15 (KLK15), transcript variant 4, mRNA", gi|20302142|ref|NM_017509.2|[20302142]; 472: NM_017528 , "Homo sapiens Williams Beuren syndrome chromosome region 22 (WBSCR22), mRNA", gi|23199994|ref|NM_017528.2|[23199994]; 473: NM_017534 , "Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA", gi|42476189|ref|NM_017534.2|[42476189]; 474: NM_017582 , "Homo sapiens ubiquitin-conjugating enzyme E2Q (putative) (UBE2Q), mRNA", gi|38045949|ref|NM_017582.5|[38045949]; 475: NM_017704 , "Homo sapiens fetal globin-inducing factor (FGIF), mRNA", gi|41350197|ref|NM_017704.2|[41350197]; 476: NM_017705 , "Homo sapiens membrane progestin receptor gamma (MPRG), mRNA", gi|31377751|ref|NM_017705.2|[31377751]; 477: NM_017738 , "Homo sapiens chromosome 9 open reading frame 39 (C9orf39), mRNA", gi|8923250|ref|NM_017738.1|[8923250]; 478: NM_017740 , "Homo sapiens zinc finger, DHHC domain containing 7 (ZDHHC7), mRNA", gi|8923254|ref|NM_017740.1|[8923254]; 479: NM_017745 , "Homo sapiens BCL6 co-repressor (BCOR), transcript variant 1, mRNA", gi|21071036|ref|NM_017745.4|[21071036]; 480: NM_017746 , "Homo sapiens testis expressed gene 10 (TEX10), mRNA", gi|8923268|ref|NM_017746.1|[8923268]; 481: NM_017786 , "Homo sapiens hypothetical protein FLJ20366 (FLJ20366), mRNA", gi|8923340|ref|NM_017786.1|[8923340]; 482: NM_017793 , "Homo sapiens RNase P protein subunit p25 (Rpp25), mRNA", gi|8923354|ref|NM_017793.1|[8923354]; 483: NM_017806 , "Homo sapiens hypothetical protein FLJ20406 (FLJ20406), mRNA", gi|8923377|ref|NM_017806.1|[8923377]; 484: NM_017815 , "Homo sapiens chromosome 14 open reading frame 94 (C14orf94), mRNA", gi|8923395|ref|NM_017815.1|[8923395]; 485: NM_017847 , "Homo sapiens chromosome 1 open reading frame 27 (C1orf27), mRNA", gi|20127566|ref|NM_017847.2|[20127566]; 486: NM_017865 , "Homo sapiens hypothetical protein FLJ20531 (FLJ20531), mRNA", gi|21361765|ref|NM_017865.2|[21361765]; 487: NM_017893 , "Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM)", "and short cytoplasmic domain, (semaphorin) 4G (SEMA4G), mRNA", gi|28872813|ref|NM_017893.2|[28872813]; 488: NM_017901 , "Homo sapiens two pore segment channel 1 (TPCN1), mRNA", gi|29725621|ref|NM_017901.3|[29725621]; 489: NM_017915 , "Homo sapiens hypothetical protein FLJ20641 (FLJ20641), mRNA", gi|8923595|ref|NM_017915.1|[8923595]; 490: NM_017941 , "Homo sapiens lung cancer-related protein 8 (HLC-8), mRNA", gi|34222156|ref|NM_017941.3|[34222156]; 491: NM_017961 , , ref|NM_017961.3|[31982883], This record was temporarily removed by RefSeq staff for additional review., , 492: NM_017991 , "Homo sapiens hypothetical protein FLJ10081 (FLJ10081), mRNA", gi|21361733|ref|NM_017991.3|[21361733]; 493: NM_018005 , , ref|NM_018005.1|[8922245], This record was replaced or removed. See revision history for details., , 494: NM_018019 , "Homo sapiens mediator subunit 25 (MED25), mRNA", gi|22907057|ref|NM_018019.2|[22907057]; 495: NM_018026 , "Homo sapiens phosphofurin

acidic cluster sorting protein 1 (PACS1), mRNA", gi|30089915|ref|NM_018026.2|[30089915]; 496: NM_018058 , "Homo sapiens cartilage acidic protein 1 (CRTAC1), mRNA", gi|42415498|ref|NM_018058.2|[42415498]; 497: NM_018125 , "Homo sapiens hypothetical protein FLJ10521 (FLJ10521), mRNA", gi|33354274|ref|NM_018125.2|[33354274]; 498: NM_018157 , "Homo sapiens brain synembryn (hSyn), mRNA", gi|8922554|ref|NM_018157.1|[8922554]; 499: NM_018163 , "Homo sapiens hypothetical protein FLJ10634 (FLJ10634), mRNA", gi|8922562|ref|NM_018163.1|[8922562]; 500: NM_018176 , "Homo sapiens leucine-rich repeat LGI family, member 2 (LGI2), mRNA", gi|21313637|ref|NM_018176.2|[21313637]; 501: NM_018180 , "Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 32 (DHX32), mRNA", gi|20336299|ref|NM_018180.2|[20336299]; 502: NM_018192 , "Homo sapiens myxoid liposarcoma associated protein 4 (MLAT4), mRNA", gi|27764881|ref|NM_018192.2|[27764881]; 503: NM_018195 , "Homo sapiens hypothetical protein FLJ10726 (FLJ10726), mRNA", gi|40254918|ref|NM_018195.2|[40254918]; 504: NM_018206 , "Homo sapiens vacuolar protein sorting 35 (yeast) (VPS35), mRNA", gi|41352714|ref|NM_018206.3|[41352714]; 505: NM_018233 , "Homo sapiens hypothetical protein FLJ10826 (FLJ10826), mRNA", gi|42476029|ref|NM_018233.2|[42476029]; 506: NM_018245 , "Homo sapiens hypothetical protein FLJ10851 (FLJ10851), mRNA", gi|8922715|ref|NM_018245.1|[8922715]; 507: NM_018261 , "Homo sapiens SEC3-like 1 (S. cerevisiae) (SEC3L1), transcript variant 1, mRNA", gi|30410719|ref|NM_018261.2|[30410719]; 508: NM_018303 , "Homo sapiens SEC5-like 1 (S. cerevisiae) (SEC5L1), mRNA", gi|30581133|ref|NM_018303.4|[30581133]; 509: NM_018306 , "Homo sapiens hypothetical protein FLJ11036 (FLJ11036), mRNA", gi|31542666|ref|NM_018306.2|[31542666]; 510: NM_018327 , "Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA", gi|8922874|ref|NM_018327.1|[8922874]; 511: NM_018330 , "Homo sapiens KIAA1598 protein (KIAA1598), mRNA", gi|21314680|ref|NM_018330.2|[21314680]; 512: NM_018404 , "Homo sapiens centaurin, alpha 2 (CENTA2), mRNA", gi|8923762|ref|NM_018404.1|[8923762]; 513: NM_018430 , "Homo sapiens translin-associated factor X interacting protein 1 (TSNAXIP1), mRNA", gi|8923845|ref|NM_018430.1|[8923845]; 514: NM_018431 , "Homo sapiens docking protein 5 (DOK5), transcript variant 1, mRNA", gi|29544725|ref|NM_018431.2|[29544725]; 515: NM_018459 , , ref|NM_018459.1|[8922103], This record was replaced or removed. See revision history for details., , 516: NM_018465 , "Homo sapiens chromosome 9 open reading frame 46 (C9orf46), mRNA", gi|8923931|ref|NM_018465.1|[8923931]; 517: NM_018484 , "Homo sapiens solute carrier family 22 (organic anion/cation transporter), member", "11 (SLC22A11), mRNA", gi|24497483|ref|NM_018484.2|[24497483]; 518: NM_018518 , Homo sapiens MCM10 minichromosome maintenance deficient 10 (S. cerevisiae), "(MCM10), transcript variant 2, mRNA", gi|33383234|ref|NM_018518.3|[33383234]; 519: NM_018558 , "Homo sapiens gamma-aminobutyric acid (GABA) receptor, theta (GABRQ), mRNA", gi|8924257|ref|NM_018558.1|[8924257]; 520: NM_018562 , , ref|NM_018562.1|[8923971], This record was temporarily removed by RefSeq staff for additional review., , 521: NM_018584 , "Homo sapiens calcium/calmodulin-dependent protein kinase II (CaMKIINalpha), mRNA", gi|31324542|ref|NM_018584.4|[31324542]; 522: NM_018608 , , ref|NM_018608.1|[8924095], This record was temporarily removed by RefSeq staff for additional review., , 523: NM_018641 , "Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 12 (CHST12), mRNA", gi|20070291|ref|NM_018641.2|[20070291]; 524: NM_018947 , "Homo sapiens cytochrome c, somatic (CYCS), nuclear gene encoding mitochondrial", "protein, mRNA",

gi|34328939|ref|NM_018947.4|[34328939]; 525: NM_018957 , "Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA", gi|15147251|ref|NM_018957.2|[15147251]; 526: NM_018959 , "Homo sapiens DAZ associated protein 1 (DAZAP1), transcript variant 2, mRNA", gi|25470885|ref|NM_018959.2|[25470885]; 527: NM_018970 , "Homo sapiens G protein-coupled receptor 85 (GPR85), mRNA", gi|31377760|ref|NM_018970.3|[31377760]; 528: NM_018993 , "Homo sapiens Ras and Rab interactor 2 (RIN2), mRNA", gi|35493905|ref|NM_018993.2|[35493905]; 529: NM_019028 , "Homo sapiens HIP14-related protein (HIP14L), mRNA", gi|9506622|ref|NM_019028.1|[9506622]; 530: NM_019044 , "Homo sapiens hypothetical protein FLJ10996 (FLJ10996), mRNA", gi|21361622|ref|NM_019044.2|[21361622]; 531: NM_019063 , "Homo sapiens echinoderm microtubule associated protein like 4 (EML4), mRNA", gi|19923496|ref|NM_019063.2|[19923496]; 532: NM_019099 , "Homo sapiens hypothetical protein LOC55924 (LOC55924), transcript variant 1,", mRNA, gi|39545578|ref|NM_019099.3|[39545578]; 533: NM_019617 , "Homo sapiens gastrokine 1 (GKN1), mRNA", gi|27894363|ref|NM_019617.2|[27894363]; 534: NM_019618 , "Homo sapiens interleukin 1 family, member 9 (IL1F9), mRNA", gi|27894314|ref|NM_019618.2|[27894314]; 535: NM_020170 , "Homo sapiens hypothetical protein from EUROIMAGE 2021883 (LOC56926), mRNA", gi|24308184|ref|NM_020170.1|[24308184]; 536: NM_020188 , "Homo sapiens DC13 protein (DC13), mRNA", gi|42476040|ref|NM_020188.2|[42476040]; 537: NM_020228 , "Homo sapiens PR domain containing 10 (PRDM10), transcript variant 1, mRNA", gi|41349457|ref|NM_020228.2|[41349457]; 538: NM_020237 , "Homo sapiens chromosome 8 open reading frame 17 (C8orf17), mRNA", gi|9910447|ref|NM_020237.1|[9910447]; 539: NM_020346 , Homo sapiens solute carrier family 17 (sodium-dependent inorganic phosphate, "cotransporter), member 6 (SLC17A6), mRNA", gi|9966810|ref|NM_020346.1|[9966810]; 540: NM_020418 , "Homo sapiens poly(rC) binding protein 4 (PCBP4), transcript variant 1, mRNA", gi|14670367|ref|NM_020418.2|[14670367]; 541: NM_020456 , "Homo sapiens chromosome 13 open reading frame 1 (C13orf1), mRNA", gi|20531764|ref|NM_020456.1|[20531764]; 542: NM_020465 , "Homo sapiens NDRG family member 4 (NDRG4), mRNA", gi|14165263|ref|NM_020465.1|[14165263]; 543: NM_020470 , "Homo sapiens Yip1 interacting factor homolog (S. cerevisiae) (YIF1), mRNA", gi|9994168|ref|NM_020470.1|[9994168]; 544: NM_020547 , "Homo sapiens anti-Mullerian hormone receptor, type II (AMHR2), mRNA", gi|10198655|ref|NM_020547.1|[10198655]; 545: NM_020990 , "Homo sapiens creatine kinase, mitochondrial 1 (ubiquitous) (CKMT1), nuclear gene", "encoding mitochondrial protein, mRNA", gi|11641403|ref|NM_020990.2|[11641403]; 546: NM_020999 , "Homo sapiens neurogenin 3 (NEUROG3), mRNA", gi|10337610|ref|NM_020999.1|[10337610]; 547: NM_021018 , "Homo sapiens histone 1, H3f (HIST1H3F), mRNA", gi|21396497|ref|NM_021018.2|[21396497]; 548: NM_021025 , "Homo sapiens T-cell leukemia, homeobox 3 (TLX3), mRNA", gi|10440563|ref|NM_021025.1|[10440563]; 549: NM_021062 , "Homo sapiens histone 1, H2bb (HIST1H2BB), mRNA", gi|19924303|ref|NM_021062.2|[19924303]; 550: NM_021067 , , ref|NM_021067.1|[10800147], This record was temporarily removed by RefSeq staff for additional review., , 551: NM_021082 , "Homo sapiens solute carrier family 15 (H+/peptide transporter), member 2", "(SLC15A2), mRNA", gi|31543623|ref|NM_021082.2|[31543623]; 552: NM_021161 , "Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript", "variant 1, mRNA", gi|20143942|ref|NM_021161.3|[20143942]; 553: NM_021174 , "Homo sapiens p30 DBC protein

(DBC-1), transcript variant 1, mRNA", gi|40548406|ref|NM_021174.4|[40548406]; 554: NM_021176 , Homo sapiens islet-specific glucose-6-phosphatase catalytic subunit-related, "protein (IGRP), mRNA", gi|10863974|ref|NM_021176.1|[10863974]; 555: NM_021184 , "Homo sapiens chromosome 6 open reading frame 47 (C6orf47), mRNA", gi|10863984|ref|NM_021184.1|[10863984]; 556: NM_021198 , "Homo sapiens CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A)", "small phosphatase 1 (CTDSP1), mRNA", gi|10864008|ref|NM_021198.1|[10864008]; 557: NM_021249 , "Homo sapiens sorting nexin 6 (SNX6), transcript variant 1, mRNA", gi|23111048|ref|NM_021249.2|[23111048]; 558: NM_021259 , "Homo sapiens transmembrane protein 8 (five membrane-spanning domains) (TMEM8),", mRNA, gi|10864068|ref|NM_021259.1|[10864068]; 559: NM_021639 , "Homo sapiens hypothetical protein SP192 (SP192), mRNA", gi|40255032|ref|NM_021639.3|[40255032]; 560: NM_021812 , "Homo sapiens blepharophimosis, epicanthus inversus and ptosis, candidate 1", "(BPESC1), mRNA", gi|11141882|ref|NM_021812.1|[11141882]; 561: NM_021815 , "Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7),", mRNA, gi|21361898|ref|NM_021815.2|[21361898]; 562: NM_021819 , "Homo sapiens lectin, mannose-binding, 1 like (LMAN1L), mRNA", gi|11141890|ref|NM_021819.1|[11141890]; 563: NM_021830 , "Homo sapiens progressive external ophthalmoplegia 1 (PEO1), mRNA", gi|39725941|ref|NM_021830.3|[39725941]; 564: NM_021833 , "Homo sapiens uncoupling protein 1 (mitochondrial, proton carrier) (UCP1),", "nuclear gene encoding mitochondrial protein, mRNA", gi|21614550|ref|NM_021833.3|[21614550]; 565: NM_021926 , "Homo sapiens aristaless-like homeobox 4 (ALX4), mRNA", gi|11496266|ref|NM_021926.1|[11496266]; 566: NM_021934 , "Homo sapiens hypothetical protein FLJ11773 (FLJ11773), mRNA", gi|34222337|ref|NM_021934.3|[34222337]; 567: NM_021969 , "Homo sapiens nuclear receptor subfamily 0, group B, member 2 (NR0B2), mRNA", gi|13259502|ref|NM_021969.1|[13259502]; 568: NM_021981 , , ref|NM_021981.1|[11415055], This record was temporarily removed by RefSeq staff for additional review., , 569: NM_022039 , "Homo sapiens split hand/foot malformation (ectrodactyly) type 3 (SHFM3), mRNA", gi|24475655|ref|NM_022039.2|[24475655]; 570: NM_022054 , "Homo sapiens potassium channel, subfamily K, member 13 (KCNK13), mRNA", gi|16306554|ref|NM_022054.2|[16306554]; 571: NM_022064 , "Homo sapiens ring finger protein 123 (RNF123), mRNA", gi|37588868|ref|NM_022064.2|[37588868]; 572: NM_022082 , "Homo sapiens chromosome 20 open reading frame 59 (C20orf59), mRNA", gi|31542262|ref|NM_022082.2|[31542262]; 573: NM_022114 , "Homo sapiens PR domain containing 16 (PRDM16), transcript variant 1, mRNA", gi|41349469|ref|NM_022114.2|[41349469]; 574: NM_022120 , "Homo sapiens 3-oxoacid CoA transferase 2 (OXCT2), mRNA", gi|11545840|ref|NM_022120.1|[11545840]; 575: NM_022131 , "Homo sapiens calsyntenin 2 (CLSTN2), mRNA", gi|11545860|ref|NM_022131.1|[11545860]; 576: NM_022135 , "Homo sapiens popeye domain containing 2 (POPDC2), mRNA", gi|22209003|ref|NM_022135.2|[22209003]; 577: NM_022168 , "Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA", gi|27886567|ref|NM_022168.2|[27886567]; 578: NM_022354 , "Homo sapiens spermatogenesis associated 1 (SPATA1), mRNA", gi|11641266|ref|NM_022354.1|[11641266]; 579: NM_022449 , "Homo sapiens RAB17, member RAS oncogene family (RAB17), mRNA", gi|11967980|ref|NM_022449.1|[11967980]; 580: NM_022452 , "Homo sapiens fibrosin 1 (FBS1), mRNA", gi|11967986|ref|NM_022452.1|[11967986]; 581: NM_022489 , "Homo sapiens

hypothetical protein FLJ22056 (FLJ22056), mRNA", gi|11968044|ref|NM_022489.1|[11968044]; 582: NM_022494 , "Homo sapiens zinc finger, DHHC domain containing 6 (ZDHHC6), mRNA", gi|11968052|ref|NM_022494.1|[11968052]; 583: NM_022568 , "Homo sapiens aldehyde dehydrogenase 8 family, member A1 (ALDH8A1), transcript", "variant 1, mRNA", gi|25952149|ref|NM_022568.2|[25952149]; 584: NM_022569 , "Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4 (NDST4),", mRNA, gi|12007649|ref|NM_022569.1|[12007649]; 585: NM_022727 , "Homo sapiens HpaII tiny fragments locus 9C (HTF9C), transcript variant 2, mRNA", gi|21361611|ref|NM_022727.3|[21361611]; 586: NM_022748 , "Homo sapiens tensin-like SH2 domain-containing 1 (TENS1), mRNA", gi|17511208|ref|NM_022748.6|[17511208]; 587: NM_022751 , "Homo sapiens chromosome 18 open reading frame 11 (C18orf11), mRNA", gi|12232414|ref|NM_022751.1|[12232414]; 588: NM_022754 , "Homo sapiens sideroflexin 1 (SFXN1), mRNA", gi|40255158|ref|NM_022754.4|[40255158]; 589: NM_022765 , Homo sapiens NEDD9 interacting protein with calponin homology and LIM domains, "(NICAL), mRNA", gi|20127615|ref|NM_022765.2|[20127615]; 590: NM_022766 , "Homo sapiens ceramide kinase (CERK), transcript variant 1, mRNA", gi|32967301|ref|NM_022766.4|[32967301]; 591: NM_022771 , "Homo sapiens TBC1 domain family, member 15 (TBC1D15), mRNA", gi|37059748|ref|NM_022771.3|[37059748]; 592: NM_022779 , "Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 (DDX31), transcript", "variant 1, mRNA", gi|20336296|ref|NM_022779.7|[20336296]; 593: NM_023009 , "Homo sapiens MARCKS-like protein (MLP), mRNA", gi|32401423|ref|NM_023009.4|[32401423]; 594: NM_023112 , "Homo sapiens chromosome 14 open reading frame 137 (C14orf137), mRNA", gi|31881722|ref|NM_023112.2|[31881722]; 595: NM_023933 , "Homo sapiens hypothetical protein MGC2494 (MGC2494), mRNA", gi|13027599|ref|NM_023933.1|[13027599]; 596: NM_024034 , Homo sapiens ganglioside-induced differentiation-associated protein 1-like 1, "(GDAP1L1), mRNA", gi|30581159|ref|NM_024034.3|[30581159]; 597: NM_024057 , "Homo sapiens nucleoporin Nup37 (Nup37), mRNA", gi|34222120|ref|NM_024057.2|[34222120]; 598: NM_024294 , "Homo sapiens hypothetical protein MGC4614 (MGC4614), mRNA", gi|13236513|ref|NM_024294.1|[13236513]; 599: NM_024323 , "Homo sapiens hypothetical protein MGC11271 (MGC11271), mRNA", gi|31543147|ref|NM_024323.3|[31543147]; 600: NM_024334 , "Homo sapiens hypothetical protein MGC3222 (MGC3222), mRNA", gi|13236586|ref|NM_024334.1|[13236586]; 601: NM_024493 , "Homo sapiens zinc finger protein 306 (ZNF306), mRNA", gi|24308296|ref|NM_024493.1|[24308296]; 602: NM_024506 , "Homo sapiens galactosidase, beta 1-like (GLB1L), mRNA", gi|40255042|ref|NM_024506.3|[40255042]; 603: NM_024515 , "Homo sapiens hypothetical protein MGC4645 (MGC4645), mRNA", gi|34147381|ref|NM_024515.2|[34147381]; 604: NM_024523 , "Homo sapiens GRIP and coiled-coil domain-containing 1 (GCC1), mRNA", gi|34305454|ref|NM_024523.5|[34305454]; 605: NM_024546 , "Homo sapiens chromosome 13 open reading frame 7 (C13orf7), mRNA", gi|21362045|ref|NM_024546.2|[21362045]; 606: NM_024560 , "Homo sapiens FLJ21963 protein (FLJ21963), mRNA", gi|38505216|ref|NM_024560.2|[38505216]; 607: NM_024589 , "Homo sapiens leucine zipper domain protein (FLJ22386), mRNA", gi|13375778|ref|NM_024589.1|[13375778]; 608: NM_024604 , "Homo sapiens hypothetical protein FLJ21908 (FLJ21908), mRNA", gi|13375808|ref|NM_024604.1|[13375808]; 609: NM_024624 , Homo sapiens SMC6 structural maintenance of chromosomes 6-like 1 (yeast), "(SMC6L1), mRNA",

gi|31543646|ref|NM_024624.2|[31543646]; 610: NM_024626 , "Homo sapiens immune costimulatory protein B7-H4 (B7-H4), mRNA", gi|13375849|ref|NM_024626.1|[13375849]; 611: NM_024630 , "Homo sapiens zinc finger, DHHC domain containing 14 (ZDHHC14), mRNA", gi|24371240|ref|NM_024630.2|[24371240]; 612: NM_024643 , "Homo sapiens chromosome 14 open reading frame 140 (C14orf140), mRNA", gi|13375882|ref|NM_024643.1|[13375882]; 613: NM_024671 , "Homo sapiens hypothetical protein FLJ23436 (FLJ23436), mRNA", gi|20127628|ref|NM_024671.2|[20127628]; 614: NM_024696 , "Homo sapiens hypothetical protein FLJ23058 (FLJ23058), mRNA", gi|13375978|ref|NM_024696.1|[13375978]; 615: NM_024713 , "Homo sapiens hypothetical protein FLJ22557 (FLJ22557), mRNA", gi|13376012|ref|NM_024713.1|[13376012]; 616: NM_024728 , "Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA", gi|13376041|ref|NM_024728.1|[13376041]; 617: NM_024731 , "Homo sapiens chromosome 16 open reading frame 44 (C16orf44), mRNA", gi|31542245|ref|NM_024731.2|[31542245]; 618: NM_024734 , "Homo sapiens calmin (calponin-like, transmembrane) (CLMN), mRNA", gi|19923598|ref|NM_024734.2|[19923598]; 619: NM_024754 , "Homo sapiens hypothetical protein FLJ12598 (FLJ12598), mRNA", gi|20127633|ref|NM_024754.2|[20127633]; 620: NM_024778 , "Homo sapiens ring finger protein 127 (RNF127), mRNA", gi|37622895|ref|NM_024778.3|[37622895]; 621: NM_024783 , "Homo sapiens hypothetical protein FLJ23598 (FLJ23598), mRNA", gi|31657118|ref|NM_024783.2|[31657118]; 622: NM_024799 , "Homo sapiens hypothetical protein FLJ13224 (FLJ13224), mRNA", gi|13376172|ref|NM_024799.1|[13376172]; 623: NM_024807 , "Homo sapiens chromosome 6 open reading frame 76 (C6orf76), mRNA", gi|13376188|ref|NM_024807.1|[13376188]; 624: NM_024820 , "Homo sapiens KIAA1608 (KIAA1608), mRNA", gi|13449264|ref|NM_024820.1|[13449264]; 625: NM_024827 , "Homo sapiens histone deacetylase 11 (HDAC11), mRNA", gi|13376227|ref|NM_024827.1|[13376227]; 626: NM_024874 , "Homo sapiens polycystic kidney disease 1-like (PKD1-like), transcript variant 1,", mRNA, gi|33359220|ref|NM_024874.3|[33359220]; 627: NM_024882 , "Homo sapiens chromosome 6 open reading frame 155 (C6orf155), mRNA", gi|13376326|ref|NM_024882.1|[13376326]; 628: NM_024912 , , ref|NM_024912.1|[13376375], This record was temporarily removed by RefSeq staff for additional review., , 629: NM_024958 , "Homo sapiens chromosome 20 open reading frame 98 (C20orf98), mRNA", gi|13376446|ref|NM_024958.1|[13376446]; 630: NM_024969 , "Homo sapiens TGF-beta induced apotosis protein 2 (TAIP-2), mRNA", gi|23346411|ref|NM_024969.2|[23346411]; 631: NM_025026 , "Homo sapiens hypothetical protein FLJ14107 (FLJ14107), mRNA", gi|13376547|ref|NM_025026.1|[13376547]; 632: NM_025079 , "Homo sapiens hypothetical protein FLJ23231 (FLJ23231), mRNA", gi|13376631|ref|NM_025079.1|[13376631]; 633: NM_025093 , , ref|NM_025093.1|[13376653], This record was temporarily removed by RefSeq staff for additional review., , 634: NM_025100 , "Homo sapiens chromosome 14 open reading frame 157 (C14orf157), mRNA", gi|13376666|ref|NM_025100.1|[13376666]; 635: NM_025137 , "Homo sapiens hypothetical protein FLJ21439 (FLJ21439), mRNA", gi|33636747|ref|NM_025137.2|[33636747]; 636: NM_025140 , "Homo sapiens limkain beta 2 (FLJ22471), mRNA", gi|13376724|ref|NM_025140.1|[13376724]; 637: NM_025152 , "Homo sapiens chromosome 14 open reading frame 127 (C14orf127), mRNA", gi|13376746|ref|NM_025152.1|[13376746]; 638: NM_025212 , "Homo sapiens CXXC finger 4 (CXXC4), mRNA", gi|13376815|ref|NM_025212.1|[13376815]; 639: NM_025236 , "Homo sapiens ring finger protein 39 (RNF39), transcript variant 1, mRNA",

gi|25777714|ref|NM_025236.2|[25777714]; 640: NM_030769 , Homo sapiens N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase), "(NPL), mRNA", gi|13540532|ref|NM_030769.1|[13540532]; 641: NM_030785 , "Homo sapiens radial spokehead-like 1 (RSHL1), mRNA", gi|13540558|ref|NM_030785.1|[13540558]; 642: NM_030786 , "Homo sapiens intermediate filament protein syncoilin (SYNCOILIN), mRNA", gi|13540560|ref|NM_030786.1|[13540560]; 643: NM_030804 , , ref|NM_030804.1|[13540591], This record was temporarily removed by RefSeq staff for additional review., , 644: NM_030818 , "Homo sapiens hypothetical protein MGC10471 (MGC10471), mRNA", gi|34147391|ref|NM_030818.2|[34147391]; 645: NM_030903 , "Homo sapiens olfactory receptor, family 2, subfamily W, member 1 (OR2W1), mRNA", gi|13624328|ref|NM_030903.1|[13624328]; 646: NM_030981 , "Homo sapiens RAB1B, member RAS oncogene family (RAB1B), mRNA", gi|13569961|ref|NM_030981.1|[13569961]; 647: NM_031219 , "Homo sapiens hypothetical protein MGC12904 (MGC12904), mRNA", gi|31377665|ref|NM_031219.2|[31377665]; 648: NM_031269 , , ref|NM_031269.1|[13775169], This record was temporarily removed by RefSeq staff for additional review., , 649: NM_031284 , "Homo sapiens ATP-dependent glucokinase (ADP-GK), mRNA", gi|31542508|ref|NM_031284.3|[31542508]; 650: NM_031294 , "Homo sapiens hypothetical protein DKFZp586M1120 (DKFZP586M1120), mRNA", gi|33636688|ref|NM_031294.2|[33636688]; 651: NM_031298 , "Homo sapiens hypothetical protein MGC2963 (MGC2963), mRNA", gi|13775219|ref|NM_031298.1|[13775219]; 652: NM_031450 , "Homo sapiens hypothetical protein p5326 (P5326), mRNA", gi|31543378|ref|NM_031450.2|[31543378]; 653: NM_032042 , "Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA", gi|37059749|ref|NM_032042.3|[37059749]; 654: NM_032179 , "Homo sapiens hypothetical protein FLJ20542 (FLJ20542), mRNA", gi|14149862|ref|NM_032179.1|[14149862]; 655: NM_032204 , "Homo sapiens ASC-1 complex subunit P100 (ASC1p100), mRNA", gi|34147616|ref|NM_032204.3|[34147616]; 656: NM_032209 , "Homo sapiens hypothetical protein FLJ21777 (FLJ21777), mRNA", gi|14149905|ref|NM_032209.1|[14149905]; 657: NM_032338 , "Homo sapiens hypothetical protein MGC14817 (MGC14817), mRNA", gi|31543151|ref|NM_032338.2|[31543151]; 658: NM_032348 , "Homo sapiens hypothetical protein MGC3047 (MGC3047), mRNA", gi|39725651|ref|NM_032348.2|[39725651]; 659: NM_032389 , "Homo sapiens zinc finger protein 289, ID1 regulated (ZNF289), mRNA", gi|31543982|ref|NM_032389.2|[31543982]; 660: NM_032842 , "Homo sapiens hypothetical protein FLJ14803 (FLJ14803), mRNA", gi|14249557|ref|NM_032842.1|[14249557]; 661: NM_033100 , "Homo sapiens protocadherin 21 (PCDH21), mRNA", gi|16933564|ref|NM_033100.1|[16933564]; 662: NM_033184 , "Homo sapiens keratin associated protein 2-4 (KRTAP2-4), mRNA", gi|15743557|ref|NM_033184.2|[15743557]; 663: NM_080284 , "Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 6 (ABCA6),", "transcript variant 1, mRNA", gi|27436952|ref|NM_080284.2|[27436952]; 664: NM_080603 , "Homo sapiens zinc finger, SWIM domain containing 1 (ZSWIM1), mRNA", gi|29126221|ref|NM_080603.2|[29126221]; 665: NM_130463 , "Homo sapiens ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 2", "(ATP6V1G2), transcript variant 1, mRNA", gi|20357536|ref|NM_130463.2|[20357536]; 666: NM_138340 , "Homo sapiens abhydrolase domain containing 3 (ABHD3), mRNA", gi|34304337|ref|NM_138340.3|[34304337]; 667: NM_138967 , "Homo sapiens secretory carrier membrane protein 5 (SCAMP5), mRNA", gi|42544128|ref|NM_138967.2|[42544128]; 668:

NM_144563 , Homo sapiens ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase), "(RPIA), mRNA", gi|21389336|ref|NM_144563.1|[21389336]; 669: NM_144718 , "Homo sapiens hypothetical protein AY099107 (LOC152185), mRNA", gi|40255074|ref|NM_144718.2|[40255074]; 670: NM_145021 , "Homo sapiens c-mir, cellular modulator of immune recognition (MIR), mRNA", gi|34222177|ref|NM_145021.2|[34222177]; 671: NM_145804 , "Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), mRNA", gi|21956638|ref|NM_145804.1|[21956638]; 672: NM_152344 , "Homo sapiens hypothetical protein FLJ30656 (FLJ30656), mRNA", gi|22748746|ref|NM_152344.1|[22748746]; 673: NM_152470 , "Homo sapiens hypothetical protein FLJ34218 (FLJ34218), mRNA", gi|22748990|ref|NM_152470.1|[22748990]; 674: NM_153045 , "Homo sapiens DKFZp547P234 protein (DKFZp547P234), mRNA", gi|33356141|ref|NM_153045.2|[33356141]; 675: NM_153354 , "Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA", gi|34222213|ref|NM_153354.2|[34222213]; 676: NM_174975 , "Homo sapiens SEC14-like 3 (S. cerevisiae) (SEC14L3), mRNA", gi|30410717|ref|NM_174975.2|[30410717]; 677: NM_174977 , "Homo sapiens SEC14-like 4 (S. cerevisiae) (SEC14L4), mRNA", gi|30410718|ref|NM_174977.2|[30410718]; 678: NM_175852 , "Homo sapiens taxilin (DKFZp451J0118), mRNA", gi|39725959|ref|NM_175852.3|[39725959],

Table 12: Genes having an Gabpa binding site motif

1: NM_000028 , "Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen", "debranching enzyme, glycogen storage disease type III) (AGL), transcript variant", "4, mRNA", gi|4557274|ref|NM_000028.1|[4557274]; 2: NM_000029 , "Homo sapiens angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A", "(alpha-1 antiproteinase, antitrypsin), member 8) (AGT), mRNA", gi|4557286|ref|NM_000029.1|[4557286]; 3: NM_000033 , "Homo sapiens ATP-binding cassette, sub-family D (ALD), member 1 (ABCD1), mRNA", gi|7262392|ref|NM_000033.2|[7262392]; 4: NM_000040 , "Homo sapiens apolipoprotein C-III (APOC3), mRNA", gi|4557322|ref|NM_000040.1|[4557322]; 5: NM_000045 , "Homo sapiens arginase, liver (ARG1), mRNA", gi|10947138|ref|NM_000045.2|[10947138]; 6: NM_000049 , "Homo sapiens aspartoacylase (aminoacylase 2, Canavan disease) (ASPA), mRNA", gi|4557334|ref|NM_000049.1|[4557334]; 7: NM_000053 , "Homo sapiens ATPase, Cu++ transporting, beta polypeptide (Wilson disease)", "(ATP7B), mRNA", gi|4502322|ref|NM_000053.1|[4502322]; 8: NM_000055 , "Homo sapiens butyrylcholinesterase (BCHE), mRNA", gi|4557350|ref|NM_000055.1|[4557350]; 9: NM_000057 , "Homo sapiens Bloom syndrome (BLM), mRNA", gi|4557364|ref|NM_000057.1|[4557364]; 10: NM_000063 , "Homo sapiens complement component 2 (C2), mRNA", gi|20631970|ref|NM_000063.3|[20631970]; 11: NM_000069 , "Homo sapiens calcium channel, voltage-dependent, L type, alpha 1S subunit", "(CACNA1S), mRNA", gi|4557400|ref|NM_000069.1|[4557400]; 12: NM_000075 , "Homo sapiens cyclin-dependent kinase 4 (CDK4), mRNA", gi|16936531|ref|NM_000075.2|[16936531]; 13: NM_000092 , "Homo sapiens collagen, type IV, alpha 4 (COL4A4), mRNA", gi|15890083|ref|NM_000092.2|[15890083]; 14: NM_000103 , "Homo sapiens cytochrome P450, family 19, subfamily A, polypeptide 1 (CYP19A1),", "transcript variant 1, mRNA", gi|13904857|ref|NM_000103.2|[13904857]; 15: NM_000110 , "Homo sapiens dihydropyrimidine dehydrogenase (DPYD), mRNA", gi|4557874|ref|NM_000110.2|[4557874]; 16: NM_000122 , "Homo sapiens excision repair cross-complementing rodent repair deficiency,", "complementation group 3 (xeroderma pigmentosum group B complementing) (ERCC3),", mRNA, gi|4557562|ref|NM_000122.1|[4557562]; 17: NM_000123 , "Homo sapiens excision repair cross-complementing rodent repair deficiency,", "complementation group 5 (xeroderma pigmentosum, complementation group G", "(Cockayne syndrome)) (ERCC5), mRNA", gi|4503600|ref|NM_000123.1|[4503600]; 18: NM_000124 , "Homo sapiens excision repair cross-complementing rodent repair deficiency,", "complementation group 6 (ERCC6), mRNA", gi|4557564|ref|NM_000124.1|[4557564]; 19: NM_000127 , "Homo sapiens exostoses (multiple) 1 (EXT1), mRNA", gi|4557570|ref|NM_000127.1|[4557570]; 20: NM_000129 , "Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA", gi|9961355|ref|NM_000129.2|[9961355]; 21: NM_000147 , "Homo sapiens fucosidase, alpha-L-1, tissue (FUCA1), mRNA", gi|24475878|ref|NM_000147.2|[24475878]; 22: NM_000148 , Homo sapiens fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase), "(FUT1), mRNA", gi|4503804|ref|NM_000148.1|[4503804]; 23: NM_000158 , "Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme,", "Andersen disease, glycogen storage disease type IV) (GBE1), mRNA", gi|4557618|ref|NM_000158.1|[4557618]; 24: NM_000164 , "Homo sapiens gastric inhibitory polypeptide receptor (GIPR), mRNA", gi|4503998|ref|NM_000164.1|[4503998]; 25: NM_000168 , Homo sapiens GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly, "syndrome) (GLI3), mRNA",

gi|13518031|ref|NM_000168.2|[13518031]; 26: NM_000174 , "Homo sapiens glycoprotein IX (platelet) (GP9), mRNA", gi|4504076|ref|NM_000174.1|[4504076]; 27: NM_000183 , Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A, "thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit", "(HADHB), mRNA", gi|4504326|ref|NM_000183.1|[4504326]; 28: NM_000188 , "Homo sapiens hexokinase 1 (HK1), nuclear gene encoding mitochondrial protein,", "transcript variant 1, mRNA", gi|4504390|ref|NM_000188.1|[4504390]; 29: NM_000190 , "Homo sapiens hydroxymethylbilane synthase (HMBS), mRNA", gi|20149499|ref|NM_000190.2|[20149499]; 30: NM_000191 , Homo sapiens 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase, "(hydroxymethylglutaricaciduria) (HMGCL), mRNA", gi|4504426|ref|NM_000191.1|[4504426]; 31: NM_000193 , "Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), mRNA", gi|21071042|ref|NM_000193.2|[21071042]; 32: NM_000230 , "Homo sapiens leptin (obesity homolog, mouse) (LEP), mRNA", gi|4557714|ref|NM_000230.1|[4557714]; 33: NM_000234 , "Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA", gi|4557718|ref|NM_000234.1|[4557718]; 34: NM_000248 , "Homo sapiens microphthalmia-associated transcription factor (MITF), transcript", "variant 4, mRNA", gi|38156695|ref|NM_000248.2|[38156695]; 35: NM_000249 , "Homo sapiens mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli) (MLH1),", mRNA, gi|28559089|ref|NM_000249.2|[28559089]; 36: NM_000251 , "Homo sapiens mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli) (MSH2),", mRNA, gi|4557760|ref|NM_000251.1|[4557760]; 37: NM_000254 , "Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase (MTR), mRNA", gi|4557764|ref|NM_000254.1|[4557764]; 38: NM_000261 , "Homo sapiens myocilin, trabecular meshwork inducible glucocorticoid response", "(MYOC), mRNA", gi|4557778|ref|NM_000261.1|[4557778]; 39: NM_000274 , "Homo sapiens ornithine aminotransferase (gyrate atrophy) (OAT), nuclear gene", "encoding mitochondrial protein, mRNA", gi|4557808|ref|NM_000274.1|[4557808]; 40: NM_000277 , "Homo sapiens phenylalanine hydroxylase (PAH), mRNA", gi|4557818|ref|NM_000277.1|[4557818]; 41: NM_000278 , "Homo sapiens paired box gene 2 (PAX2), transcript variant b, mRNA", gi|34878700|ref|NM_000278.2|[34878700]; 42: NM_000280 , "Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), mRNA", gi|4505614|ref|NM_000280.1|[4505614]; 43: NM_000286 , "Homo sapiens peroxisomal biogenesis factor 12 (PEX12), mRNA", gi|4505720|ref|NM_000286.1|[4505720]; 44: NM_000294 , "Homo sapiens phosphorylase kinase, gamma 2 (testis) (PHKG2), mRNA", gi|4505784|ref|NM_000294.1|[4505784]; 45: NM_000297 , "Homo sapiens polycystic kidney disease 2 (autosomal dominant) (PKD2), mRNA", gi|33286447|ref|NM_000297.2|[33286447]; 46: NM_000300 , "Homo sapiens phospholipase A2, group IIA (platelets, synovial fluid) (PLA2G2A),", mRNA, gi|20149501|ref|NM_000300.2|[20149501]; 47: NM_000302 , "Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine", "hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD), mRNA", gi|32307143|ref|NM_000302.2|[32307143]; 48: NM_000304 , "Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, mRNA", gi|24430161|ref|NM_000304.2|[24430161]; 49: NM_000308 , Homo sapiens protective protein for beta-galactosidase (galactosialidosis), "(PPGB), mRNA", gi|4505988|ref|NM_000308.1|[4505988]; 50: NM_000316 , "Homo sapiens parathyroid hormone receptor 1 (PTHR1), mRNA", gi|39995096|ref|NM_000316.2|[39995096]; 51: NM_000317 , "Homo sapiens 6-pyruvoyltetrahydropterin synthase (PTS), mRNA",

gi|4506330|ref|NM_000317.1|[4506330]; 52: NM_000318 , "Homo sapiens peroxisomal membrane protein 3, 35kDa (Zellweger syndrome) (PXMP3),", mRNA, gi|4506342|ref|NM_000318.1|[4506342]; 53: NM_000328 , "Homo sapiens retinitis pigmentosa GTPase regulator (RPGR), mRNA", gi|4506580|ref|NM_000328.1|[4506580]; 54: NM_000347 , "Homo sapiens spectrin, beta, erythrocytic (includes spherocytosis, clinical type", "I) (SPTB), mRNA", gi|22507315|ref|NM_000347.3|[22507315]; 55: NM_000348 , "Homo sapiens steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5", "alpha-steroid delta 4-dehydrogenase alpha 2) (SRD5A2), mRNA", gi|39812446|ref|NM_000348.2|[39812446]; 56: NM_000359 , "Homo sapiens transglutaminase 1 (K polypeptide epidermal type I,", "protein-glutamine-gamma-glutamyltransferase) (TGM1), mRNA", gi|4507474|ref|NM_000359.1|[4507474]; 57: NM_000364 , "Homo sapiens troponin T2, cardiac (TNNT2), mRNA", gi|4507626|ref|NM_000364.1|[4507626]; 58: NM_000368 , "Homo sapiens tuberous sclerosis 1 (TSC1), mRNA", gi|24475626|ref|NM_000368.2|[24475626]; 59: NM_000375 , Homo sapiens uroporphyrinogen III synthase (congenital erythropoietic porphyria), "(UROS), mRNA", gi|4557872|ref|NM_000375.1|[4557872]; 60: NM_000383 , Homo sapiens autoimmune regulator (autoimmune polyendocrinopathy candidiasis, "ectodermal dystrophy) (AIRE), transcript variant AIRE-1, mRNA", gi|4557290|ref|NM_000383.1|[4557290]; 61: NM_000387 , "Homo sapiens solute carrier family 25 (carnitine/acylcarnitine translocase),", "member 20 (SLC25A20), nuclear gene encoding mitochondrial protein, mRNA", gi|6006040|ref|NM_000387.2|[6006040]; 62: NM_000389 , "Homo sapiens cyclin-dependent kinase inhibitor 1A (p21, Cip1) (CDKN1A),", "transcript variant 1, mRNA", gi|17978496|ref|NM_000389.2|[17978496]; 63: NM_000396 , "Homo sapiens cathepsin K (pycnodysostosis) (CTSK), mRNA", gi|23110958|ref|NM_000396.2|[23110958]; 64: NM_000399 , "Homo sapiens early growth response 2 (Krox-20 homolog, Drosophila) (EGR2), mRNA", gi|9845523|ref|NM_000399.2|[9845523]; 65: NM_000402 , "Homo sapiens glucose-6-phosphate dehydrogenase (G6PD), nuclear gene encoding", "mitochondrial protein, mRNA", gi|21614519|ref|NM_000402.2|[21614519]; 66: NM_000403 , "Homo sapiens galactose-4-epimerase, UDP (GALE), mRNA", gi|9945333|ref|NM_000403.2|[9945333]; 67: NM_000429 , "Homo sapiens methionine adenosyltransferase I, alpha (MAT1A), mRNA", gi|4557736|ref|NM_000429.1|[4557736]; 68: NM_000434 , "Homo sapiens sialidase 1 (lysosomal sialidase) (NEU1), mRNA", gi|40806202|ref|NM_000434.2|[40806202]; 69: NM_000474 , Homo sapiens twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome), "(Drosophila) (TWIST1), mRNA", gi|17978464|ref|NM_000474.2|[17978464]; 70: NM_000483 , "Homo sapiens apolipoprotein C-II (APOC2), mRNA", gi|32130517|ref|NM_000483.3|[32130517]; 71: NM_000499 , "Homo sapiens cytochrome P450, family 1, subfamily A, polypeptide 1 (CYP1A1),", mRNA, gi|13325053|ref|NM_000499.2|[13325053]; 72: NM_000503 , "Homo sapiens eyes absent homolog 1 (Drosophila) (EYA1), transcript variant 3,", mRNA, gi|26667213|ref|NM_000503.3|[26667213]; 73: NM_000512 , "Homo sapiens galactosamine (N-acetyl)-6-sulfate sulfatase (Morquio syndrome,", "mucopolysaccharidosis type IVA) (GALNS), mRNA", gi|9945384|ref|NM_000512.2|[9945384]; 74: NM_000514 , "Homo sapiens glial cell derived neurotrophic factor (GDNF), transcript variant", "1, mRNA", gi|40549401|ref|NM_000514.2|[40549401]; 75: NM_000524 , "Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), mRNA", gi|4504530|ref|NM_000524.1|[4504530]; 76: NM_000526 , "Homo sapiens keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)", "(KRT14), mRNA",

gi|15431309|ref|NM_000526.3|[15431309]; 77: NM_000528 , "Homo sapiens mannosidase, alpha, class 2B, member 1 (MAN2B1), mRNA", gi|10834967|ref|NM_000528.1|[10834967]; 78: NM_000534 , "Homo sapiens PMS1 postmeiotic segregation increased 1 (S. cerevisiae) (PMS1),", mRNA, gi|11496979|ref|NM_000534.2|[11496979]; 79: NM_000547 , "Homo sapiens thyroid peroxidase (TPO), transcript variant 1, mRNA", gi|28558981|ref|NM_000547.3|[28558981]; 80: NM_000548 , "Homo sapiens tuberous sclerosis 2 (TSC2), transcript variant 1, mRNA", gi|10938006|ref|NM_000548.2|[10938006]; 81: NM_000581 , "Homo sapiens glutathione peroxidase 1 (GPX1), transcript variant 1, mRNA", gi|41406083|ref|NM_000581.2|[41406083]; 82: NM_000582 , "Homo sapiens secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early", "T-lymphocyte activation 1) (SPP1), mRNA", gi|38146097|ref|NM_000582.2|[38146097]; 83: NM_000585 , "Homo sapiens interleukin 15 (IL15), transcript variant 3, mRNA", gi|26787979|ref|NM_000585.2|[26787979]; 84: NM_000588 , "Homo sapiens interleukin 3 (colony-stimulating factor, multiple) (IL3), mRNA", gi|28416914|ref|NM_000588.3|[28416914]; 85: NM_000592 , "Homo sapiens complement component 4B (C4B), mRNA", gi|14577920|ref|NM_000592.3|[14577920]; 86: NM_000593 , "Homo sapiens transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) (TAP1),", mRNA, gi|24797159|ref|NM_000593.4|[24797159]; 87: NM_000594 , "Homo sapiens tumor necrosis factor (TNF superfamily, member 2) (TNF), mRNA", gi|25952110|ref|NM_000594.2|[25952110]; 88: NM_000595 , "Homo sapiens lymphotoxin alpha (TNF superfamily, member 1) (LTA), mRNA", gi|6806892|ref|NM_000595.2|[6806892]; 89: NM_000600 , "Homo sapiens interleukin 6 (interferon, beta 2) (IL6), mRNA", gi|10834983|ref|NM_000600.1|[10834983]; 90: NM_000603 , "Homo sapiens nitric oxide synthase 3 (endothelial cell) (NOS3), mRNA", gi|40254421|ref|NM_000603.2|[40254421]; 91: NM_000606 , "Homo sapiens complement component 8, gamma polypeptide (C8G), mRNA", gi|4557392|ref|NM_000606.1|[4557392]; 92: NM_000623 , "Homo sapiens bradykinin receptor B2 (BDKRB2), mRNA", gi|17352499|ref|NM_000623.2|[17352499]; 93: NM_000626 , "Homo sapiens CD79B antigen (immunoglobulin-associated beta) (CD79B), transcript", "variant 1, mRNA", gi|11038673|ref|NM_000626.1|[11038673]; 94: NM_000628 , "Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA", gi|24430214|ref|NM_000628.3|[24430214]; 95: NM_000635 , "Homo sapiens regulatory factor X, 2 (influences HLA class II expression) (RFX2),", "transcript variant 1, mRNA", gi|19743880|ref|NM_000635.2|[19743880]; 96: NM_000637 , "Homo sapiens glutathione reductase (GSR), mRNA", gi|10835188|ref|NM_000637.1|[10835188]; 97: NM_000638 , "Homo sapiens vitronectin (serum spreading factor, somatomedin B, complement", "S-protein) (VTN), mRNA", gi|18201910|ref|NM_000638.2|[18201910]; 98: NM_000661 , "Homo sapiens ribosomal protein L9 (RPL9), mRNA", gi|15431302|ref|NM_000661.2|[15431302]; 99: NM_000673 , "Homo sapiens alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide (ADH7),", mRNA, gi|11496969|ref|NM_000673.2|[11496969]; 100: NM_000679 , "Homo sapiens adrenergic, alpha-1B-, receptor (ADRA1B), mRNA", gi|15451783|ref|NM_000679.2|[15451783]; 101: NM_000681 , "Homo sapiens adrenergic, alpha-2A-, receptor (ADRA2A), mRNA", gi|15718669|ref|NM_000681.2|[15718669]; 102: NM_000682 , "Homo sapiens adrenergic, alpha-2B-, receptor (ADRA2B), mRNA", gi|33598959|ref|NM_000682.3|[33598959]; 103: NM_000684 , "Homo sapiens adrenergic, beta-1-, receptor (ADRB1), mRNA", gi|4557264|ref|NM_000684.1|[4557264]; 104: NM_000687 , "Homo sapiens S-adenosylhomocysteine hydrolase (AHCY), mRNA", gi|9951914|ref|NM_000687.1|[9951914]; 105: NM_000688 , "Homo sapiens aminolevulinate, delta-, synthase 1 (ALAS1), transcript

variant 1,", mRNA, gi|40316942|ref|NM_000688.4|[40316942]; 106: NM_000697 , "Homo sapiens arachidonate 12-lipoxygenase (ALOX12), mRNA", gi|4502050|ref|NM_000697.1|[4502050]; 107: NM_000721 , "Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E),", mRNA, gi|4502528|ref|NM_000721.1|[4502528]; 108: NM_000747 , "Homo sapiens cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)", "(CHRNB1), mRNA", gi|41327725|ref|NM_000747.2|[41327725]; 109: NM_000751 , "Homo sapiens cholinergic receptor, nicotinic, delta polypeptide (CHRND), mRNA", gi|4557460|ref|NM_000751.1|[4557460]; 110: NM_000760 , "Homo sapiens colony stimulating factor 3 receptor (granulocyte) (CSF3R),", "transcript variant 1, mRNA", gi|27437046|ref|NM_000760.2|[27437046]; 111: NM_000781 , "Homo sapiens cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1),", "nuclear gene encoding mitochondrial protein, mRNA", gi|4503188|ref|NM_000781.1|[4503188]; 112: NM_000782 , "Homo sapiens cytochrome P450, family 24, subfamily A, polypeptide 1 (CYP24A1),", "nuclear gene encoding mitochondrial protein, mRNA", gi|13904862|ref|NM_000782.2|[13904862]; 113: NM_000784 , "Homo sapiens cytochrome P450, family 27, subfamily A, polypeptide 1 (CYP27A1),", "nuclear gene encoding mitochondrial protein, mRNA", gi|13904863|ref|NM_000784.2|[13904863]; 114: NM_000785 , "Homo sapiens cytochrome P450, family 27, subfamily B, polypeptide 1 (CYP27B1),", "nuclear gene encoding mitochondrial protein, mRNA", gi|13904864|ref|NM_000785.2|[13904864]; 115: NM_000794 , "Homo sapiens dopamine receptor D1 (DRD1), mRNA", gi|16445404|ref|NM_000794.2|[16445404]; 116: NM_000798 , "Homo sapiens dopamine receptor D5 (DRD5), mRNA", gi|34328907|ref|NM_000798.3|[34328907]; 117: NM_000806 , "Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 1 (GABRA1), mRNA", gi|38327553|ref|NM_000806.3|[38327553]; 118: NM_000809 , "Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 4 (GABRA4), mRNA", gi|34452722|ref|NM_000809.2|[34452722]; 119: NM_000813 , "Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 2 (GABRB2),", "transcript variant 2, mRNA", gi|4503864|ref|NM_000813.1|[4503864]; 120: NM_000831 , "Homo sapiens glutamate receptor, ionotropic, kainate 3 (GRIK3), mRNA", gi|28605144|ref|NM_000831.2|[28605144]; 121: NM_000835 , "Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2C (GRIN2C),", mRNA, gi|6006004|ref|NM_000835.2|[6006004]; 122: NM_000839 , "Homo sapiens glutamate receptor, metabotropic 2 (GRM2), mRNA", gi|4504136|ref|NM_000839.1|[4504136]; 123: NM_000841 , "Homo sapiens glutamate receptor, metabotropic 4 (GRM4), mRNA", gi|4504140|ref|NM_000841.1|[4504140]; 124: NM_000849 , "Homo sapiens glutathione S-transferase M3 (brain) (GSTM3), mRNA", gi|39995110|ref|NM_000849.3|[39995110]; 125: NM_000863 , "Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B), mRNA", gi|4504532|ref|NM_000863.1|[4504532]; 126: NM_000880 , "Homo sapiens interleukin 7 (IL7), mRNA", gi|28610152|ref|NM_000880.2|[28610152]; 127: NM_000883 , "Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), transcript", "variant 1, mRNA", gi|34328929|ref|NM_000883.2|[34328929]; 128: NM_000894 , "Homo sapiens luteinizing hormone beta polypeptide (LHB), mRNA", gi|15431286|ref|NM_000894.2|[15431286]; 129: NM_000901 , "Homo sapiens nuclear receptor subfamily 3, group C, member 2 (NR3C2), mRNA", gi|4505198|ref|NM_000901.1|[4505198]; 130: NM_000905 , "Homo sapiens neuropeptide Y (NPY), mRNA", gi|31542152|ref|NM_000905.2|[31542152]; 131: NM_000915 ,

"Homo sapiens oxytocin, prepro- (neurophysin I) (OXT), mRNA", gi|12707574|ref|NM_000915.2|[12707574]; 132: NM_000932 , "Homo sapiens phospholipase C, beta 3 (phosphatidylinositol-specific) (PLCB3),", mRNA, gi|11386138|ref|NM_000932.1|[11386138]; 133: NM_000939 , Homo sapiens proopiomelanocortin (adrenocorticotropin/ beta-lipotropin/, alpha-melanocyte stimulating hormone/ beta-melanocyte stimulating hormone/, "beta-endorphin) (POMC), mRNA", gi|4505948|ref|NM_000939.1|[4505948]; 134: NM_000951 , "Homo sapiens proline-rich Gla (G-carboxyglutamic acid) polypeptide 2 (PRRG2),", mRNA, gi|4506136|ref|NM_000951.1|[4506136]; 135: NM_000963 , Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase, "and cyclooxygenase) (PTGS2), mRNA", gi|4506264|ref|NM_000963.1|[4506264]; 136: NM_000970 , "Homo sapiens ribosomal protein L6 (RPL6), mRNA", gi|16753226|ref|NM_000970.2|[16753226]; 137: NM_000973 , "Homo sapiens ribosomal protein L8 (RPL8), transcript variant 1, mRNA", gi|15431304|ref|NM_000973.2|[15431304]; 138: NM_000975 , "Homo sapiens ribosomal protein L11 (RPL11), mRNA", gi|15431289|ref|NM_000975.2|[15431289]; 139: NM_000980 , "Homo sapiens ribosomal protein L18a (RPL18A), mRNA", gi|15431299|ref|NM_000980.2|[15431299]; 140: NM_000981 , "Homo sapiens ribosomal protein L19 (RPL19), mRNA", gi|17158042|ref|NM_000981.2|[17158042]; 141: NM_000982 , "Homo sapiens ribosomal protein L21 (RPL21), mRNA", gi|18104947|ref|NM_000982.2|[18104947]; 142: NM_000993 , "Homo sapiens ribosomal protein L31 (RPL31), mRNA", gi|15812219|ref|NM_000993.2|[15812219]; 143: NM_000994 , "Homo sapiens ribosomal protein L32 (RPL32), mRNA", gi|15812220|ref|NM_000994.2|[15812220]; 144: NM_000995 , "Homo sapiens ribosomal protein L34 (RPL34), transcript variant 1, mRNA", gi|16117786|ref|NM_000995.2|[16117786]; 145: NM_000997 , "Homo sapiens ribosomal protein L37 (RPL37), mRNA", gi|16306560|ref|NM_000997.2|[16306560]; 146: NM_001000 , "Homo sapiens ribosomal protein L39 (RPL39), mRNA", gi|16306563|ref|NM_001000.2|[16306563]; 147: NM_001001 , "Homo sapiens ribosomal protein L36a-like (RPL36AL), mRNA", gi|34335143|ref|NM_001001.3|[34335143]; 148: NM_001003 , "Homo sapiens ribosomal protein, large, P1 (RPLP1), mRNA", gi|16905511|ref|NM_001003.2|[16905511]; 149: NM_001009 , "Homo sapiens ribosomal protein S5 (RPS5), mRNA", gi|13904869|ref|NM_001009.2|[13904869]; 150: NM_001018 , "Homo sapiens ribosomal protein S15 (RPS15), mRNA", gi|14591911|ref|NM_001018.2|[14591911]; 151: NM_001019 , "Homo sapiens ribosomal protein S15a (RPS15A), mRNA", gi|34335150|ref|NM_001019.3|[34335150]; 152: NM_001026 , "Homo sapiens ribosomal protein S24 (RPS24), transcript variant 2, mRNA", gi|14916502|ref|NM_001026.2|[14916502]; 153: NM_001028 , "Homo sapiens ribosomal protein S25 (RPS25), mRNA", gi|14591916|ref|NM_001028.2|[14591916]; 154: NM_001029 , "Homo sapiens ribosomal protein S26 (RPS26), mRNA", gi|15011935|ref|NM_001029.2|[15011935]; 155: NM_001030 , "Homo sapiens ribosomal protein S27 (metallopanstimulin 1) (RPS27), mRNA", gi|15011937|ref|NM_001030.2|[15011937]; 156: NM_001031 , "Homo sapiens ribosomal protein S28 (RPS28), mRNA", gi|15011938|ref|NM_001031.2|[15011938]; 157: NM_001040 , "Homo sapiens sex hormone-binding globulin (SHBG), mRNA", gi|7382459|ref|NM_001040.2|[7382459]; 158: NM_001046 , "Homo sapiens solute carrier family 12 (sodium/potassium/chloride transporters),", "member 2 (SLC12A2), mRNA", gi|38569461|ref|NM_001046.2|[38569461]; 159: NM_001049 , "Homo sapiens somatostatin

receptor 1 (SSTR1), mRNA", gi|33946330|ref|NM_001049.2|[33946330]; 160: NM_001051 , "Homo sapiens somatostatin receptor 3 (SSTR3), mRNA", gi|4557860|ref|NM_001051.1|[4557860]; 161: NM_001057 , "Homo sapiens tachykinin receptor 2 (TACR2), mRNA", gi|4507344|ref|NM_001057.1|[4507344]; 162: NM_001068 , "Homo sapiens topoisomerase (DNA) II beta 180kDa (TOP2B), mRNA", gi|19913407|ref|NM_001068.2|[19913407]; 163: NM_001083 , "Homo sapiens phosphodiesterase 5A, cGMP-specific (PDE5A), transcript variant 1,", mRNA, gi|15812210|ref|NM_001083.2|[15812210]; 164: NM_001087 , "Homo sapiens angio-associated, migratory cell protein (AAMP), mRNA", gi|4557228|ref|NM_001087.1|[4557228]; 165: NM_001090 , "Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 1 (ABCF1), mRNA", gi|10947134|ref|NM_001090.1|[10947134]; 166: NM_001094 , "Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1),", "transcript variant 2, mRNA", gi|34452696|ref|NM_001094.4|[34452696]; 167: NM_001098 , "Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding", "mitochondrial protein, mRNA", gi|4501866|ref|NM_001098.1|[4501866]; 168: NM_001099 , "Homo sapiens acid phosphatase, prostate (ACPP), mRNA", gi|6382063|ref|NM_001099.2|[6382063]; 169: NM_001104 , "Homo sapiens actinin, alpha 3 (ACTN3), mRNA", gi|4557240|ref|NM_001104.1|[4557240]; 170: NM_001105 , "Homo sapiens activin A receptor, type I (ACVR1), mRNA", gi|10862690|ref|NM_001105.2|[10862690]; 171: NM_001117 , "Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) (ADCYAP1),", mRNA, gi|10947062|ref|NM_001117.2|[10947062]; 172: NM_001120 , "Homo sapiens tetracycline transporter-like protein (TETRAN), mRNA", gi|20127439|ref|NM_001120.2|[20127439]; 173: NM_001124 , "Homo sapiens adrenomedullin (ADM), mRNA", gi|4501944|ref|NM_001124.1|[4501944]; 174: NM_001125 , "Homo sapiens ADP-ribosylarginine hydrolase (ADPRH), mRNA", gi|40549393|ref|NM_001125.2|[40549393]; 175: NM_001126 , "Homo sapiens adenylosuccinate synthase (ADSS), mRNA", gi|34577062|ref|NM_001126.2|[34577062]; 176: NM_001127 , "Homo sapiens adaptor-related protein complex 1, beta 1 subunit (AP1B1),", "transcript variant 1, mRNA", gi|22027650|ref|NM_001127.2|[22027650]; 177: NM_001129 , "Homo sapiens AE binding protein 1 (AEBP1), mRNA", gi|4755145|ref|NM_001129.2|[4755145]; 178: NM_001138 , "Homo sapiens agouti related protein homolog (mouse) (AGRP), transcript variant", "1, mRNA", gi|4501994|ref|NM_001138.1|[4501994]; 179: NM_001151 , Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide, "translocator), member 4 (SLC25A4), mRNA", gi|4502096|ref|NM_001151.1|[4502096]; 180: NM_001158 , "Homo sapiens amine oxidase, copper containing 2 (retina-specific) (AOC2),", "transcript variant 1, mRNA", gi|6806880|ref|NM_001158.2|[6806880]; 181: NM_001161 , Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 2, "(NUDT2), transcript variant 1, mRNA", gi|22265329|ref|NM_001161.3|[22265329]; 182: NM_001164 , "Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 1", "(Fe65) (APBB1), transcript variant 1, mRNA", gi|22035552|ref|NM_001164.2|[22035552]; 183: NM_001166 , "Homo sapiens baculoviral IAP repeat-containing 2 (BIRC2), mRNA", gi|41349435|ref|NM_001166.3|[41349435]; 184: NM_001170 , "Homo sapiens aquaporin 7 (AQP7), mRNA", gi|4502186|ref|NM_001170.1|[4502186]; 185: NM_001188 , "Homo sapiens BCL2-antagonist/killer 1 (BAK1), mRNA", gi|33457353|ref|NM_001188.2|[33457353]; 186: NM_001197 , "Homo sapiens BCL2-interacting killer (apoptosis-inducing) (BIK), mRNA", gi|21536418|ref|NM_001197.3|[21536418]; 187: NM_001211 , Homo sapiens BUB1 budding

uninhibited by benzimidazoles 1 homolog beta (yeast), "(BUB1B), mRNA", gi|20149508|ref|NM_001211.3|[20149508]; 188: NM_001231 , "Homo sapiens calsequestrin 1 (fast-twitch, skeletal muscle) (CASQ1), nuclear", "gene encoding mitochondrial protein, mRNA", gi|21536273|ref|NM_001231.2|[21536273]; 189: NM_001237 , "Homo sapiens cyclin A2 (CCNA2), mRNA", gi|16950653|ref|NM_001237.2|[16950653]; 190: NM_001239 , "Homo sapiens cyclin H (CCNH), mRNA", gi|17738313|ref|NM_001239.2|[17738313]; 191: NM_001242 , "Homo sapiens tumor necrosis factor receptor superfamily, member 7 (TNFRSF7),", mRNA, gi|23510435|ref|NM_001242.3|[23510435]; 192: NM_001246 , "Homo sapiens ectonucleoside triphosphate diphosphohydrolase 2 (ENTPD2), mRNA", gi|4557420|ref|NM_001246.1|[4557420]; 193: NM_001255 , "Homo sapiens CDC20 cell division cycle 20 homolog (S. cerevisiae) (CDC20), mRNA", gi|4557436|ref|NM_001255.1|[4557436]; 194: NM_001257 , "Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA", gi|16507956|ref|NM_001257.2|[16507956]; 195: NM_001261 , "Homo sapiens cyclin-dependent kinase 9 (CDC2-related kinase) (CDK9), mRNA", gi|17017983|ref|NM_001261.2|[17017983]; 196: NM_001265 , "Homo sapiens caudal type homeo box transcription factor 2 (CDX2), mRNA", gi|24431948|ref|NM_001265.2|[24431948]; 197: NM_001278 , "Homo sapiens conserved helix-loop-helix ubiquitous kinase (CHUK), mRNA", gi|19923133|ref|NM_001278.2|[19923133]; 198: NM_001286 , "Homo sapiens chloride channel 6 (CLCN6), transcript variant ClC-6a, mRNA", gi|4502872|ref|NM_001286.1|[4502872]; 199: NM_001288 , "Homo sapiens chloride intracellular channel 1 (CLIC1), mRNA", gi|14251208|ref|NM_001288.3|[14251208]; 200: NM_001291 , "Homo sapiens CDC-like kinase 2 (CLK2), transcript variant phclk2/139, mRNA", gi|4557476|ref|NM_001291.1|[4557476]; 201: NM_001293 , "Homo sapiens chloride channel, nucleotide-sensitive, 1A (CLNS1A), mRNA", gi|4502890|ref|NM_001293.1|[4502890]; 202: NM_001303 , "Homo sapiens COX10 homolog, cytochrome c oxidase assembly protein, heme A:", "farnesyltransferase (yeast) (COX10), nuclear gene encoding mitochondrial", "protein, mRNA", gi|17921981|ref|NM_001303.2|[17921981]; 203: NM_001307 , "Homo sapiens claudin 7 (CLDN7), mRNA", gi|34222214|ref|NM_001307.3|[34222214]; 204: NM_001311 , "Homo sapiens cysteine-rich protein 1 (intestinal) (CRIP1), mRNA", gi|39725694|ref|NM_001311.3|[39725694]; 205: NM_001313 , "Homo sapiens collapsin response mediator protein 1 (CRMP1), mRNA", gi|21359849|ref|NM_001313.2|[21359849]; 206: NM_001320 , "Homo sapiens casein kinase 2, beta polypeptide (CSNK2B), mRNA", gi|26787971|ref|NM_001320.5|[26787971]; 207: NM_001326 , "Homo sapiens cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa (CSTF3),", mRNA, gi|4557494|ref|NM_001326.1|[4557494]; 208: NM_001338 , "Homo sapiens coxsackie virus and adenovirus receptor (CXADR), mRNA", gi|20149514|ref|NM_001338.2|[20149514]; 209: NM_001347 , "Homo sapiens diacylglycerol kinase, theta 110kDa (DGKQ), mRNA", gi|40806174|ref|NM_001347.2|[40806174]; 210: NM_001362 , "Homo sapiens deiodinase, iodothyronine, type III (DIO3), mRNA", gi|4503334|ref|NM_001362.1|[4503334]; 211: NM_001374 , "Homo sapiens deoxyribonuclease I-like 2 (DNASE1L2), mRNA", gi|41393584|ref|NM_001374.2|[41393584]; 212: NM_001378 , "Homo sapiens dynein, cytoplasmic, intermediate polypeptide 2 (DNCI2), mRNA", gi|24307878|ref|NM_001378.1|[24307878]; 213: NM_001382 , , ref|NM_001382.2|[42794008]; 214: NM_001384 , "Homo sapiens DPH2-like 2 (S. cerevisiae) (DPH2L2), transcript variant 1, mRNA", gi|41352701|ref|NM_001384.3|[41352701]; 215: NM_001386 , "Homo sapiens dihydropyrimidinase-like 2 (DPYSL2), mRNA", gi|19923654|ref|NM_001386.3|[19923654];

216: NM_001389 , "Homo sapiens Down syndrome cell adhesion molecule (DSCAM), mRNA", gi|20127421|ref|NM_001389.2|[20127421]; 217: NM_001395 , "Homo sapiens dual specificity phosphatase 9 (DUSP9), mRNA", gi|4503420|ref|NM_001395.1|[4503420]; 218: NM_001414 , "Homo sapiens eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa", "(EIF2B1), mRNA", gi|4503502|ref|NM_001414.1|[4503502]; 219: NM_001415 , "Homo sapiens eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa", "(EIF2S3), mRNA", gi|21314612|ref|NM_001415.2|[21314612]; 220: NM_001420 , "Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu", "antigen C) (ELAVL3), mRNA", gi|5231299|ref|NM_001420.2|[5231299]; 221: NM_001424 , "Homo sapiens epithelial membrane protein 2 (EMP2), mRNA", gi|42716292|ref|NM_001424.3|[42716292]; 222: NM_001425 , "Homo sapiens epithelial membrane protein 3 (EMP3), mRNA", gi|4503562|ref|NM_001425.1|[4503562]; 223: NM_001426 , "Homo sapiens engrailed homolog 1 (EN1), mRNA", gi|7710118|ref|NM_001426.2|[7710118]; 224: NM_001430 , "Homo sapiens endothelial PAS domain protein 1 (EPAS1), mRNA", gi|41327154|ref|NM_001430.3|[41327154]; 225: NM_001433 , "Homo sapiens ER to nucleus signalling 1 (ERN1), mRNA", gi|4557568|ref|NM_001433.1|[4557568]; 226: NM_001436 , "Homo sapiens fibrillarin (FBL), mRNA", gi|12056464|ref|NM_001436.2|[12056464]; 227: NM_001450 , "Homo sapiens four and a half LIM domains 2 (FHL2), transcript variant 1, mRNA", gi|42403584|ref|NM_001450.3|[42403584]; 228: NM_001451 , "Homo sapiens forkhead box F1 (FOXF1), mRNA", gi|4503732|ref|NM_001451.1|[4503732]; 229: NM_001454 , "Homo sapiens forkhead box J1 (FOXJ1), mRNA", gi|4557023|ref|NM_001454.1|[4557023]; 230: NM_001467 , "Homo sapiens solute carrier family 37 (glycerol-6-phosphate transporter), member", "4 (SLC37A4), mRNA", gi|21361125|ref|NM_001467.2|[21361125]; 231: NM_001469 , "Homo sapiens thyroid autoantigen 70kDa (Ku antigen) (G22P1), mRNA", gi|20070134|ref|NM_001469.2|[20070134]; 232: NM_001481 , "Homo sapiens growth arrest-specific 8 (GAS8), mRNA", gi|4503916|ref|NM_001481.1|[4503916]; 233: NM_001485 , "Homo sapiens gastrulation brain homeo box 2 (GBX2), mRNA", gi|4503940|ref|NM_001485.1|[4503940]; 234: NM_001486 , "Homo sapiens glucokinase (hexokinase 4) regulatory protein (GCKR), mRNA", gi|30795244|ref|NM_001486.2|[30795244]; 235: NM_001487 , Homo sapiens GCN5 general control of amino-acid synthesis 5-like 1 (yeast), "(GCN5L1), mRNA", gi|4503954|ref|NM_001487.1|[4503954]; 236: NM_001491 , "Homo sapiens glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (GCNT2),", "transcript variant 2, mRNA", gi|30061504|ref|NM_001491.2|[30061504]; 237: NM_001501 , "Homo sapiens gonadotropin-releasing hormone 2 (GNRH2), transcript variant 1,", mRNA, gi|4504056|ref|NM_001501.1|[4504056]; 238: NM_001511 , Homo sapiens chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating, "activity, alpha) (CXCL1), mRNA", gi|4504152|ref|NM_001511.1|[4504152]; 239: NM_001513 , Homo sapiens glutathione transferase zeta 1 (maleylacetoacetate isomerase), "(GSTZ1), transcript variant 3, mRNA", gi|22202621|ref|NM_001513.2|[22202621]; 240: NM_001516 , "Homo sapiens general transcription factor IIH, polypeptide 3, 34kDa (GTF2H3),", mRNA, gi|28376643|ref|NM_001516.3|[28376643]; 241: NM_001517 , , ref|NM_001517.3|[34222289], This record was temporarily removed by RefSeq staff for additional review., , 242: NM_001523 , "Homo sapiens hyaluronan synthase 1 (HAS1), mRNA", gi|4504338|ref|NM_001523.1|[4504338]; 243: NM_001527 , "Homo sapiens histone deacetylase 2 (HDAC2), mRNA", gi|4557640|ref|NM_001527.1|[4557640]; 244: NM_001528 , "Homo sapiens HGF activator (HGFAC), mRNA", gi|32455241|ref|NM_001528.2|[32455241]; 245:

NM_001536 , "Homo sapiens HMT1 hnRNP methyltransferase-like 2 (S. cerevisiae) (HRMT1L2),", "transcript variant 1, mRNA", gi|38195088|ref|NM_001536.2|[38195088]; 246: NM_001538 , "Homo sapiens heat shock transcription factor 4 (HSF4), mRNA", gi|4557650|ref|NM_001538.1|[4557650]; 247: NM_001542 , "Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA", gi|4504626|ref|NM_001542.1|[4504626]; 248: NM_001544 , "Homo sapiens intercellular adhesion molecule 4, Landsteiner-Wiener blood group", "(ICAM4), transcript variant 1, mRNA", gi|12545400|ref|NM_001544.2|[12545400]; 249: NM_001545 , "Homo sapiens immature colon carcinoma transcript 1 (ICT1), mRNA", gi|4557656|ref|NM_001545.1|[4557656]; 250: NM_001562 , "Homo sapiens interleukin 18 (interferon-gamma-inducing factor) (IL18), mRNA", gi|27502389|ref|NM_001562.2|[27502389]; 251: NM_001567 , "Homo sapiens inositol polyphosphate phosphatase-like 1 (INPPL1), mRNA", gi|4755141|ref|NM_001567.2|[4755141]; 252: NM_001569 , "Homo sapiens interleukin-1 receptor-associated kinase 1 (IRAK1), mRNA", gi|4755143|ref|NM_001569.2|[4755143]; 253: NM_001571 , "Homo sapiens interferon regulatory factor 3 (IRF3), mRNA", gi|4504724|ref|NM_001571.1|[4504724]; 254: NM_001585 , "Homo sapiens chromosome 22 open reading frame 1 (C22orf1), mRNA", gi|31542268|ref|NM_001585.2|[31542268]; 255: NM_001610 , "Homo sapiens acid phosphatase 2, lysosomal (ACP2), mRNA", gi|4557009|ref|NM_001610.1|[4557009]; 256: NM_001615 , "Homo sapiens actin, gamma 2, smooth muscle, enteric (ACTG2), mRNA", gi|11038625|ref|NM_001615.2|[11038625]; 257: NM_001616 , "Homo sapiens activin A receptor, type II (ACVR2), mRNA", gi|10862696|ref|NM_001616.2|[10862696]; 258: NM_001618 , Homo sapiens ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase), "(ADPRT), mRNA", gi|11496989|ref|NM_001618.2|[11496989]; 259: NM_001621 , "Homo sapiens aryl hydrocarbon receptor (AHR), mRNA", gi|5016091|ref|NM_001621.2|[5016091]; 260: NM_001622 , "Homo sapiens alpha-2-HS-glycoprotein (AHSG), mRNA", gi|4502004|ref|NM_001622.1|[4502004]; 261: NM_001628 , "Homo sapiens aldo-keto reductase family 1, member B1 (aldose reductase)", "(AKR1B1), mRNA", gi|24497579|ref|NM_001628.2|[24497579]; 262: NM_001629 , "Homo sapiens arachidonate 5-lipoxygenase-activating protein (ALOX5AP), mRNA", gi|15718674|ref|NM_001629.2|[15718674]; 263: NM_001637 , "Homo sapiens acyloxyacyl hydrolase (neutrophil) (AOAH), mRNA", gi|4502114|ref|NM_001637.1|[4502114]; 264: NM_001649 , "Homo sapiens apical protein-like (Xenopus laevis) (APXL), mRNA", gi|18375508|ref|NM_001649.2|[18375508]; 265: NM_001654 , "Homo sapiens v-raf murine sarcoma 3611 viral oncogene homolog 1 (ARAF1), mRNA", gi|4502192|ref|NM_001654.1|[4502192]; 266: NM_001655 , "Homo sapiens archain 1 (ARCN1), mRNA", gi|21626463|ref|NM_001655.3|[21626463]; 267: NM_001662 , "Homo sapiens ADP-ribosylation factor 5 (ARF5), mRNA", gi|6995999|ref|NM_001662.2|[6995999]; 268: NM_001664 , "Homo sapiens ras homolog gene family, member A (ARHA), mRNA", gi|10835048|ref|NM_001664.1|[10835048]; 269: NM_001666 , "Homo sapiens Rho GTPase activating protein 4 (ARHGAP4), mRNA", gi|41327157|ref|NM_001666.2|[41327157]; 270: NM_001671 , "Homo sapiens asialoglycoprotein receptor 1 (ASGR1), mRNA", gi|18426870|ref|NM_001671.2|[18426870]; 271: NM_001673 , "Homo sapiens asparagine synthetase (ASNS), transcript variant 2, mRNA", gi|19718771|ref|NM_001673.2|[19718771]; 272: NM_001674 , "Homo sapiens activating transcription factor 3 (ATF3), mRNA", gi|4502262|ref|NM_001674.1|[4502262]; 273: NM_001675 , Homo sapiens activating transcription factor 4 (tax-responsive enhancer element, "B67) (ATF4), transcript variant 1,

mRNA", gi|33469975|ref|NM_001675.2|[33469975]; 274: NM_001678 , "Homo sapiens ATPase, Na+/K+ transporting, beta 2 polypeptide (ATP1B2), mRNA", gi|40254453|ref|NM_001678.2|[40254453]; 275: NM_001688 , "Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b,", "isoform 1 (ATP5F1), mRNA", gi|21361564|ref|NM_001688.2|[21361564]; 276: NM_001702 , "Homo sapiens brain-specific angiogenesis inhibitor 1 (BAI1), mRNA", gi|4502354|ref|NM_001702.1|[4502354]; 277: NM_001722 , "Homo sapiens polymerase (RNA) III (DNA directed) polypeptide D, 44kDa (POLR3D),", mRNA, gi|4502436|ref|NM_001722.1|[4502436]; 278: NM_001724 , "Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), transcript variant 1, mRNA", gi|40353767|ref|NM_001724.3|[40353767]; 279: NM_001725 , "Homo sapiens bactericidal/permeability-increasing protein (BPI), mRNA", gi|4502446|ref|NM_001725.1|[4502446]; 280: NM_001739 , "Homo sapiens carbonic anhydrase VA, mitochondrial (CA5A), nuclear gene encoding", "mitochondrial protein, mRNA", gi|4502520|ref|NM_001739.1|[4502520]; 281: NM_001744 , "Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4), mRNA", gi|27477118|ref|NM_001744.3|[27477118]; 282: NM_001747 , "Homo sapiens capping protein (actin filament), gelsolin-like (CAPG), mRNA", gi|4502560|ref|NM_001747.1|[4502560]; 283: NM_001760 , "Homo sapiens cyclin D3 (CCND3), mRNA", gi|16950657|ref|NM_001760.2|[16950657]; 284: NM_001769 , "Homo sapiens CD9 antigen (p24) (CD9), mRNA", gi|21237762|ref|NM_001769.2|[21237762]; 285: NM_001780 , "Homo sapiens CD63 antigen (melanoma 1 antigen) (CD63), mRNA", gi|34328936|ref|NM_001780.3|[34328936]; 286: NM_001796 , "Homo sapiens cadherin 8, type 2 (CDH8), mRNA", gi|16306538|ref|NM_001796.2|[16306538]; 287: NM_001799 , "Homo sapiens cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis,", "cdk-activating kinase) (CDK7), mRNA", gi|16950659|ref|NM_001799.2|[16950659]; 288: NM_001806 , "Homo sapiens CCAAT/enhancer binding protein (C/EBP), gamma (CEBPG), mRNA", gi|34452718|ref|NM_001806.2|[34452718]; 289: NM_001810 , "Homo sapiens centromere protein B, 80kDa (CENPB), mRNA", gi|26105977|ref|NM_001810.4|[26105977]; 290: NM_001821 , "Homo sapiens choroideremia-like (Rab escort protein 2) (CHML), mRNA", gi|4502810|ref|NM_001821.1|[4502810]; 291: NM_001823 , "Homo sapiens creatine kinase, brain (CKB), mRNA", gi|34335231|ref|NM_001823.3|[34335231]; 292: NM_001841 , "Homo sapiens cannabinoid receptor 2 (macrophage) (CNR2), mRNA", gi|4502928|ref|NM_001841.1|[4502928]; 293: NM_001842 , "Homo sapiens ciliary neurotrophic factor receptor (CNTFR), transcript variant 2,", mRNA, gi|22212916|ref|NM_001842.3|[22212916]; 294: NM_001843 , "Homo sapiens contactin 1 (CNTN1), transcript variant 1, mRNA", gi|28373116|ref|NM_001843.2|[28373116]; 295: NM_001853 , "Homo sapiens collagen, type IX, alpha 3 (COL9A3), mRNA", gi|17921994|ref|NM_001853.2|[17921994]; 296: NM_001855 , "Homo sapiens collagen, type XV, alpha 1 (COL15A1), mRNA", gi|18641349|ref|NM_001855.2|[18641349]; 297: NM_001856 , "Homo sapiens collagen, type XVI, alpha 1 (COL16A1), mRNA", gi|18641351|ref|NM_001856.2|[18641351]; 298: NM_001859 , "Homo sapiens solute carrier family 31 (copper transporters), member 1 (SLC31A1),", mRNA, gi|40254457|ref|NM_001859.2|[40254457]; 299: NM_001863 , "Homo sapiens cytochrome c oxidase subunit VIb (COX6B), mRNA", gi|17999530|ref|NM_001863.3|[17999530]; 300: NM_001864 , "Homo sapiens cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1),", mRNA, gi|18105034|ref|NM_001864.2|[18105034]; 301: NM_001878 , "Homo

sapiens cellular retinoic acid binding protein 2 (CRABP2), mRNA", gi|6382069|ref|NM_001878.2|[6382069]; 302: NM_001880 , "Homo sapiens activating transcription factor 2 (ATF2), mRNA", gi|22538421|ref|NM_001880.2|[22538421]; 303: NM_001885 , "Homo sapiens crystallin, alpha B (CRYAB), mRNA", gi|4503056|ref|NM_001885.1|[4503056]; 304: NM_001887 , "Homo sapiens crystallin, beta B1 (CRYBB1), mRNA", gi|21536279|ref|NM_001887.3|[21536279]; 305: NM_001889 , "Homo sapiens crystallin, zeta (quinone reductase) (CRYZ), mRNA", gi|14251216|ref|NM_001889.2|[14251216]; 306: NM_001893 , "Homo sapiens casein kinase 1, delta (CSNK1D), transcript variant 1, mRNA", gi|20544143|ref|NM_001893.3|[20544143]; 307: NM_001895 , "Homo sapiens casein kinase 2, alpha 1 polypeptide (CSNK2A1), transcript variant", "2, mRNA", gi|29570794|ref|NM_001895.2|[29570794]; 308: NM_001905 , "Homo sapiens CTP synthase (CTPS), mRNA", gi|4503132|ref|NM_001905.1|[4503132]; 309: NM_001917 , "Homo sapiens D-amino-acid oxidase (DAO), mRNA", gi|21536469|ref|NM_001917.3|[21536469]; 310: NM_001923 , "Homo sapiens damage-specific DNA binding protein 1, 127kDa (DDB1), mRNA", gi|13435358|ref|NM_001923.2|[13435358]; 311: NM_001924 , "Homo sapiens growth arrest and DNA-damage-inducible, alpha (GADD45A), mRNA", gi|9790904|ref|NM_001924.2|[9790904]; 312: NM_001928 , "Homo sapiens D component of complement (adipsin) (DF), mRNA", gi|42544238|ref|NM_001928.2|[42544238]; 313: NM_001932 , "Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)", "(MPP3), mRNA", gi|21536463|ref|NM_001932.2|[21536463]; 314: NM_001933 , Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of, "2-oxo-glutarate complex) (DLST), mRNA", gi|32307170|ref|NM_001933.3|[32307170]; 315: NM_001944 , "Homo sapiens desmoglein 3 (pemphigus vulgaris antigen) (DSG3), mRNA", gi|4503404|ref|NM_001944.1|[4503404]; 316: NM_001955 , "Homo sapiens endothelin 1 (EDN1), mRNA", gi|21359861|ref|NM_001955.2|[21359861]; 317: NM_001958 , "Homo sapiens eukaryotic translation elongation factor 1 alpha 2 (EEF1A2), mRNA", gi|25453470|ref|NM_001958.2|[25453470]; 318: NM_001959 , "Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2),", "transcript variant 1, mRNA", gi|16519564|ref|NM_001959.2|[16519564]; 319: NM_001962 , "Homo sapiens ephrin-A5 (EFNA5), mRNA", gi|4503486|ref|NM_001962.1|[4503486]; 320: NM_001967 , "Homo sapiens eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2),", mRNA, gi|9945313|ref|NM_001967.2|[9945313]; 321: NM_001974 , "Homo sapiens egf-like module containing, mucin-like, hormone receptor-like 1", "(EMR1), mRNA", gi|40807488|ref|NM_001974.3|[40807488]; 322: NM_001978 , "Homo sapiens erythrocyte membrane protein band 4.9 (dematin) (EPB49), mRNA", gi|4503580|ref|NM_001978.1|[4503580]; 323: NM_001985 , "Homo sapiens electron-transfer-flavoprotein, beta polypeptide (ETFB), mRNA", gi|4503608|ref|NM_001985.1|[4503608]; 324: NM_001989 , "Homo sapiens eve, even-skipped homeo box homolog 1 (Drosophila) (EVX1), mRNA", gi|24497610|ref|NM_001989.2|[24497610]; 325: NM_001990 , "Homo sapiens eyes absent homolog 3 (Drosophila) (EYA3), transcript variant 1,", mRNA, gi|26667242|ref|NM_001990.2|[26667242]; 326: NM_001992 , "Homo sapiens coagulation factor II (thrombin) receptor (F2R), mRNA", gi|6031164|ref|NM_001992.2|[6031164]; 327: NM_002004 , "Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase,", "dimethylallyltranstransferase, geranyltranstransferase) (FDPS), mRNA", gi|41281370|ref|NM_002004.2|[41281370]; 328: NM_002005 , "Homo sapiens feline sarcoma

oncogene (FES), mRNA", gi|13376997|ref|NM_002005.2|[13376997]; 329: NM_002010 , "Homo sapiens fibroblast growth factor 9 (glia-activating factor) (FGF9), mRNA", gi|4503706|ref|NM_002010.1|[4503706]; 330: NM_002012 , "Homo sapiens fragile histidine triad gene (FHIT), mRNA", gi|4503718|ref|NM_002012.1|[4503718]; 331: NM_002020 , "Homo sapiens fms-related tyrosine kinase 4 (FLT4), transcript variant 2, mRNA", gi|4503752|ref|NM_002020.1|[4503752]; 332: NM_002022 , "Homo sapiens flavin containing monooxygenase 4 (FMO4), mRNA", gi|4503758|ref|NM_002022.1|[4503758]; 333: NM_002032 , "Homo sapiens ferritin, heavy polypeptide 1 (FTH1), mRNA", gi|4503794|ref|NM_002032.1|[4503794]; 334: NM_002041 , "Homo sapiens GA binding protein transcription factor, beta subunit 2, 47kDa", "(GABPB2), transcript variant gamma-1, mRNA", gi|8051596|ref|NM_002041.2|[8051596]; 335: NM_002044 , "Homo sapiens galactokinase 2 (GALK2), mRNA", gi|4503896|ref|NM_002044.1|[4503896]; 336: NM_002047 , "Homo sapiens glycyl-tRNA synthetase (GARS), mRNA", gi|6996009|ref|NM_002047.1|[6996009]; 337: NM_002052 , "Homo sapiens GATA binding protein 4 (GATA4), mRNA", gi|33188460|ref|NM_002052.2|[33188460]; 338: NM_002083 , "Homo sapiens glutathione peroxidase 2 (gastrointestinal) (GPX2), mRNA", gi|32967606|ref|NM_002083.2|[32967606]; 339: NM_002086 , "Homo sapiens growth factor receptor-bound protein 2 (GRB2), mRNA", gi|34452726|ref|NM_002086.2|[34452726]; 340: NM_002093 , "Homo sapiens glycogen synthase kinase 3 beta (GSK3B), mRNA", gi|21361339|ref|NM_002093.2|[21361339]; 341: NM_002095 , "Homo sapiens general transcription factor IIE, polypeptide 2, beta 34kDa", "(GTF2E2), mRNA", gi|34222295|ref|NM_002095.3|[34222295]; 342: NM_002110 , "Homo sapiens hemopoietic cell kinase (HCK), mRNA", gi|30795228|ref|NM_002110.2|[30795228]; 343: NM_002115 , "Homo sapiens hexokinase 3 (white cell) (HK3), nuclear gene encoding", "mitochondrial protein, mRNA", gi|4504394|ref|NM_002115.1|[4504394]; 344: NM_002137 , "Homo sapiens heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1),", "transcript variant A2, mRNA", gi|14043073|ref|NM_002137.2|[14043073]; 345: NM_002148 , "Homo sapiens homeo box D10 (HOXD10), mRNA", gi|23510365|ref|NM_002148.2|[23510365]; 346: NM_002151 , "Homo sapiens hepsin (transmembrane protease, serine 1) (HPN), transcript variant", "2, mRNA", gi|4504480|ref|NM_002151.1|[4504480]; 347: NM_002152 , "Homo sapiens histidine rich calcium binding protein (HRC), mRNA", gi|4504486|ref|NM_002152.1|[4504486]; 348: NM_002157 , "Homo sapiens heat shock 10kDa protein 1 (chaperonin 10) (HSPE1), mRNA", gi|4504522|ref|NM_002157.1|[4504522]; 349: NM_002158 , "Homo sapiens human T-cell leukemia virus enhancer factor (HTLF), mRNA", gi|40549453|ref|NM_002158.2|[40549453]; 350: NM_002162 , "Homo sapiens intercellular adhesion molecule 3 (ICAM3), mRNA", gi|12545399|ref|NM_002162.2|[12545399]; 351: NM_002193 , "Homo sapiens inhibin, beta B (activin AB beta polypeptide) (INHBB), mRNA", gi|9257224|ref|NM_002193.1|[9257224]; 352: NM_002194 , "Homo sapiens inositol polyphosphate-1-phosphatase (INPP1), mRNA", gi|4755138|ref|NM_002194.2|[4755138]; 353: NM_002196 , "Homo sapiens insulinoma-associated 1 (INSM1), mRNA", gi|4504712|ref|NM_002196.1|[4504712]; 354: NM_002198 , "Homo sapiens interferon regulatory factor 1 (IRF1), mRNA", gi|4504720|ref|NM_002198.1|[4504720]; 355: NM_002199 , "Homo sapiens interferon regulatory factor 2 (IRF2), mRNA", gi|4755144|ref|NM_002199.2|[4755144]; 356: NM_002210 , "Homo sapiens integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen", "CD51) (ITGAV), mRNA", gi|40217844|ref|NM_002210.2|[40217844]; 357: NM_002212 , "Homo sapiens integrin beta 4 binding protein (ITGB4BP), transcript variant 1,", mRNA,

gi|31563381|ref|NM_002212.2|[31563381]; 358: NM_002217 , "Homo sapiens pre-alpha (globulin) inhibitor, H3 polypeptide (ITIH3), mRNA", gi|10092578|ref|NM_002217.1|[10092578]; 359: NM_002221 , "Homo sapiens inositol 1,4,5-trisphosphate 3-kinase B (ITPKB), mRNA", gi|38569399|ref|NM_002221.2|[38569399]; 360: NM_002229 , "Homo sapiens jun B proto-oncogene (JUNB), mRNA", gi|4504808|ref|NM_002229.1|[4504808]; 361: NM_002231 , "Homo sapiens kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen", "(R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4)) (KAI1),", mRNA, gi|13259537|ref|NM_002231.2|[13259537]; 362: NM_002232 , "Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 3", "(KCNA3), mRNA", gi|25952081|ref|NM_002232.2|[25952081]; 363: NM_002238 , "Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member", "1 (KCNH1), transcript variant 2, mRNA", gi|27436999|ref|NM_002238.2|[27436999]; 364: NM_002241 , "Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 10", "(KCNJ10), mRNA", gi|25121965|ref|NM_002241.2|[25121965]; 365: NM_002248 , "Homo sapiens potassium intermediate/small conductance calcium-activated channel,", "subfamily N, member 1 (KCNN1), mRNA", gi|25777642|ref|NM_002248.3|[25777642]; 366: NM_002252 , "Homo sapiens potassium voltage-gated channel, delayed-rectifier, subfamily S,", "member 3 (KCNS3), mRNA", gi|25952107|ref|NM_002252.3|[25952107]; 367: NM_002257 , "Homo sapiens kallikrein 1, renal/pancreas/salivary (KLK1), mRNA", gi|22027643|ref|NM_002257.2|[22027643]; 368: NM_002268 , "Homo sapiens karyopherin alpha 4 (importin alpha 3) (KPNA4), mRNA", gi|27477125|ref|NM_002268.3|[27477125]; 369: NM_002277 , "Homo sapiens keratin, hair, acidic, 1 (KRTHA1), mRNA", gi|14917114|ref|NM_002277.2|[14917114]; 370: NM_002280 , "Homo sapiens keratin, hair, acidic, 5 (KRTHA5), mRNA", gi|15431313|ref|NM_002280.3|[15431313]; 371: NM_002283 , "Homo sapiens keratin, hair, basic, 5 (KRTHB5), mRNA", gi|15431324|ref|NM_002283.2|[15431324]; 372: NM_002286 , "Homo sapiens lymphocyte-activation gene 3 (LAG3), mRNA", gi|15718681|ref|NM_002286.4|[15718681]; 373: NM_002298 , "Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA", gi|7382490|ref|NM_002298.2|[7382490]; 374: NM_002305 , "Homo sapiens lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA", gi|6006015|ref|NM_002305.2|[6006015]; 375: NM_002309 , Homo sapiens leukemia inhibitory factor (cholinergic differentiation factor), "(LIF), mRNA", gi|6006018|ref|NM_002309.2|[6006018]; 376: NM_002312 , "Homo sapiens ligase IV, DNA, ATP-dependent (LIG4), mRNA", gi|23199992|ref|NM_002312.2|[23199992]; 377: NM_002316 , "Homo sapiens LIM homeobox transcription factor 1, beta (LMX1B), mRNA", gi|4505006|ref|NM_002316.1|[4505006]; 378: NM_002335 , "Homo sapiens low density lipoprotein receptor-related protein 5 (LRP5), mRNA", gi|4505018|ref|NM_002335.1|[4505018]; 379: NM_002339 , "Homo sapiens lymphocyte-specific protein 1 (LSP1), mRNA", gi|10880978|ref|NM_002339.1|[10880978]; 380: NM_002342 , "Homo sapiens lymphotoxin beta receptor (TNFR superfamily, member 3) (LTBR), mRNA", gi|4505038|ref|NM_002342.1|[4505038]; 381: NM_002347 , "Homo sapiens lymphocyte antigen 6 complex, locus H (LY6H), mRNA", gi|4505050|ref|NM_002347.1|[4505050]; 382: NM_002357 , "Homo sapiens MAX dimerization protein 1 (MAD), mRNA", gi|4505068|ref|NM_002357.1|[4505068]; 383: NM_002372 , "Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA", gi|4758697|ref|NM_002372.1|[4758697]; 384: NM_002378 , "Homo sapiens megakaryocyte-

associated tyrosine kinase (MATK), transcript variant", "2, mRNA", gi|21450841|ref|NM_002378.2|[21450841]; 385: NM_002381 , "Homo sapiens matrilin 3 (MATN3), mRNA", gi|13518040|ref|NM_002381.2|[13518040]; 386: NM_002386 , Homo sapiens melanocortin 1 receptor (alpha melanocyte stimulating hormone, "receptor) (MC1R), mRNA", gi|27477128|ref|NM_002386.2|[27477128]; 387: NM_002388 , "Homo sapiens MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) (MCM3),", mRNA, gi|33356548|ref|NM_002388.3|[33356548]; 388: NM_002390 , "Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11), transcript", "variant 1, mRNA", gi|4585709|ref|NM_002390.2|[4585709]; 389: NM_002391 , "Homo sapiens midkine (neurite growth-promoting factor 2) (MDK), mRNA", gi|24475622|ref|NM_002391.2|[24475622]; 390: NM_002393 , "Homo sapiens Mdm4, transformed 3T3 cell double minute 4, p53 binding protein", "(mouse) (MDM4), mRNA", gi|4505138|ref|NM_002393.1|[4505138]; 391: NM_002398 , "Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse)", "(MEIS1), mRNA", gi|4505150|ref|NM_002398.1|[4505150]; 392: NM_002399 , "Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse)", "(MEIS2), transcript variant f, mRNA", gi|27502374|ref|NM_002399.2|[27502374]; 393: NM_002401 , , ref|NM_002401.3|[42794764]; 394: NM_002406 , "Homo sapiens mannosyl (alpha-1,3-)-glycoprotein", "beta-1,2-N-acetylglucosaminyltransferase (MGAT1), mRNA", gi|6031182|ref|NM_002406.2|[6031182]; 395: NM_002412 , "Homo sapiens O-6-methylguanine-DNA methyltransferase (MGMT), mRNA", gi|4505176|ref|NM_002412.1|[4505176]; 396: NM_002419 , "Homo sapiens mitogen-activated protein kinase kinase kinase 11 (MAP3K11), mRNA", gi|21735553|ref|NM_002419.2|[21735553]; 397: NM_002427 , "Homo sapiens matrix metalloproteinase 13 (collagenase 3) (MMP13), mRNA", gi|13027796|ref|NM_002427.2|[13027796]; 398: NM_002428 , "Homo sapiens matrix metalloproteinase 15 (membrane-inserted) (MMP15), mRNA", gi|4505210|ref|NM_002428.1|[4505210]; 399: NM_002434 , "Homo sapiens N-methylpurine-DNA glycosylase (MPG), mRNA", gi|4505232|ref|NM_002434.1|[4505232]; 400: NM_002437 , "Homo sapiens MpV17 transgene, murine homolog, glomerulosclerosis (MPV17), mRNA", gi|37059781|ref|NM_002437.3|[37059781]; 401: NM_002446 , "Homo sapiens mitogen-activated protein kinase kinase kinase 10 (MAP3K10), mRNA", gi|21735549|ref|NM_002446.2|[21735549]; 402: NM_002447 , Homo sapiens macrophage stimulating 1 receptor (c-met-related tyrosine kinase), "(MST1R), mRNA", gi|4505264|ref|NM_002447.1|[4505264]; 403: NM_002452 , Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 1, "(NUDT1), transcript variant 1, mRNA", gi|40288273|ref|NM_002452.3|[40288273]; 404: NM_002453 , "Homo sapiens mitochondrial translational initiation factor 2 (MTIF2), nuclear", "gene encoding mitochondrial protein, mRNA", gi|4505276|ref|NM_002453.1|[4505276]; 405: NM_002461 , "Homo sapiens mevalonate (diphospho) decarboxylase (MVD), mRNA", gi|4505288|ref|NM_002461.1|[4505288]; 406: NM_002470 , "Homo sapiens myosin, heavy polypeptide 3, skeletal muscle, embryonic (MYH3),", mRNA, gi|11342671|ref|NM_002470.1|[11342671]; 407: NM_002471 , "Homo sapiens myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy,", "hypertrophic 1) (MYH6), mRNA", gi|27764860|ref|NM_002471.1|[27764860]; 408: NM_002475 , "Homo sapiens myosin light chain 1 slow a (MLC1SA), mRNA", gi|17986280|ref|NM_002475.2|[17986280]; 409: NM_002487 , "Homo sapiens necdin homolog (mouse) (NDN), mRNA",

gi|10800414|ref|NM_002487.2|[10800414]; 410: NM_002492 , "Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa", "(NDUFB5), nuclear gene encoding mitochondrial protein, mRNA", gi|33519467|ref|NM_002492.2|[33519467]; 411: NM_002500 , "Homo sapiens neurogenic differentiation 1 (NEUROD1), mRNA", gi|4505376|ref|NM_002500.1|[4505376]; 412: NM_002506 , "Homo sapiens nerve growth factor, beta polypeptide (NGFB), mRNA", gi|4505390|ref|NM_002506.1|[4505390]; 413: NM_002513 , "Homo sapiens non-metastatic cells 3, protein expressed in (NME3), mRNA", gi|37693992|ref|NM_002513.2|[37693992]; 414: NM_002522 , "Homo sapiens neuronal pentraxin I (NPTX1), mRNA", gi|4505442|ref|NM_002522.1|[4505442]; 415: NM_002525 , "Homo sapiens nardilysin (N-arginine dibasic convertase) (NRD1), mRNA", gi|4505452|ref|NM_002525.1|[4505452]; 416: NM_002528 , "Homo sapiens nth endonuclease III-like 1 (E. coli) (NTHL1), mRNA", gi|38455392|ref|NM_002528.4|[38455392]; 417: NM_002529 , "Homo sapiens neurotrophic tyrosine kinase, receptor, type 1 (NTRK1), mRNA", gi|4585711|ref|NM_002529.2|[4585711]; 418: NM_002531 , "Homo sapiens neurotensin receptor 1 (high affinity) (NTSR1), mRNA", gi|4505476|ref|NM_002531.1|[4505476]; 419: NM_002555 , "Homo sapiens solute carrier family 22 (organic cation transporter), member 18", "(SLC22A18), transcript variant 1, mRNA", gi|34734074|ref|NM_002555.3|[34734074]; 420: NM_002559 , "Homo sapiens purinergic receptor P2X, ligand-gated ion channel, 3 (P2RX3), mRNA", gi|28416924|ref|NM_002559.2|[28416924]; 421: NM_002560 , "Homo sapiens purinergic receptor P2X, ligand-gated ion channel, 4 (P2RX4),", "transcript variant 1, mRNA", gi|28416926|ref|NM_002560.2|[28416926]; 422: NM_002562 , "Homo sapiens purinergic receptor P2X, ligand-gated ion channel, 7 (P2RX7),", "transcript variant 1, mRNA", gi|34335273|ref|NM_002562.4|[34335273]; 423: NM_002563 , "Homo sapiens purinergic receptor P2Y, G-protein coupled, 1 (P2RY1), mRNA", gi|28872741|ref|NM_002563.2|[28872741]; 424: NM_002566 , "Homo sapiens purinergic receptor P2Y, G-protein coupled, 11 (P2RY11), mRNA", gi|29029602|ref|NM_002566.3|[29029602]; 425: NM_002568 , "Homo sapiens poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA", gi|4505574|ref|NM_002568.1|[4505574]; 426: NM_002569 , "Homo sapiens furin (paired basic amino acid cleaving enzyme) (FURIN), mRNA", gi|20336193|ref|NM_002569.2|[20336193]; 427: NM_002572 , "Homo sapiens platelet-activating factor acetylhydrolase, isoform Ib, beta", "subunit 30kDa (PAFAH1B2), mRNA", gi|4505584|ref|NM_002572.1|[4505584]; 428: NM_002576 , , ref|NM_002576.3|[42794768]; 429: NM_002582 , "Homo sapiens poly(A)-specific ribonuclease (deadenylation nuclease) (PARN), mRNA", gi|4505610|ref|NM_002582.1|[4505610]; 430: NM_002584 , "Homo sapiens paired box gene 7 (PAX7), transcript variant 1, mRNA", gi|4505618|ref|NM_002584.1|[4505618]; 431: NM_002590 , "Homo sapiens protocadherin 8 (PCDH8), transcript variant 1, mRNA", gi|6631101|ref|NM_002590.2|[6631101]; 432: NM_002591 , "Homo sapiens phosphoenolpyruvate carboxykinase 1 (soluble) (PCK1), mRNA", gi|32483400|ref|NM_002591.2|[32483400]; 433: NM_002599 , "Homo sapiens phosphodiesterase 2A, cGMP-stimulated (PDE2A), mRNA", gi|4505656|ref|NM_002599.1|[4505656]; 434: NM_002615 , "Homo sapiens serine (or cysteine) proteinase inhibitor, clade F (alpha-2", "antiplasmin, pigment epithelium derived factor), member 1 (SERPINF1), mRNA", gi|39725933|ref|NM_002615.3|[39725933]; 435: NM_002618 , "Homo sapiens peroxisome biogenesis factor 13 (PEX13), mRNA", gi|4505722|ref|NM_002618.1|[4505722]; 436: NM_002620 , "Homo sapiens platelet factor 4 variant 1 (PF4V1), mRNA", gi|4505734|ref|NM_002620.1|[4505734]; 437: NM_002628 ,

"Homo sapiens profilin 2 (PFN2), transcript variant 2, mRNA", gi|16753216|ref|NM_002628.2|[16753216]; 438: NM_002630 , "Homo sapiens progastricsin (pepsinogen C) (PGC), mRNA", gi|4505756|ref|NM_002630.1|[4505756]; 439: NM_002635 , Homo sapiens solute carrier family 25 (mitochondrial carrier; phosphate, "carrier), member 3 (SLC25A3), nuclear gene encoding mitochondrial protein,", "transcript variant 1b, mRNA", gi|4505774|ref|NM_002635.1|[4505774]; 440: NM_002639 , "Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin),", "member 5 (SERPINB5), mRNA", gi|4505788|ref|NM_002639.1|[4505788]; 441: NM_002640 , "Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin),", "member 8 (SERPINB8), transcript variant 1, mRNA", gi|38504672|ref|NM_002640.3|[38504672]; 442: NM_002641 , "Homo sapiens phosphatidylinositol glycan, class A (paroxysmal nocturnal", "hemoglobinuria) (PIGA), transcript variant 1, mRNA", gi|11863129|ref|NM_002641.1|[11863129]; 443: NM_002648 , "Homo sapiens pim-1 oncogene (PIM1), mRNA", gi|31543400|ref|NM_002648.2|[31543400]; 444: NM_002654 , "Homo sapiens pyruvate kinase, muscle (PKM2), transcript variant 1, mRNA", gi|33286417|ref|NM_002654.3|[33286417]; 445: NM_002655 , "Homo sapiens pleiomorphic adenoma gene 1 (PLAG1), mRNA", gi|4505854|ref|NM_002655.1|[4505854]; 446: NM_002676 , "Homo sapiens phosphomannomutase 1 (PMM1), mRNA", gi|4505904|ref|NM_002676.1|[4505904]; 447: NM_002692 , "Homo sapiens polymerase (DNA directed), epsilon 2 (p59 subunit) (POLE2), mRNA", gi|32189368|ref|NM_002692.2|[32189368]; 448: NM_002697 , "Homo sapiens POU domain, class 2, transcription factor 1 (POU2F1), mRNA", gi|42476163|ref|NM_002697.2|[42476163]; 449: NM_002707 , "Homo sapiens protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma", "isoform (PPM1G), transcript variant 2, mRNA", gi|29826283|ref|NM_002707.3|[29826283]; 450: NM_002708 , "Homo sapiens protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA),", mRNA, gi|31543430|ref|NM_002708.2|[31543430]; 451: NM_002715 , "Homo sapiens protein phosphatase 2 (formerly 2A), catalytic subunit, alpha", "isoform (PPP2CA), mRNA", gi|4506016|ref|NM_002715.1|[4506016]; 452: NM_002728 , "Homo sapiens proteoglycan 2, bone marrow (natural killer cell activator,", "eosinophil granule major basic protein) (PRG2), mRNA", gi|32261294|ref|NM_002728.3|[32261294]; 453: NM_002739 , "Homo sapiens protein kinase C, gamma (PRKCG), mRNA", gi|31377808|ref|NM_002739.2|[31377808]; 454: NM_002763 , "Homo sapiens prospero-related homeobox 1 (PROX1), mRNA", gi|34147628|ref|NM_002763.3|[34147628]; 455: NM_002766 , Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 1, "(PRPSAP1), mRNA", gi|4506130|ref|NM_002766.1|[4506130]; 456: NM_002768 , "Homo sapiens procollagen (type III) N-endopeptidase (PCOLN3), mRNA", gi|4506138|ref|NM_002768.1|[4506138]; 457: NM_002774 , "Homo sapiens kallikrein 6 (neurosin, zyme) (KLK6), mRNA", gi|21327702|ref|NM_002774.2|[21327702]; 458: NM_002779 , "Homo sapiens pleckstrin and Sec7 domain protein (PSD), mRNA", gi|28626518|ref|NM_002779.2|[28626518]; 459: NM_002789 , "Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 4 (PSMA4),", mRNA, gi|23110940|ref|NM_002789.3|[23110940]; 460: NM_002790 , "Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5),", mRNA, gi|23110941|ref|NM_002790.2|[23110941]; 461: NM_002791 , "Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 6 (PSMA6),", mRNA, gi|23110943|ref|NM_002791.1|[23110943]; 462: NM_002795 , "Homo sapiens proteasome (prosome, macropain) subunit, beta type, 3 (PSMB3), mRNA",

gi|22538464|ref|NM_002795.2|[22538464]; 463: NM_002799 , "Homo sapiens proteasome (prosome, macropain) subunit, beta type, 7 (PSMB7), mRNA", gi|23110926|ref|NM_002799.2|[23110926]; 464: NM_002800 , "Homo sapiens proteasome (prosome, macropain) subunit, beta type, 9 (large", "multifunctional protease 2) (PSMB9), transcript variant 1, mRNA", gi|23110930|ref|NM_002800.3|[23110930]; 465: NM_002802 , "Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 1 (PSMC1),", mRNA, gi|24430150|ref|NM_002802.2|[24430150]; 466: NM_002805 , "Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 5 (PSMC5),", mRNA, gi|24497434|ref|NM_002805.4|[24497434]; 467: NM_002818 , "Homo sapiens proteasome (prosome, macropain) activator subunit 2 (PA28 beta)", "(PSME2), mRNA", gi|30410791|ref|NM_002818.2|[30410791]; 468: NM_002821 , "Homo sapiens PTK7 protein tyrosine kinase 7 (PTK7), transcript variant PTK7-1,", mRNA, gi|27886610|ref|NM_002821.3|[27886610]; 469: NM_002826 , "Homo sapiens quiescin Q6 (QSCN6), mRNA", gi|13325074|ref|NM_002826.2|[13325074]; 470: NM_002831 , "Homo sapiens protein tyrosine phosphatase, non-receptor type 6 (PTPN6),", "transcript variant 1, mRNA", gi|34328900|ref|NM_002831.3|[34328900]; 471: NM_002832 , "Homo sapiens protein tyrosine phosphatase, non-receptor type 7 (PTPN7),", "transcript variant 1, mRNA", gi|18375657|ref|NM_002832.2|[18375657]; 472: NM_002833 , "Homo sapiens protein tyrosine phosphatase, non-receptor type 9 (PTPN9), mRNA", gi|18375663|ref|NM_002833.2|[18375663]; 473: NM_002837 , "Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), mRNA", gi|18491009|ref|NM_002837.2|[18491009]; 474: NM_002841 , "Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA", gi|18860897|ref|NM_002841.2|[18860897]; 475: NM_002845 , "Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA", gi|18860903|ref|NM_002845.2|[18860903]; 476: NM_002851 , "Homo sapiens protein tyrosine phosphatase, receptor-type, Z polypeptide 1", "(PTPRZ1), mRNA", gi|4506328|ref|NM_002851.1|[4506328]; 477: NM_002854 , "Homo sapiens parvalbumin (PVALB), mRNA", gi|4506334|ref|NM_002854.1|[4506334]; 478: NM_002856 , Homo sapiens poliovirus receptor-related 2 (herpesvirus entry mediator B), "(PVRL2), mRNA", gi|5360209|ref|NM_002856.1|[5360209]; 479: NM_002860 , Homo sapiens pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde, "synthetase) (PYCS), mRNA", gi|21361367|ref|NM_002860.2|[21361367]; 480: NM_002863 , "Homo sapiens phosphorylase, glycogen; liver (Hers disease, glycogen storage", "disease type VI) (PYGL), mRNA", gi|42476165|ref|NM_002863.2|[42476165]; 481: NM_002868 , "Homo sapiens RAB5B, member RAS oncogene family (RAB5B), mRNA", gi|33943097|ref|NM_002868.2|[33943097]; 482: NM_002887 , "Homo sapiens arginyl-tRNA synthetase (RARS), mRNA", gi|40068503|ref|NM_002887.3|[40068503]; 483: NM_002891 , Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1, "(RASGRF1), transcript variant 1, mRNA", gi|24797098|ref|NM_002891.3|[24797098]; 484: NM_002892 , "Homo sapiens AT rich interactive domain 4A (RBP1-like) (ARID4A), transcript", "variant 1, mRNA", gi|13259496|ref|NM_002892.2|[13259496]; 485: NM_002900 , "Homo sapiens retinol binding protein 3, interstitial (RBP3), mRNA", gi|4506452|ref|NM_002900.1|[4506452]; 486: NM_002901 , "Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA", gi|4506454|ref|NM_002901.1|[4506454]; 487: NM_002904 , "Homo sapiens RD RNA binding protein (RDBP), mRNA", gi|20631983|ref|NM_002904.4|[20631983]; 488: NM_002912 , "Homo sapiens REV3-like, catalytic subunit of DNA polymerase zeta (yeast)", "(REV3L), mRNA", gi|4506482|ref|NM_002912.1|[4506482]; 489: NM_002916 , "Homo sapiens

replication factor C (activator 1) 4, 37kDa (RFC4), transcript", "variant 1, mRNA", gi|31881681|ref|NM_002916.3|[31881681]; 490: NM_002919 , "Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3),", "transcript variant 1, mRNA", gi|19743882|ref|NM_002919.2|[19743882]; 491: NM_002921 , "Homo sapiens retinal G protein coupled receptor (RGR), mRNA", gi|21361328|ref|NM_002921.2|[21361328]; 492: NM_002923 , "Homo sapiens regulator of G-protein signalling 2, 24kDa (RGS2), mRNA", gi|4506516|ref|NM_002923.1|[4506516]; 493: NM_002930 , "Homo sapiens Ras-like without CAAX 2 (RIT2), mRNA", gi|4506532|ref|NM_002930.1|[4506532]; 494: NM_002938 , "Homo sapiens ring finger protein 4 (RNF4), mRNA", gi|34305289|ref|NM_002938.2|[34305289]; 495: NM_002941 , "Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1),", "transcript variant 1, mRNA", gi|19743804|ref|NM_002941.2|[19743804]; 496: NM_002946 , "Homo sapiens replication protein A2, 32kDa (RPA2), mRNA", gi|34147622|ref|NM_002946.3|[34147622]; 497: NM_002954 , "Homo sapiens ribosomal protein S27a (RPS27A), mRNA", gi|27436941|ref|NM_002954.3|[27436941]; 498: NM_002965 , "Homo sapiens S100 calcium binding protein A9 (calgranulin B) (S100A9), mRNA", gi|9845520|ref|NM_002965.2|[9845520]; 499: NM_002966 , "Homo sapiens S100 calcium binding protein A10 (annexin II ligand, calpactin I,", "light polypeptide (p11)) (S100A10), mRNA", gi|4506760|ref|NM_002966.1|[4506760]; 500: NM_002968 , "Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA", gi|6997248|ref|NM_002968.1|[6997248]; 501: NM_002971 , Homo sapiens special AT-rich sequence binding protein 1 (binds to nuclear, "matrix/scaffold-associating DNA's) (SATB1), mRNA", gi|33356175|ref|NM_002971.2|[33356175]; 502: NM_002973 , "Homo sapiens spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal", "dominant, ataxin 2) (SCA2), mRNA", gi|4506794|ref|NM_002973.1|[4506794]; 503: NM_002987 , "Homo sapiens chemokine (C-C motif) ligand 17 (CCL17), mRNA", gi|22538801|ref|NM_002987.2|[22538801]; 504: NM_003002 , "Homo sapiens succinate dehydrogenase complex, subunit D, integral membrane", "protein (SDHD), nuclear gene encoding mitochondrial protein, mRNA", gi|4506864|ref|NM_003002.1|[4506864]; 505: NM_003025 , "Homo sapiens SH3-domain GRB2-like 1 (SH3GL1), mRNA", gi|42476326|ref|NM_003025.2|[42476326]; 506: NM_003028 , "Homo sapiens SHB (Src homology 2 domain containing) adaptor protein B (SHB),", mRNA, gi|4506934|ref|NM_003028.1|[4506934]; 507: NM_003034 , Homo sapiens sialyltransferase 8A (alpha-N-acetylneuraminate:, "alpha-2,8-sialyltransferase, GD3 synthase) (SIAT8A), mRNA", gi|28373095|ref|NM_003034.2|[28373095]; 508: NM_003035 , "Homo sapiens TAL1 (SCL) interrupting locus (SIL), mRNA", gi|4506958|ref|NM_003035.1|[4506958]; 509: NM_003040 , "Homo sapiens solute carrier family 4, anion exchanger, member 2 (erythrocyte", "membrane protein band 3-like 1) (SLC4A2), mRNA", gi|21361550|ref|NM_003040.2|[21361550]; 510: NM_003042 , "Homo sapiens solute carrier family 6 (neurotransmitter transporter, GABA),", "member 1 (SLC6A1), mRNA", gi|40254466|ref|NM_003042.2|[40254466]; 511: NM_003054 , "Homo sapiens solute carrier family 18 (vesicular monoamine), member 2 (SLC18A2),", mRNA, gi|42476324|ref|NM_003054.2|[42476324]; 512: NM_003055 , "Homo sapiens solute carrier family 18 (vesicular acetylcholine), member 3", "(SLC18A3), mRNA", gi|4506990|ref|NM_003055.1|[4506990]; 513: NM_003058 , "Homo sapiens solute carrier family 22 (organic cation transporter), member 2", "(SLC22A2), transcript variant 1, mRNA", gi|23510411|ref|NM_003058.2|[23510411]; 514: NM_003068 , "Homo sapiens snail homolog 2 (Drosophila) (SNAI2), mRNA", gi|24497625|ref|NM_003068.3|[24497625]; 515: NM_003077 , "Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of", "chromatin,

subfamily d, member 2 (SMARCD2), mRNA", gi|21264350|ref|NM_003077.2|[21264350]; 516: NM_003092 , "Homo sapiens small nuclear ribonucleoprotein polypeptide B" (SNRPB2),", "transcript variant 1, mRNA", gi|38149917|ref|NM_003092.3|[38149917]; 517: NM_003093 , "Homo sapiens small nuclear ribonucleoprotein polypeptide C (SNRPC), mRNA", gi|4507126|ref|NM_003093.1|[4507126]; 518: NM_003096 , "Homo sapiens small nuclear ribonucleoprotein polypeptide G (SNRPG), mRNA", gi|21359839|ref|NM_003096.2|[21359839]; 519: NM_003115 , "Homo sapiens UDP-N-acteylglucosamine pyrophosphorylase 1 (UAP1), mRNA", gi|34147515|ref|NM_003115.3|[34147515]; 520: NM_003132 , "Homo sapiens spermidine synthase (SRM), mRNA", gi|4507208|ref|NM_003132.1|[4507208]; 521: NM_003134 , Homo sapiens signal recognition particle 14kDa (homologous Alu RNA binding, "protein) (SRP14), mRNA", gi|31543652|ref|NM_003134.2|[31543652]; 522: NM_003135 , "Homo sapiens signal recognition particle 19kDa (SRP19), mRNA", gi|4507212|ref|NM_003135.1|[4507212]; 523: NM_003140 , "Homo sapiens sex determining region Y (SRY), mRNA", gi|4507224|ref|NM_003140.1|[4507224]; 524: NM_003141 , "Homo sapiens Sjogren syndrome antigen A1 (52kDa, ribonucleoprotein autoantigen", "SS-A/Ro) (SSA1), mRNA", gi|15208659|ref|NM_003141.2|[15208659]; 525: NM_003149 , "Homo sapiens src homology three (SH3) and cysteine rich domain (STAC), mRNA", gi|4507246|ref|NM_003149.1|[4507246]; 526: NM_003150 , Homo sapiens signal transducer and activator of transcription 3 (acute-phase, "response factor) (STAT3), transcript variant 2, mRNA", gi|21618337|ref|NM_003150.2|[21618337]; 527: NM_003156 , "Homo sapiens stromal interaction molecule 1 (STIM1), mRNA", gi|21070996|ref|NM_003156.2|[21070996]; 528: NM_003159 , "Homo sapiens cyclin-dependent kinase-like 5 (CDKL5), mRNA", gi|4507280|ref|NM_003159.1|[4507280]; 529: NM_003162 , "Homo sapiens striatin, calmodulin binding protein (STRN), mRNA", gi|4507282|ref|NM_003162.1|[4507282]; 530: NM_003165 , "Homo sapiens syntaxin binding protein 1 (STXBP1), mRNA", gi|4507296|ref|NM_003165.1|[4507296]; 531: NM_003181 , "Homo sapiens T, brachyury homolog (mouse) (T), mRNA", gi|19743811|ref|NM_003181.2|[19743811]; 532: NM_003184 , "Homo sapiens TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated", "factor, 150kDa (TAF2), mRNA", gi|20357590|ref|NM_003184.2|[20357590]; 533: NM_003186 , "Homo sapiens transgelin (TAGLN), mRNA", gi|12621918|ref|NM_003186.2|[12621918]; 534: NM_003192 , "Homo sapiens tubulin-specific chaperone c (TBCC), mRNA", gi|4507372|ref|NM_003192.1|[4507372]; 535: NM_003194 , "Homo sapiens TATA box binding protein (TBP), mRNA", gi|20544178|ref|NM_003194.2|[20544178]; 536: NM_003216 , "Homo sapiens thyrotrophic embryonic factor (TEF), mRNA", gi|34486096|ref|NM_003216.2|[34486096]; 537: NM_003223 , Homo sapiens transcription factor AP-4 (activating enhancer binding protein 4), "(TFAP4), mRNA", gi|4507446|ref|NM_003223.1|[4507446]; 538: NM_003239 , "Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA", gi|4507464|ref|NM_003239.1|[4507464]; 539: NM_003245 , "Homo sapiens transglutaminase 3 (E polypeptide,", "protein-glutamine-gamma-glutamyltransferase) (TGM3), mRNA", gi|39777600|ref|NM_003245.2|[39777600]; 540: NM_003256 , "Homo sapiens tissue inhibitor of metalloproteinase 4 (TIMP4), mRNA", gi|4507514|ref|NM_003256.1|[4507514]; 541: NM_003259 , "Homo sapiens intercellular adhesion molecule 5, telencephalin (ICAM5), mRNA", gi|12545403|ref|NM_003259.2|[12545403]; 542: NM_003269 , "Homo sapiens nuclear receptor subfamily 2, group E, member 1 (NR2E1), mRNA", gi|21361108|ref|NM_003269.2|[21361108]; 543: NM_003273 , "Homo sapiens transmembrane 7 superfamily member 2 (TM7SF2),

mRNA", gi|4507546|ref|NM_003273.1|[4507546]; 544: NM_003277 , Homo sapiens claudin 5 (transmembrane protein deleted in velocardiofacial, "syndrome) (CLDN5), mRNA", gi|38570041|ref|NM_003277.2|[38570041]; 545: NM_003280 , "Homo sapiens troponin C, slow (TNNC1), mRNA", gi|4507614|ref|NM_003280.1|[4507614]; 546: NM_003281 , "Homo sapiens troponin I, skeletal, slow (TNNI1), mRNA", gi|21361554|ref|NM_003281.2|[21361554]; 547: NM_003282 , "Homo sapiens troponin I, skeletal, fast (TNNI2), mRNA", gi|4507620|ref|NM_003282.1|[4507620]; 548: NM_003288 , "Homo sapiens tumor protein D52-like 2 (TPD52L2), transcript variant 5, mRNA", gi|40805859|ref|NM_003288.2|[40805859]; 549: NM_003291 , "Homo sapiens tripeptidyl peptidase II (TPP2), mRNA", gi|4507656|ref|NM_003291.1|[4507656]; 550: NM_003296 , "Homo sapiens cysteine-rich secretory protein 2 (CRISP2), mRNA", gi|4507670|ref|NM_003296.1|[4507670]; 551: NM_003298 , "Homo sapiens nuclear receptor subfamily 2, group C, member 2 (NR2C2), mRNA", gi|36950990|ref|NM_003298.2|[36950990]; 552: NM_003312 , "Homo sapiens thiosulfate sulfurtransferase (rhodanese) (TST), nuclear gene", "encoding mitochondrial protein, mRNA", gi|34335291|ref|NM_003312.4|[34335291]; 553: NM_003314 , "Homo sapiens tetratricopeptide repeat domain 1 (TTC1), mRNA", gi|4507710|ref|NM_003314.1|[4507710]; 554: NM_003315 , "Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 7 (DNAJC7), mRNA", gi|4507712|ref|NM_003315.1|[4507712]; 555: NM_003323 , "Homo sapiens tubby like protein 2 (TULP2), mRNA", gi|4507736|ref|NM_003323.1|[4507736]; 556: NM_003325 , Homo sapiens HIR histone cell cycle regulation defective homolog A (S., "cerevisiae) (HIRA), mRNA", gi|21536484|ref|NM_003325.3|[21536484]; 557: NM_003328 , "Homo sapiens TXK tyrosine kinase (TXK), mRNA", gi|4507742|ref|NM_003328.1|[4507742]; 558: NM_003331 , "Homo sapiens tyrosine kinase 2 (TYK2), mRNA", gi|34222294|ref|NM_003331.3|[34222294]; 559: NM_003333 , "Homo sapiens ubiquitin A-52 residue ribosomal protein fusion product 1 (UBA52),", mRNA, gi|15451941|ref|NM_003333.2|[15451941]; 560: NM_003334 , Homo sapiens ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature, "sensitivity complementing) (UBE1), transcript variant 1, mRNA", gi|23510337|ref|NM_003334.2|[23510337]; 561: NM_003341 , "Homo sapiens ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)", "(UBE2E1), transcript variant 1, mRNA", gi|33359692|ref|NM_003341.3|[33359692]; 562: NM_003350 , "Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA", gi|12025664|ref|NM_003350.2|[12025664]; 563: NM_003369 , "Homo sapiens UV radiation resistance associated gene (UVRAG), mRNA", gi|21687211|ref|NM_003369.2|[21687211]; 564: NM_003374 , "Homo sapiens voltage-dependent anion channel 1 (VDAC1), mRNA", gi|4507878|ref|NM_003374.1|[4507878]; 565: NM_003375 , "Homo sapiens voltage-dependent anion channel 2 (VDAC2), mRNA", gi|42476280|ref|NM_003375.2|[42476280]; 566: NM_003383 , "Homo sapiens very low density lipoprotein receptor (VLDLR), mRNA", gi|40254472|ref|NM_003383.2|[40254472]; 567: NM_003389 , "Homo sapiens coronin, actin binding protein, 2A (CORO2A), transcript variant 1,", mRNA, gi|16554582|ref|NM_003389.2|[16554582]; 568: NM_003391 , "Homo sapiens wingless-type MMTV integration site family member 2 (WNT2), mRNA", gi|4507926|ref|NM_003391.1|[4507926]; 569: NM_003399 , "Homo sapiens X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound", "(XPNPEP2), mRNA", gi|10880125|ref|NM_003399.3|[10880125]; 570: NM_003400 , "Homo sapiens exportin 1 (CRM1 homolog, yeast) (XPO1), mRNA", gi|8051634|ref|NM_003400.2|[8051634]; 571: NM_003404 , Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase

activation, "protein, beta polypeptide (YWHAB), transcript variant 1, mRNA", gi|31742479|ref|NM_003404.3|[31742479]; 572: NM_003407 , "Homo sapiens zinc finger protein 36, C3H type, homolog (mouse) (ZFP36), mRNA", gi|4507960|ref|NM_003407.1|[4507960]; 573: NM_003408 , "Homo sapiens zinc finger protein 37 homolog (mouse) (ZFP37), mRNA", gi|4507962|ref|NM_003408.1|[4507962]; 574: NM_003412 , "Homo sapiens Zic family member 1 (odd-paired homolog, Drosophila) (ZIC1), mRNA", gi|22547181|ref|NM_003412.2|[22547181]; 575: NM_003413 , "Homo sapiens Zic family member 3 heterotaxy 1 (odd-paired homolog, Drosophila)", "(ZIC3), mRNA", gi|22547199|ref|NM_003413.2|[22547199]; 576: NM_003418 , Homo sapiens zinc finger protein 9 (a cellular retroviral nucleic acid binding, "protein) (ZNF9), mRNA", gi|4827070|ref|NM_003418.1|[4827070]; 577: NM_003441 , "Homo sapiens zinc finger protein 141 (clone pHZ-44) (ZNF141), mRNA", gi|4507992|ref|NM_003441.1|[4507992]; 578: NM_003446 , "Homo sapiens zinc finger protein 157 (HZF22) (ZNF157), mRNA", gi|23510453|ref|NM_003446.2|[23510453]; 579: NM_003449 , "Homo sapiens tripartite motif-containing 26 (TRIM26), mRNA", gi|16445440|ref|NM_003449.2|[16445440]; 580: NM_003460 , "Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2), mRNA", gi|4508044|ref|NM_003460.1|[4508044]; 581: NM_003462 , "Homo sapiens dynein, axonemal, light intermediate polypeptide 1 (DNALI1), mRNA", gi|37595559|ref|NM_003462.3|[37595559]; 582: NM_003468 , "Homo sapiens frizzled homolog 5 (Drosophila) (FZD5), mRNA", gi|27894384|ref|NM_003468.2|[27894384]; 583: NM_003472 , "Homo sapiens DEK oncogene (DNA binding) (DEK), mRNA", gi|31542502|ref|NM_003472.2|[31542502]; 584: NM_003473 , Homo sapiens signal transducing adaptor molecule (SH3 domain and ITAM motif) 1, "(STAM), mRNA", gi|21265027|ref|NM_003473.2|[21265027]; 585: NM_003483 , "Homo sapiens high mobility group AT-hook 2 (HMGA2), mRNA", gi|14141182|ref|NM_003483.3|[14141182]; 586: NM_003491 , "Homo sapiens ARD1 homolog, N-acetyltransferase (S. cerevisiae) (ARD1), mRNA", gi|34222259|ref|NM_003491.2|[34222259]; 587: NM_003492 , "Homo sapiens chromosome X open reading frame 12 (CXorf12), mRNA", gi|4504738|ref|NM_003492.1|[4504738]; 588: NM_003495 , "Homo sapiens histone 1, H4i (HIST1H4I), mRNA", gi|18105065|ref|NM_003495.2|[18105065]; 589: NM_003502 , "Homo sapiens axin 1 (AXIN1), transcript variant 1, mRNA", gi|31083149|ref|NM_003502.2|[31083149]; 590: NM_003504 , "Homo sapiens CDC45 cell division cycle 45-like (S. cerevisiae) (CDC45L), mRNA", gi|34335230|ref|NM_003504.3|[34335230]; 591: NM_003509 , "Homo sapiens histone 1, H2ai (HIST1H2AI), mRNA", gi|15718713|ref|NM_003509.2|[15718713]; 592: NM_003524 , "Homo sapiens histone 1, H2bh (HIST1H2BH), mRNA", gi|21166386|ref|NM_003524.2|[21166386]; 593: NM_003529 , "Homo sapiens histone 1, H3a (HIST1H3A), mRNA", gi|19743828|ref|NM_003529.2|[19743828]; 594: NM_003532 , "Homo sapiens histone 1, H3e (HIST1H3E), mRNA", gi|21264566|ref|NM_003532.2|[21264566]; 595: NM_003536 , "Homo sapiens histone 1, H3h (HIST1H3H), mRNA", gi|15718725|ref|NM_003536.2|[15718725]; 596: NM_003538 , "Homo sapiens histone 1, H4a (HIST1H4A), mRNA", gi|21166390|ref|NM_003538.3|[21166390]; 597: NM_003549 , "Homo sapiens hyaluronoglucosaminidase 3 (HYAL3), mRNA", gi|15208650|ref|NM_003549.2|[15208650]; 598: NM_003550 , "Homo sapiens MAD1 mitotic arrest deficient-like 1 (yeast) (MAD1L1), mRNA", gi|4505064|ref|NM_003550.1|[4505064]; 599: NM_003553 , "Homo sapiens olfactory receptor, family 1, subfamily E, member 1 (OR1E1), mRNA",

gi|11496274|ref|NM_003553.1|[11496274]; 600: NM_003554 , "Homo sapiens olfactory receptor, family 1, subfamily E, member 2 (OR1E2), mRNA", gi|11386152|ref|NM_003554.1|[11386152]; 601: NM_003581 , "Homo sapiens NCK adaptor protein 2 (NCK2), mRNA", gi|4505346|ref|NM_003581.1|[4505346]; 602: NM_003582 , Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3, "(DYRK3), mRNA", gi|4503428|ref|NM_003582.1|[4503428]; 603: NM_003585 , "Homo sapiens double C2-like domains, beta (DOC2B), mRNA", gi|6005996|ref|NM_003585.1|[6005996]; 604: NM_003587 , "Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 16 (DHX16), mRNA", gi|21237727|ref|NM_003587.3|[21237727]; 605: NM_003592 , "Homo sapiens cullin 1 (CUL1), mRNA", gi|32307160|ref|NM_003592.2|[32307160]; 606: NM_003594 , "Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA", gi|40807470|ref|NM_003594.3|[40807470]; 607: NM_003608 , "Homo sapiens G protein-coupled receptor 65 (GPR65), mRNA", gi|33695103|ref|NM_003608.2|[33695103]; 608: NM_003611 , "Homo sapiens oral-facial-digital syndrome 1 (OFD1), mRNA", gi|4503178|ref|NM_003611.1|[4503178]; 609: NM_003614 , "Homo sapiens galanin receptor 3 (GALR3), mRNA", gi|4503906|ref|NM_003614.1|[4503906]; 610: NM_003618 , "Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3),", mRNA, gi|15451901|ref|NM_003618.2|[15451901]; 611: NM_003625 , "Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF),", "interacting protein (liprin), alpha 2 (PPFIA2), mRNA", gi|29171754|ref|NM_003625.2|[29171754]; 612: NM_003627 , "Homo sapiens solute carrier family 43, member 1 (SLC43A1), mRNA", gi|42476323|ref|NM_003627.4|[42476323]; 613: NM_003632 , "Homo sapiens contactin associated protein 1 (CNTNAP1), mRNA", gi|4505462|ref|NM_003632.1|[4505462]; 614: NM_003635 , "Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2 (NDST2),", mRNA, gi|31377809|ref|NM_003635.2|[31377809]; 615: NM_003642 , "Homo sapiens histone acetyltransferase 1 (HAT1), mRNA", gi|4504340|ref|NM_003642.1|[4504340]; 616: NM_003646 , "Homo sapiens diacylglycerol kinase, zeta 104kDa (DGKZ), transcript variant 2,", mRNA, gi|41872506|ref|NM_003646.2|[41872506]; 617: NM_003648 , "Homo sapiens diacylglycerol kinase, delta 130kDa (DGKD), transcript variant 1,", mRNA, gi|25777595|ref|NM_003648.2|[25777595]; 618: NM_003653 , Homo sapiens COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis), "(COPS3), mRNA", gi|23238221|ref|NM_003653.2|[23238221]; 619: NM_003654 , "Homo sapiens carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 (CHST1),", mRNA, gi|31542307|ref|NM_003654.2|[31542307]; 620: NM_003655 , "Homo sapiens chromobox homolog 4 (Pc class homolog, Drosophila) (CBX4), mRNA", gi|4502602|ref|NM_003655.1|[4502602]; 621: NM_003656 , "Homo sapiens calcium/calmodulin-dependent protein kinase I (CAMK1), mRNA", gi|21536281|ref|NM_003656.3|[21536281]; 622: NM_003658 , "Homo sapiens BarH-like homeobox 2 (BARX2), mRNA", gi|21536440|ref|NM_003658.3|[21536440]; 623: NM_003669 , "Homo sapiens inactivation escape 1 (INE1), mRNA", gi|4504692|ref|NM_003669.1|[4504692]; 624: NM_003680 , "Homo sapiens tyrosyl-tRNA synthetase (YARS), mRNA", gi|38202242|ref|NM_003680.2|[38202242]; 625: NM_003684 , "Homo sapiens MAP kinase-interacting serine/threonine kinase 1 (MKNK1), mRNA", gi|34147650|ref|NM_003684.3|[34147650]; 626: NM_003686 , "Homo sapiens exonuclease 1 (EXO1), transcript variant 3, mRNA", gi|39995068|ref|NM_003686.3|[39995068]; 627: NM_003691 , "Homo sapiens serine/threonine kinase 16 (STK16), mRNA",

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gi|4758343|ref|NM_004106.1|[4758343]; 682: NM_004107 , "Homo sapiens Fc fragment of IgG, receptor, transporter, alpha (FCGRT), mRNA", gi|34222296|ref|NM_004107.3|[34222296]; 683: NM_004110 , "Homo sapiens ferredoxin reductase (FDXR), nuclear gene encoding mitochondrial", "protein, transcript variant 2, mRNA", gi|13435351|ref|NM_004110.2|[13435351]; 684: NM_004114 , "Homo sapiens fibroblast growth factor 13 (FGF13), transcript variant 1A, mRNA", gi|16306544|ref|NM_004114.2|[16306544]; 685: NM_004115 , "Homo sapiens fibroblast growth factor 14 (FGF14), transcript variant 1, mRNA", gi|28872754|ref|NM_004115.2|[28872754]; 686: NM_004117 , "Homo sapiens FK506 binding protein 5 (FKBP5), mRNA", gi|17149847|ref|NM_004117.2|[17149847]; 687: NM_004120 , "Homo sapiens guanylate binding protein 2, interferon-inducible (GBP2), mRNA", gi|38327557|ref|NM_004120.3|[38327557]; 688: NM_004125 , "Homo sapiens guanine nucleotide binding protein (G protein), gamma 10 (GNG10),", mRNA, gi|21361096|ref|NM_004125.2|[21361096]; 689: NM_004127 , "Homo sapiens G protein pathway suppressor 1 (GPS1), mRNA", gi|13435380|ref|NM_004127.3|[13435380]; 690: NM_004153 , "Homo sapiens origin recognition complex, subunit 1-like (yeast) (ORC1L), mRNA", gi|31795543|ref|NM_004153.2|[31795543]; 691: NM_004154 , "Homo sapiens pyrimidinergic receptor P2Y, G-protein coupled, 6 (P2RY6),", "transcript variant 4, mRNA", gi|29029606|ref|NM_004154.3|[29029606]; 692: NM_004159 , "Homo sapiens proteasome (prosome, macropain) subunit, beta type, 8 (large", "multifunctional protease 7) (PSMB8), transcript variant 1, mRNA", gi|34335277|ref|NM_004159.3|[34335277]; 693: NM_004178 , "Homo sapiens TAR (HIV) RNA binding protein 2 (TARBP2), transcript variant 3,", mRNA, gi|19743837|ref|NM_004178.3|[19743837]; 694: NM_004182 , "Homo sapiens ubiquitously-expressed transcript (UXT), transcript variant 2, mRNA", gi|24041015|ref|NM_004182.2|[24041015]; 695: NM_004188 , "Homo sapiens growth factor independent 1B (potential regulator of CDKN1A,", "translocated in CML) (GFI1B), mRNA", gi|40254479|ref|NM_004188.2|[40254479]; 696: NM_004189 , "Homo sapiens SRY (sex determining region Y)-box 14 (SOX14), mRNA", gi|31563384|ref|NM_004189.2|[31563384]; 697: NM_004196 , "Homo sapiens cyclin-dependent kinase-like 1 (CDC2-related kinase) (CDKL1), mRNA", gi|37596296|ref|NM_004196.3|[37596296]; 698: NM_004202 , "Homo sapiens thymosin, beta 4, Y-linked (TMSB4Y), mRNA", gi|34328944|ref|NM_004202.2|[34328944]; 699: NM_004203 , Homo sapiens membrane-associated tyrosine- and threonine-specific, "cdc2-inhibitory kinase (PKMYT1), transcript variant 1, mRNA", gi|33383240|ref|NM_004203.3|[33383240]; 700: NM_004204 , "Homo sapiens phosphatidylinositol glycan, class Q (PIGQ), transcript variant 2,", mRNA, gi|22538449|ref|NM_004204.2|[22538449]; 701: NM_004214 , Homo sapiens fibroblast growth factor (acidic) intracellular binding protein, "(FIBP), transcript variant 2, mRNA", gi|38683847|ref|NM_004214.4|[38683847]; 702: NM_004217 , "Homo sapiens aurora kinase B (AURKB), mRNA", gi|4759177|ref|NM_004217.1|[4759177]; 703: NM_004219 , "Homo sapiens pituitary tumor-transforming 1 (PTTG1), mRNA", gi|11038651|ref|NM_004219.2|[11038651]; 704: NM_004223 , "Homo sapiens ubiquitin-conjugating enzyme E2L 6 (UBE2L6), transcript variant 1,", mRNA, gi|38157980|ref|NM_004223.3|[38157980]; 705: NM_004224 , "Homo sapiens G protein-coupled receptor 50 (GPR50), mRNA", gi|4758467|ref|NM_004224.1|[4758467]; 706: NM_004226 , "Homo sapiens serine/threonine kinase 17b (apoptosis-inducing) (STK17B), mRNA", gi|31543661|ref|NM_004226.2|[31543661]; 707: NM_004227 , "Homo sapiens pleckstrin homology, Sec7 and coiled-coil domains 3 (PSCD3), mRNA",

gi|33946275|ref|NM_004227.3|[33946275]; 708: NM_004233 , "Homo sapiens CD83 antigen (activated B lymphocytes, immunoglobulin superfamily)", "(CD83), mRNA", gi|24475618|ref|NM_004233.2|[24475618]; 709: NM_004237 , "Homo sapiens thyroid hormone receptor interactor 13 (TRIP13), mRNA", gi|20149561|ref|NM_004237.2|[20149561]; 710: NM_004238 , , ref|NM_004238.1|[10863902], This record was temporarily removed by RefSeq staff for additional review., , 711: NM_004257 , "Homo sapiens transforming growth factor, beta receptor associated protein 1", "(TGFBRAP1), mRNA", gi|34222146|ref|NM_004257.3|[34222146]; 712: NM_004260 , "Homo sapiens RecQ protein-like 4 (RECQL4), mRNA", gi|4759029|ref|NM_004260.1|[4759029]; 713: NM_004261 , "Homo sapiens 15 kDa selenoprotein (SEP15), transcript variant 1, mRNA", gi|42741647|ref|NM_004261.3|[42741647]; 714: NM_004267 , "Homo sapiens carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 (CHST2),", mRNA, gi|27369496|ref|NM_004267.2|[27369496]; 715: NM_004272 , "Homo sapiens homer homolog 1 (Drosophila) (HOMER1), mRNA", gi|20127465|ref|NM_004272.2|[20127465]; 716: NM_004281 , "Homo sapiens BCL2-associated athanogene 3 (BAG3), mRNA", gi|14043023|ref|NM_004281.2|[14043023]; 717: NM_004285 , "Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD),", mRNA, gi|4758497|ref|NM_004285.1|[4758497]; 718: NM_004294 , "Homo sapiens mitochondrial translational release factor 1 (MTRF1), nuclear gene", "encoding mitochondrial protein, mRNA", gi|34577119|ref|NM_004294.2|[34577119]; 719: NM_004298 , "Homo sapiens nucleoporin 155kDa (NUP155), transcript variant 2, mRNA", gi|24430147|ref|NM_004298.2|[24430147]; 720: NM_004314 , "Homo sapiens ADP-ribosyltransferase 1 (ART1), mRNA", gi|4757783|ref|NM_004314.1|[4757783]; 721: NM_004330 , "Homo sapiens BCL2/adenovirus E1B 19kDa interacting protein 2 (BNIP2), mRNA", gi|4757855|ref|NM_004330.1|[4757855]; 722: NM_004339 , "Homo sapiens pituitary tumor-transforming 1 interacting protein (PTTG1IP), mRNA", gi|11038670|ref|NM_004339.2|[11038670]; 723: NM_004341 , "Homo sapiens carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and", "dihydroorotase (CAD), mRNA", gi|18105006|ref|NM_004341.2|[18105006]; 724: NM_004344 , "Homo sapiens centrin, EF-hand protein, 2 (CETN2), mRNA", gi|4757901|ref|NM_004344.1|[4757901]; 725: NM_004346 , "Homo sapiens caspase 3, apoptosis-related cysteine protease (CASP3), transcript", "variant alpha, mRNA", gi|14790118|ref|NM_004346.2|[14790118]; 726: NM_004356 , "Homo sapiens CD81 antigen (target of antiproliferative antibody 1) (CD81), mRNA", gi|21237760|ref|NM_004356.2|[21237760]; 727: NM_004357 , "Homo sapiens CD151 antigen (CD151), transcript variant 1, mRNA", gi|34328913|ref|NM_004357.3|[34328913]; 728: NM_004358 , "Homo sapiens cell division cycle 25B (CDC25B), transcript variant 1, mRNA", gi|11641416|ref|NM_004358.2|[11641416]; 729: NM_004359 , "Homo sapiens cell division cycle 34 (CDC34), mRNA", gi|16357476|ref|NM_004359.1|[16357476]; 730: NM_004365 , "Homo sapiens centrin, EF-hand protein, 3 (CDC31 homolog, yeast) (CETN3), mRNA", gi|4757975|ref|NM_004365.1|[4757975]; 731: NM_004366 , "Homo sapiens chloride channel 2 (CLCN2), mRNA", gi|5803001|ref|NM_004366.2|[5803001]; 732: NM_004367 , "Homo sapiens chemokine (C-C motif) receptor 6 (CCR6), transcript variant 1, mRNA", gi|37187859|ref|NM_004367.3|[37187859]; 733: NM_004374 , "Homo sapiens cytochrome c oxidase subunit VIc (COX6C), mRNA", gi|17999531|ref|NM_004374.2|[17999531]; 734: NM_004383 , "Homo sapiens c-src tyrosine kinase (CSK), mRNA", gi|4758077|ref|NM_004383.1|[4758077]; 735: NM_004396 , "Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 (DDX5), mRNA", gi|13514826|ref|NM_004396.2|[13514826]; 736:

NM_004398 , "Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 10 (DDX10), mRNA", gi|13514830|ref|NM_004398.2|[13514830]; 737: NM_004401 , "Homo sapiens DNA fragmentation factor, 45kDa, alpha polypeptide (DFFA), mRNA", gi|4758147|ref|NM_004401.1|[4758147]; 738: NM_004402 , "Homo sapiens DNA fragmentation factor, 40kDa, beta polypeptide", "(caspase-activated DNase) (DFFB), mRNA", gi|4758149|ref|NM_004402.1|[4758149]; 739: NM_004411 , "Homo sapiens dynein, cytoplasmic, intermediate polypeptide 1 (DNCI1), mRNA", gi|4758177|ref|NM_004411.1|[4758177]; 740: NM_004415 , "Homo sapiens desmoplakin (DSP), mRNA", gi|4758199|ref|NM_004415.1|[4758199]; 741: NM_004418 , "Homo sapiens dual specificity phosphatase 2 (DUSP2), mRNA", gi|12707563|ref|NM_004418.2|[12707563]; 742: NM_004420 , "Homo sapiens dual specificity phosphatase 8 (DUSP8), mRNA", gi|4758211|ref|NM_004420.1|[4758211]; 743: NM_004426 , "Homo sapiens polyhomeotic-like 1 (Drosophila) (PHC1), mRNA", gi|11038623|ref|NM_004426.1|[11038623]; 744: NM_004427 , "Homo sapiens polyhomeotic-like 2 (Drosophila) (PHC2), transcript variant 2, mRNA", gi|37595529|ref|NM_004427.2|[37595529]; 745: NM_004432 , "Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu", "antigen B) (ELAVL2), mRNA", gi|4758261|ref|NM_004432.1|[4758261]; 746: NM_004438 , "Homo sapiens EphA4 (EPHA4), mRNA", gi|32967315|ref|NM_004438.2|[32967315]; 747: NM_004445 , "Homo sapiens EphB6 (EPHB6), mRNA", gi|4758291|ref|NM_004445.1|[4758291]; 748: NM_004447 , "Homo sapiens epidermal growth factor receptor pathway substrate 8 (EPS8), mRNA", gi|34222299|ref|NM_004447.3|[34222299]; 749: NM_004450 , "Homo sapiens enhancer of rudimentary homolog (Drosophila) (ERH), mRNA", gi|4758301|ref|NM_004450.1|[4758301]; 750: NM_004456 , "Homo sapiens enhancer of zeste homolog 2 (Drosophila) (EZH2), transcript variant", "1, mRNA", gi|23510382|ref|NM_004456.3|[23510382]; 751: NM_004466 , "Homo sapiens glypican 5 (GPC5), mRNA", gi|34106705|ref|NM_004466.3|[34106705]; 752: NM_004469 , Homo sapiens c-fos induced growth factor (vascular endothelial growth factor D), "(FIGF), mRNA", gi|19924297|ref|NM_004469.2|[19924297]; 753: NM_004470 , "Homo sapiens FK506 binding protein 2, 13kDa (FKBP2), transcript variant 1, mRNA", gi|17149841|ref|NM_004470.2|[17149841]; 754: NM_004473 , "Homo sapiens forkhead box E1 (thyroid transcription factor 2) (FOXE1), mRNA", gi|21618324|ref|NM_004473.3|[21618324]; 755: NM_004474 , "Homo sapiens forkhead box D2 (FOXD2), mRNA", gi|4758387|ref|NM_004474.1|[4758387]; 756: NM_004480 , "Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8),", "transcript variant 4, mRNA", gi|30410721|ref|NM_004480.3|[30410721]; 757: NM_004485 , "Homo sapiens guanine nucleotide binding protein (G protein), gamma 4 (GNG4),", mRNA, gi|21314630|ref|NM_004485.2|[21314630]; 758: NM_004487 , "Homo sapiens golgi autoantigen, golgin subfamily b, macrogolgin (with", "transmembrane signal), 1 (GOLGB1), mRNA", gi|4758453|ref|NM_004487.1|[4758453]; 759: NM_004490 , "Homo sapiens growth factor receptor-bound protein 14 (GRB14), mRNA", gi|4758477|ref|NM_004490.1|[4758477]; 760: NM_004492 , "Homo sapiens general transcription factor IIA, 2 (12kD subunit) (GTF2A2), mRNA", gi|4758485|ref|NM_004492.1|[4758485]; 761: NM_004496 , "Homo sapiens forkhead box A1 (FOXA1), mRNA", gi|24497500|ref|NM_004496.2|[24497500]; 762: NM_004498 , "Homo sapiens one cut domain, family member 1 (ONECUT1), mRNA", gi|24307886|ref|NM_004498.1|[24307886]; 763: NM_004499 , "Homo sapiens heterogeneous nuclear ribonucleoprotein A/B (HNRPAB), transcript", "variant 2, mRNA", gi|14110401|ref|NM_004499.2|[14110401]; 764: NM_004503 , "Homo sapiens homeo box C6

(HOXC6), transcript variant 1, mRNA", gi|24497542|ref|NM_004503.2|[24497542]; 765: NM_004512 , "Homo sapiens interleukin 11 receptor, alpha (IL11RA), transcript variant 1, mRNA", gi|22212920|ref|NM_004512.3|[22212920]; 766: NM_004524 , "Homo sapiens lethal giant larvae homolog 2 (Drosophila) (LLGL2), mRNA", gi|4758679|ref|NM_004524.1|[4758679]; 767: NM_004525 , "Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA", gi|6806918|ref|NM_004525.1|[6806918]; 768: NM_004527 , "Homo sapiens mesenchyme homeo box 1 (MEOX1), transcript variant 1, mRNA", gi|21396477|ref|NM_004527.2|[21396477]; 769: NM_004528 , "Homo sapiens microsomal glutathione S-transferase 3 (MGST3), mRNA", gi|22035640|ref|NM_004528.2|[22035640]; 770: NM_004540 , "Homo sapiens neural cell adhesion molecule 2 (NCAM2), mRNA", gi|33519480|ref|NM_004540.2|[33519480]; 771: NM_004542 , "Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa", "(NDUFA3), mRNA", gi|4758771|ref|NM_004542.1|[4758771]; 772: NM_004543 , "Homo sapiens nebulin (NEB), mRNA", gi|8400716|ref|NM_004543.2|[8400716]; 773: NM_004550 , "Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa", "(NADH-coenzyme Q reductase) (NDUFS2), mRNA", gi|34147556|ref|NM_004550.3|[34147556]; 774: NM_004551 , "Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa", "(NADH-coenzyme Q reductase) (NDUFS3), mRNA", gi|4758787|ref|NM_004551.1|[4758787]; 775: NM_004552 , "Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa", "(NADH-coenzyme Q reductase) (NDUFS5), mRNA", gi|4758789|ref|NM_004552.1|[4758789]; 776: NM_004561 , "Homo sapiens ovo-like 1(Drosophila) (OVOL1), mRNA", gi|38570157|ref|NM_004561.2|[38570157]; 777: NM_004567 , "Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (PFKFB4),", mRNA, gi|19923257|ref|NM_004567.2|[19923257]; 778: NM_004568 , "Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin),", "member 6 (SERPINB6), mRNA", gi|41152085|ref|NM_004568.4|[41152085]; 779: NM_004569 , "Homo sapiens phosphatidylinositol glycan, class H (PIGH), mRNA", gi|24430187|ref|NM_004569.2|[24430187]; 780: NM_004575 , "Homo sapiens POU domain, class 4, transcription factor 2 (POU4F2), mRNA", gi|4758947|ref|NM_004575.1|[4758947]; 781: NM_004579 , "Homo sapiens mitogen-activated protein kinase kinase kinase kinase 2 (MAP4K2),", mRNA, gi|22035599|ref|NM_004579.2|[22035599]; 782: NM_004581 , "Homo sapiens Rab geranylgeranyltransferase, alpha subunit (RABGGTA), transcript", "variant 2, mRNA", gi|33469948|ref|NM_004581.2|[33469948]; 783: NM_004584 , "Homo sapiens RAD9 homolog A (S. pombe) (RAD9A), mRNA", gi|19924112|ref|NM_004584.2|[19924112]; 784: NM_004586 , "Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 3 (RPS6KA3), mRNA", gi|4759049|ref|NM_004586.1|[4759049]; 785: NM_004597 , "Homo sapiens small nuclear ribonucleoprotein D2 polypeptide 16.5kDa (SNRPD2),", "transcript variant 1, mRNA", gi|29294622|ref|NM_004597.4|[29294622]; 786: NM_004604 , "Homo sapiens syntaxin 4A (placental) (STX4A), mRNA", gi|34147603|ref|NM_004604.3|[34147603]; 787: NM_004609 , "Homo sapiens transcription factor 15 (basic helix-loop-helix) (TCF15), mRNA", gi|38505157|ref|NM_004609.2|[38505157]; 788: NM_004612 , "Homo sapiens transforming growth factor, beta receptor I (activin A receptor", "type II-like kinase, 53kDa) (TGFBR1), mRNA", gi|4759225|ref|NM_004612.1|[4759225]; 789: NM_004619 , "Homo sapiens TNF receptor-associated factor 5 (TRAF5), transcript variant 1,", mRNA, gi|22027625|ref|NM_004619.2|[22027625]; 790: NM_004620 , "Homo sapiens TNF receptor-

associated factor 6 (TRAF6), transcript variant 2,", mRNA, gi|22027628|ref|NM_004620.2|[22027628]; 791: NM_004626 , "Homo sapiens wingless-type MMTV integration site family, member 11 (WNT11), mRNA", gi|17017973|ref|NM_004626.2|[17017973]; 792: NM_004653 , "Homo sapiens Jumonji, AT rich interactive domain 1D (RBP2-like) (JARID1D), mRNA", gi|33356559|ref|NM_004653.2|[33356559]; 793: NM_004656 , Homo sapiens BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase), "(BAP1), mRNA", gi|19718752|ref|NM_004656.2|[19718752]; 794: NM_004664 , "Homo sapiens lin-7 homolog A (C. elegans) (LIN7A), mRNA", gi|4759305|ref|NM_004664.1|[4759305]; 795: NM_004666 , "Homo sapiens vanin 1 (VNN1), mRNA", gi|4759311|ref|NM_004666.1|[4759311]; 796: NM_004667 , "Homo sapiens hect domain and RLD 2 (HERC2), mRNA", gi|5729867|ref|NM_004667.2|[5729867]; 797: NM_004669 , "Homo sapiens chloride intracellular channel 3 (CLIC3), mRNA", gi|40288289|ref|NM_004669.2|[40288289]; 798: NM_004672 , "Homo sapiens mitogen-activated protein kinase kinase kinase 6 (MAP3K6),", "transcript variant 1, mRNA", gi|24497521|ref|NM_004672.2|[24497521]; 799: NM_004691 , "Homo sapiens ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d isoform 1", "(ATP6V0D1), mRNA", gi|34335257|ref|NM_004691.3|[34335257]; 800: NM_004693 , "Homo sapiens cytokeratin type II (K6HF), mRNA", gi|4758617|ref|NM_004693.1|[4758617]; 801: NM_004694 , "Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member", "6 (SLC16A6), mRNA", gi|40789260|ref|NM_004694.2|[40789260]; 802: NM_004698 , "Homo sapiens PRP3 pre-mRNA processing factor 3 homolog (yeast) (PRPF3), mRNA", gi|4758555|ref|NM_004698.1|[4758555]; 803: NM_004699 , Homo sapiens DNA segment on chromosome X (unique) 9928 expressed sequence, "(DXS9928E), mRNA", gi|4758219|ref|NM_004699.1|[4758219]; 804: NM_004700 , "Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 4", "(KCNQ4), transcript variant 1, mRNA", gi|26638652|ref|NM_004700.2|[26638652]; 805: NM_004701 , "Homo sapiens cyclin B2 (CCNB2), mRNA", gi|10938017|ref|NM_004701.2|[10938017]; 806: NM_004704 , "Homo sapiens RNA, U3 small nucleolar interacting protein 2 (RNU3IP2), mRNA", gi|31543556|ref|NM_004704.2|[31543556]; 807: NM_004713 , "Homo sapiens serologically defined colon cancer antigen 1 (SDCCAG1), mRNA", gi|32130515|ref|NM_004713.2|[32130515]; 808: NM_004714 , Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B, "(DYRK1B), transcript variant a, mRNA", gi|4758221|ref|NM_004714.1|[4758221]; 809: NM_004716 , "Homo sapiens proprotein convertase subtilisin/kexin type 7 (PCSK7), mRNA", gi|20336247|ref|NM_004716.2|[20336247]; 810: NM_004717 , "Homo sapiens diacylglycerol kinase, iota (DGKI), mRNA", gi|32483395|ref|NM_004717.2|[32483395]; 811: NM_004728 , "Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 21 (DDX21), mRNA", gi|13787208|ref|NM_004728.1|[13787208]; 812: NM_004732 , "Homo sapiens potassium voltage-gated channel, shaker-related subfamily, beta", "member 3 (KCNAB3), mRNA", gi|27436970|ref|NM_004732.2|[27436970]; 813: NM_004742 , "Homo sapiens BAI1-associated protein 1 (BAIAP1), mRNA", gi|9257194|ref|NM_004742.1|[9257194]; 814: NM_004761 , "Homo sapiens RAB2, member RAS oncogene family-like (RAB2L), mRNA", gi|21361071|ref|NM_004761.2|[21361071]; 815: NM_004766 , "Homo sapiens coatomer protein complex, subunit beta 2 (beta prime) (COPB2), mRNA", gi|4758031|ref|NM_004766.1|[4758031]; 816: NM_004767 , "Homo sapiens endothelin type b receptor-like protein 2 (ET(B)R-LP-2), mRNA", gi|31377792|ref|NM_004767.2|[31377792];

817: NM_004784 , "Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3 (NDST3),", mRNA, gi|4758765|ref|NM_004784.1|[4758765]; 818: NM_004785 , "Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 3", "regulatory factor 2 (SLC9A3R2), mRNA", gi|4759141|ref|NM_004785.1|[4759141]; 819: NM_004787 , "Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA", gi|4759145|ref|NM_004787.1|[4759145]; 820: NM_004788 , "Homo sapiens ubiquitination factor E4A (UFD2 homolog, yeast) (UBE4A), mRNA", gi|38327028|ref|NM_004788.2|[38327028]; 821: NM_004793 , "Homo sapiens protease, serine, 15 (PRSS15), nuclear gene encoding mitochondrial", "protein, mRNA", gi|21396488|ref|NM_004793.2|[21396488]; 822: NM_004800 , "Homo sapiens transmembrane 9 superfamily member 2 (TM9SF2), mRNA", gi|4758873|ref|NM_004800.1|[4758873]; 823: NM_004804 , "Homo sapiens WD40 protein Ciao1 (CIAO1), mRNA", gi|38570089|ref|NM_004804.2|[38570089]; 824: NM_004826 , "Homo sapiens endothelin converting enzyme-like 1 (ECEL1), mRNA", gi|4758231|ref|NM_004826.1|[4758231]; 825: NM_004830 , "Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 3,", "130kDa (CRSP3), transcript variant 1, mRNA", gi|28558970|ref|NM_004830.2|[28558970]; 826: NM_004834 , "Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4),", "transcript variant 1, mRNA", gi|22035601|ref|NM_004834.2|[22035601]; 827: NM_004836 , Homo sapiens eukaryotic translation initiation factor 2-alpha kinase 3, "(EIF2AK3), mRNA", gi|21361154|ref|NM_004836.2|[21361154]; 828: NM_004854 , "Homo sapiens carbohydrate sulfotransferase 10 (CHST10), mRNA", gi|20127466|ref|NM_004854.2|[20127466]; 829: NM_004855 , "Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA", gi|22538447|ref|NM_004855.3|[22538447]; 830: NM_004856 , "Homo sapiens kinesin family member 23 (KIF23), transcript variant 2, mRNA", gi|20143965|ref|NM_004856.4|[20143965]; 831: NM_004857 , "Homo sapiens A kinase (PRKA) anchor protein 5 (AKAP5), mRNA", gi|21493042|ref|NM_004857.2|[21493042]; 832: NM_004865 , "Homo sapiens TBP-like 1 (TBPL1), mRNA", gi|21071068|ref|NM_004865.2|[21071068]; 833: NM_004869 , "Homo sapiens vacuolar protein sorting 4B (yeast) (VPS4B), mRNA", gi|17865801|ref|NM_004869.2|[17865801]; 834: NM_004870 , "Homo sapiens mannose-P-dolichol utilization defect 1 (MPDU1), mRNA", gi|4759109|ref|NM_004870.1|[4759109]; 835: NM_004872 , "Homo sapiens chromosome 1 open reading frame 8 (C1orf8), mRNA", gi|27545320|ref|NM_004872.3|[27545320]; 836: NM_004874 , "Homo sapiens BCL2-associated athanogene 4 (BAG4), mRNA", gi|14574569|ref|NM_004874.2|[14574569]; 837: NM_004882 , "Homo sapiens CBF1 interacting corepressor (CIR), transcript variant 1, mRNA", gi|40068058|ref|NM_004882.3|[40068058]; 838: NM_004891 , "Homo sapiens mitochondrial ribosomal protein L33 (MRPL33), nuclear gene encoding", "mitochondrial protein, transcript variant 1, mRNA", gi|21735607|ref|NM_004891.2|[21735607]; 839: NM_004897 , "Homo sapiens multiple inositol polyphosphate histidine phosphatase, 1 (MINPP1),", mRNA, gi|19923760|ref|NM_004897.2|[19923760]; 840: NM_004898 , "Homo sapiens clock homolog (mouse) (CLOCK), mRNA", gi|25777594|ref|NM_004898.2|[25777594]; 841: NM_004907 , "Homo sapiens immediate early response 2 (IER2), mRNA", gi|4758313|ref|NM_004907.1|[4758313]; 842: NM_004910 , "Homo sapiens phosphatidylinositol transfer protein, membrane-associated 1", "(PITPNM1), mRNA", gi|4758925|ref|NM_004910.1|[4758925]; 843: NM_004913 , "Homo sapiens chromosome 16 open reading frame 7 (C16orf7), mRNA", gi|4757805|ref|NM_004913.1|[4757805]; 844: NM_004918 , "Homo sapiens T-cell leukemia/lymphoma 1B (TCL1B), transcript variant 1,

mRNA", gi|40548373|ref|NM_004918.2|[40548373]; 845: NM_004922 , "Homo sapiens SEC24 related gene family, member C (S. cerevisiae) (SEC24C),", "transcript variant 1, mRNA", gi|38373668|ref|NM_004922.2|[38373668]; 846: NM_004927 , "Homo sapiens mitochondrial ribosomal protein L49 (MRPL49), nuclear gene encoding", "mitochondrial protein, mRNA", gi|27436906|ref|NM_004927.2|[27436906]; 847: NM_004935 , "Homo sapiens cyclin-dependent kinase 5 (CDK5), mRNA", gi|38454327|ref|NM_004935.2|[38454327]; 848: NM_004941 , "Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 8 (DHX8), mRNA", gi|4826689|ref|NM_004941.1|[4826689]; 849: NM_004944 , "Homo sapiens deoxyribonuclease I-like 3 (DNASE1L3), mRNA", gi|4826697|ref|NM_004944.1|[4826697]; 850: NM_004959 , "Homo sapiens nuclear receptor subfamily 5, group A, member 1 (NR5A1), mRNA", gi|24432033|ref|NM_004959.3|[24432033]; 851: NM_004966 , "Homo sapiens heterogeneous nuclear ribonucleoprotein F (HNRPF), mRNA", gi|14141150|ref|NM_004966.2|[14141150]; 852: NM_004970 , "Homo sapiens insulin-like growth factor binding protein, acid labile subunit", "(IGFALS), mRNA", gi|4826771|ref|NM_004970.1|[4826771]; 853: NM_004974 , "Homo sapiens potassium voltage-gated channel, shaker-related subfamily, member 2", "(KCNA2), mRNA", gi|25952079|ref|NM_004974.2|[25952079]; 854: NM_004975 , "Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1", "(KCNB1), mRNA", gi|27436972|ref|NM_004975.2|[27436972]; 855: NM_004978 , "Homo sapiens potassium voltage-gated channel, Shaw-related subfamily, member 4", "(KCNC4), transcript variant 1, mRNA", gi|24497461|ref|NM_004978.2|[24497461]; 856: NM_004984 , "Homo sapiens kinesin family member 5A (KIF5A), mRNA", gi|4826807|ref|NM_004984.1|[4826807]; 857: NM_004987 , "Homo sapiens LIM and senescent cell antigen-like domains 1 (LIMS1), mRNA", gi|13518025|ref|NM_004987.2|[13518025]; 858: NM_004991 , "Homo sapiens myelodysplasia syndrome 1 (MDS1), mRNA", gi|4826827|ref|NM_004991.1|[4826827]; 859: NM_004994 , "Homo sapiens matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa", "type IV collagenase) (MMP9), mRNA", gi|4826835|ref|NM_004994.1|[4826835]; 860: NM_004998 , "Homo sapiens myosin IE (MYO1E), mRNA", gi|4826843|ref|NM_004998.1|[4826843]; 861: NM_005006 , "Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa", "(NADH-coenzyme Q reductase) (NDUFS1), nuclear gene encoding mitochondrial", "protein, mRNA", gi|33519474|ref|NM_005006.5|[33519474]; 862: NM_005007 , Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells, "inhibitor-like 1 (NFKBIL1), mRNA", gi|26787990|ref|NM_005007.2|[26787990]; 863: NM_005012 , "Homo sapiens receptor tyrosine kinase-like orphan receptor 1 (ROR1), mRNA", gi|4826867|ref|NM_005012.1|[4826867]; 864: NM_005017 , "Homo sapiens phosphate cytidylyltransferase 1, choline, alpha isoform (PCYT1A),", mRNA, gi|31543384|ref|NM_005017.2|[31543384]; 865: NM_005023 , "Homo sapiens protein geranylgeranyltransferase type I, beta subunit (PGGT1B),", mRNA, gi|27597101|ref|NM_005023.2|[27597101]; 866: NM_005025 , "Homo sapiens serine (or cysteine) proteinase inhibitor, clade I (neuroserpin),", "member 1 (SERPINI1), mRNA", gi|4826903|ref|NM_005025.1|[4826903]; 867: NM_005027 , "Homo sapiens phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85", "beta) (PIK3R2), mRNA", gi|4826907|ref|NM_005027.1|[4826907]; 868: NM_005028 , "Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, alpha", "(PIP5K2A), mRNA", gi|20302162|ref|NM_005028.3|[20302162]; 869: NM_005037 , "Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG),", "transcript variant 4, mRNA", gi|20336230|ref|NM_005037.3|[20336230]; 870: NM_005041 , "Homo sapiens perforin 1 (pore

forming protein) (PRF1), mRNA", gi|40254807|ref|NM_005041.2|[40254807]; 871: NM_005048 , "Homo sapiens parathyroid hormone receptor 2 (PTHR2), mRNA", gi|39995097|ref|NM_005048.2|[39995097]; 872: NM_005049 , "Homo sapiens PWP2 periodic tryptophan protein homolog (yeast) (PWP2H), mRNA", gi|4826955|ref|NM_005049.1|[4826955]; 873: NM_005051 , "Homo sapiens glutaminyl-tRNA synthetase (QARS), mRNA", gi|4826959|ref|NM_005051.1|[4826959]; 874: NM_005074 , "Homo sapiens solute carrier family 17 (sodium phosphate), member 1 (SLC17A1),", mRNA, gi|4827009|ref|NM_005074.1|[4827009]; 875: NM_005076 , "Homo sapiens contactin 2 (axonal) (CNTN2), mRNA", gi|28373120|ref|NM_005076.2|[28373120]; 876: NM_005084 , "Homo sapiens phospholipase A2, group VII (platelet-activating factor", "acetylhydrolase, plasma) (PLA2G7), mRNA", gi|31543409|ref|NM_005084.2|[31543409]; 877: NM_005092 , "Homo sapiens tumor necrosis factor (ligand) superfamily, member 18 (TNFSF18),", mRNA, gi|40354198|ref|NM_005092.2|[40354198]; 878: NM_005097 , "Homo sapiens leucine-rich, glioma inactivated 1 (LGI1), mRNA", gi|4826815|ref|NM_005097.1|[4826815]; 879: NM_005098 , "Homo sapiens musculin (activated B-cell factor-1) (MSC), mRNA", gi|6996017|ref|NM_005098.2|[6996017]; 880: NM_005113 , "Homo sapiens golgi autoantigen, golgin subfamily a, 5 (GOLGA5), mRNA", gi|30260187|ref|NM_005113.2|[30260187]; 881: NM_005124 , "Homo sapiens nucleoporin 153kDa (NUP153), mRNA", gi|24430145|ref|NM_005124.2|[24430145]; 882: NM_005125 , "Homo sapiens copper chaperone for superoxide dismutase (CCS), mRNA", gi|4826664|ref|NM_005125.1|[4826664]; 883: NM_005132 , "Homo sapiens REC8-like 1 (yeast) (REC8L1), mRNA", gi|9845292|ref|NM_005132.1|[9845292]; 884: NM_005139 , "Homo sapiens annexin A3 (ANXA3), mRNA", gi|4826642|ref|NM_005139.1|[4826642]; 885: NM_005146 , "Homo sapiens squamous cell carcinoma antigen recognised by T cells (SART1), mRNA", gi|38788009|ref|NM_005146.3|[38788009]; 886: NM_005147 , "Homo sapiens DnaJ (Hsp40) homolog, subfamily A, member 3 (DNAJA3), mRNA", gi|40786390|ref|NM_005147.3|[40786390]; 887: NM_005154 , "Homo sapiens ubiquitin specific protease 8 (USP8), mRNA", gi|41281375|ref|NM_005154.2|[41281375]; 888: NM_005161 , "Homo sapiens angiotensin II receptor-like 1 (AGTRL1), mRNA", gi|34577064|ref|NM_005161.2|[34577064]; 889: NM_005164 , "Homo sapiens ATP-binding cassette, sub-family D (ALD), member 2 (ABCD2), mRNA", gi|21536379|ref|NM_005164.2|[21536379]; 890: NM_005169 , "Homo sapiens paired-like (aristaless) homeobox 2a (PHOX2A), mRNA", gi|4885070|ref|NM_005169.1|[4885070]; 891: NM_005170 , "Homo sapiens achaete-scute complex-like 2 (Drosophila) (ASCL2), mRNA", gi|42716308|ref|NM_005170.2|[42716308]; 892: NM_005171 , "Homo sapiens activating transcription factor 1 (ATF1), mRNA", gi|38261963|ref|NM_005171.2|[38261963]; 893: NM_005182 , "Homo sapiens carbonic anhydrase VII (CA7), mRNA", gi|4885100|ref|NM_005182.1|[4885100]; 894: NM_005186 , "Homo sapiens calpain 1, (mu/I) large subunit (CAPN1), mRNA", gi|12408655|ref|NM_005186.2|[12408655]; 895: NM_005198 , "Homo sapiens choline kinase-like (CHKL), transcript variant 1, mRNA", gi|23238259|ref|NM_005198.3|[23238259]; 896: NM_005209 , "Homo sapiens crystallin, beta A2 (CRYBA2), transcript variant 1, mRNA", gi|7019356|ref|NM_005209.1|[7019356]; 897: NM_005215 , "Homo sapiens deleted in colorectal carcinoma (DCC), mRNA", gi|4885174|ref|NM_005215.1|[4885174]; 898: NM_005221 , "Homo sapiens distal-less homeo box 5 (DLX5), mRNA", gi|41352719|ref|NM_005221.4|[41352719]; 899: NM_005222 , , ref|NM_005222.1|DLX6[4885188], This record was temporarily removed by RefSeq staff for

additional review.,, 900: NM_005223 , "Homo sapiens deoxyribonuclease I (DNASE1), mRNA", gi|21361253|ref|NM_005223.2|[21361253]; 901: NM_005224 , "Homo sapiens AT rich interactive domain 3A (BRIGHT- like) (ARID3A), mRNA", gi|4885192|ref|NM_005224.1|[4885192]; 902: NM_005227 , "Homo sapiens ephrin-A4 (EFNA4), transcript variant 1, mRNA", gi|33359684|ref|NM_005227.2|[33359684]; 903: NM_005236 , "Homo sapiens excision repair cross-complementing rodent repair deficiency,", "complementation group 4 (ERCC4), mRNA", gi|4885216|ref|NM_005236.1|[4885216]; 904: NM_005238 , "Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1),", mRNA, gi|41393580|ref|NM_005238.2|[41393580]; 905: NM_005239 , "Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 2 (avian) (ETS2),", mRNA, gi|20127471|ref|NM_005239.2|[20127471]; 906: NM_005245 , "Homo sapiens FAT tumor suppressor homolog 1 (Drosophila) (FAT), mRNA", gi|4885228|ref|NM_005245.1|[4885228]; 907: NM_005246 , "Homo sapiens fer (fps/fes related) tyrosine kinase (phosphoprotein NCP94) (FER),", mRNA, gi|4885230|ref|NM_005246.1|[4885230]; 908: NM_005251 , "Homo sapiens forkhead box C2 (MFH-1, mesenchyme forkhead 1) (FOXC2), mRNA", gi|4885236|ref|NM_005251.1|[4885236]; 909: NM_005256 , "Homo sapiens growth arrest-specific 2 (GAS2), transcript variant 1, mRNA", gi|29540560|ref|NM_005256.2|[29540560]; 910: NM_005257 , "Homo sapiens GATA binding protein 6 (GATA6), mRNA", gi|40288196|ref|NM_005257.3|[40288196]; 911: NM_005258 , "Homo sapiens GTP cyclohydrolase I feedback regulatory protein (GCHFR), mRNA", gi|6382072|ref|NM_005258.2|[6382072]; 912: NM_005260 , "Homo sapiens growth differentiation factor 9 (GDF9), mRNA", gi|6715598|ref|NM_005260.2|[6715598]; 913: NM_005264 , "Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 1, mRNA", gi|22035690|ref|NM_005264.2|[22035690]; 914: NM_005266 , "Homo sapiens gap junction protein, alpha 5, 40kDa (connexin 40) (GJA5),", "transcript variant A, mRNA", gi|32483413|ref|NM_005266.4|[32483413]; 915: NM_005268 , "Homo sapiens gap junction protein, beta 5 (connexin 31.1) (GJB5), mRNA", gi|31542847|ref|NM_005268.2|[31542847]; 916: NM_005272 , "Homo sapiens guanine nucleotide binding protein (G protein), alpha transducing", "activity polypeptide 2 (GNAT2), mRNA", gi|22027523|ref|NM_005272.2|[22027523]; 917: NM_005275 , "Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA", gi|38788318|ref|NM_005275.2|[38788318]; 918: NM_005281 , "Homo sapiens G protein-coupled receptor 3 (GPR3), mRNA", gi|31377791|ref|NM_005281.2|[31377791]; 919: NM_005286 , "Homo sapiens G protein-coupled receptor 8 (GPR8), mRNA", gi|30581163|ref|NM_005286.2|[30581163]; 920: NM_005288 , "Homo sapiens G protein-coupled receptor 12 (GPR12), mRNA", gi|4885294|ref|NM_005288.1|[4885294]; 921: NM_005299 , "Homo sapiens G protein-coupled receptor 31 (GPR31), mRNA", gi|4885316|ref|NM_005299.1|[4885316]; 922: NM_005302 , Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like), "(GPR37), mRNA", gi|31377788|ref|NM_005302.2|[31377788]; 923: NM_005306 , "Homo sapiens G protein-coupled receptor 43 (GPR43), mRNA", gi|4885332|ref|NM_005306.1|[4885332]; 924: NM_005309 , "Homo sapiens glutamic-pyruvate transaminase (alanine aminotransferase) (GPT),", mRNA, gi|4885350|ref|NM_005309.1|[4885350]; 925: NM_005312 , Homo sapiens guanine nucleotide-releasing factor 2 (specific for crk, "proto-oncogene) (GRF2), transcript variant 1, mRNA", gi|38373674|ref|NM_005312.2|[38373674]; 926: NM_005313 , "Homo sapiens glucose regulated protein, 58kDa (GRP58), mRNA", gi|21361656|ref|NM_005313.3|[21361656]; 927: NM_005318 , "Homo sapiens H1 histone

family, member 0 (H1F0), mRNA", gi|20336758|ref|NM_005318.2|[20336758]; 928: NM_005321 , "Homo sapiens histone 1, H1e (HIST1H1E), mRNA", gi|20544164|ref|NM_005321.2|[20544164]; 929: NM_005325 , "Homo sapiens histone 1, H1a (HIST1H1A), mRNA", gi|21264571|ref|NM_005325.2|[21264571]; 930: NM_005330 , "Homo sapiens hemoglobin, epsilon 1 (HBE1), mRNA", gi|28302129|ref|NM_005330.3|[28302129]; 931: NM_005341 , "Homo sapiens GLI-Kruppel family member HKR3 (HKR3), mRNA", gi|4885418|ref|NM_005341.1|[4885418]; 932: NM_005370 , "Homo sapiens RAB8A, member RAS oncogene family (RAB8A), mRNA", gi|40548385|ref|NM_005370.4|[40548385]; 933: NM_005379 , "Homo sapiens myosin IA (MYO1A), mRNA", gi|29544746|ref|NM_005379.2|[29544746]; 934: NM_005381 , "Homo sapiens nucleolin (NCL), mRNA", gi|4885510|ref|NM_005381.1|[4885510]; 935: NM_005382 , "Homo sapiens neurofilament 3 (150kDa medium) (NEF3), mRNA", gi|4885512|ref|NM_005382.1|[4885512]; 936: NM_005386 , "Homo sapiens neuronatin (NNAT), transcript variant 1, mRNA", gi|32307134|ref|NM_005386.2|[32307134]; 937: NM_005390 , "Homo sapiens pyruvate dehydrogenase (lipoamide) alpha 2 (PDHA2), mRNA", gi|38492354|ref|NM_005390.3|[38492354]; 938: NM_005393 , "Homo sapiens plexin B3 (PLXNB3), mRNA", gi|10864080|ref|NM_005393.1|[10864080]; 939: NM_005398 , "Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3C (PPP1R3C),", mRNA, gi|42476161|ref|NM_005398.3|[42476161]; 940: NM_005401 , "Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), mRNA", gi|34328898|ref|NM_005401.3|[34328898]; 941: NM_005402 , Homo sapiens v-ral simian leukemia viral oncogene homolog A (ras related), "(RALA), mRNA", gi|33946328|ref|NM_005402.2|[33946328]; 942: NM_005418 , "Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 1, mRNA", gi|21264611|ref|NM_005418.2|[21264611]; 943: NM_005423 , "Homo sapiens trefoil factor 2 (spasmolytic protein 1) (TFF2), mRNA", gi|38488723|ref|NM_005423.2|[38488723]; 944: NM_005424 , Homo sapiens tyrosine kinase with immunoglobulin and epidermal growth factor, "homology domains (TIE), mRNA", gi|31543809|ref|NM_005424.2|[31543809]; 945: NM_005426 , "Homo sapiens tumor protein p53 binding protein, 2 (TP53BP2), mRNA", gi|4885642|ref|NM_005426.1|[4885642]; 946: NM_005427 , "Homo sapiens tumor protein p73 (TP73), mRNA", gi|4885644|ref|NM_005427.1|[4885644]; 947: NM_005428 , "Homo sapiens vav 1 oncogene (VAV1), mRNA", gi|7108366|ref|NM_005428.2|[7108366]; 948: NM_005429 , "Homo sapiens vascular endothelial growth factor C (VEGFC), mRNA", gi|19924300|ref|NM_005429.2|[19924300]; 949: NM_005431 , Homo sapiens X-ray repair complementing defective repair in Chinese hamster, "cells 2 (XRCC2), mRNA", gi|4885656|ref|NM_005431.1|[4885656]; 950: NM_005432 , Homo sapiens X-ray repair complementing defective repair in Chinese hamster, "cells 3 (XRCC3), mRNA", gi|12408644|ref|NM_005432.2|[12408644]; 951: NM_005436 , "Homo sapiens coiled-coil domain containing 6 (CCDC6), mRNA", gi|4885172|ref|NM_005436.1|[4885172]; 952: NM_005439 , "Homo sapiens myeloid leukemia factor 2 (MLF2), mRNA", gi|4885486|ref|NM_005439.1|[4885486]; 953: NM_005441 , "Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA", gi|4885104|ref|NM_005441.1|[4885104]; 954: NM_005452 , "Homo sapiens chromosome 6 open reading frame 11 (C6orf11), mRNA", gi|39725662|ref|NM_005452.4|[39725662]; 955: NM_005453 , "Homo sapiens zinc finger protein 297 (ZNF297), mRNA", gi|20070223|ref|NM_005453.3|[20070223]; 956: NM_005460 , "Homo sapiens synuclein, alpha

interacting protein (synphilin) (SNCAIP), mRNA", gi|4885602|ref|NM_005460.1|[4885602]; 957: NM_005461 , Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian), "(MAFB), mRNA", gi|31652256|ref|NM_005461.3|[31652256]; 958: NM_005469 , "Homo sapiens peroxisomal acyl-CoA thioesterase (PTE1), transcript variant 1,", mRNA, gi|34577074|ref|NM_005469.2|[34577074]; 959: NM_005474 , "Homo sapiens histone deacetylase 5 (HDAC5), transcript variant 1, mRNA", gi|21237796|ref|NM_005474.3|[21237796]; 960: NM_005475 , "Homo sapiens lymphocyte adaptor protein (LNK), mRNA", gi|4885454|ref|NM_005475.1|[4885454]; 961: NM_005477 , Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium, "channel 4 (HCN4), mRNA", gi|4885406|ref|NM_005477.1|[4885406]; 962: NM_005479 , "Homo sapiens frequently rearranged in advanced T-cell lymphomas (FRAT1),", "transcript variant 1, mRNA", gi|31317235|ref|NM_005479.2|[31317235]; 963: NM_005485 , Homo sapiens ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)-like 3, "(ADPRTL3), mRNA", gi|11496992|ref|NM_005485.2|[11496992]; 964: NM_005490 , "Homo sapiens SH2 domain containing 3A (SH2D3A), mRNA", gi|4885524|ref|NM_005490.1|[4885524]; 965: NM_005499 , "Homo sapiens SUMO-1 activating enzyme subunit 2 (UBA2), mRNA", gi|4885648|ref|NM_005499.1|[4885648]; 966: NM_005505 , "Homo sapiens scavenger receptor class B, member 1 (SCARB1), mRNA", gi|33620766|ref|NM_005505.3|[33620766]; 967: NM_005507 , "Homo sapiens cofilin 1 (non-muscle) (CFL1), mRNA", gi|5031634|ref|NM_005507.1|[5031634]; 968: NM_005517 , "Homo sapiens high-mobility group nucleosomal binding domain 2 (HMGN2), mRNA", gi|5031748|ref|NM_005517.1|[5031748]; 969: NM_005522 , "Homo sapiens homeo box A1 (HOXA1), transcript variant 1, mRNA", gi|24497507|ref|NM_005522.3|[24497507]; 970: NM_005527 , "Homo sapiens heat shock 70kDa protein 1-like (HSPA1L), mRNA", gi|27436928|ref|NM_005527.2|[27436928]; 971: NM_005534 , Homo sapiens interferon gamma receptor 2 (interferon gamma transducer 1), "(IFNGR2), mRNA", gi|5031782|ref|NM_005534.1|[5031782]; 972: NM_005536 , "Homo sapiens inositol(myo)-1(or 4)-monophosphatase 1 (IMPA1), mRNA", gi|8393607|ref|NM_005536.2|[8393607]; 973: NM_005539 , "Homo sapiens inositol polyphosphate-5-phosphatase, 40kDa (INPP5A), mRNA", gi|38327536|ref|NM_005539.2|[38327536]; 974: NM_005545 , "Homo sapiens immunoglobulin superfamily containing leucine-rich repeat (ISLR),", "transcript variant 1, mRNA", gi|41582237|ref|NM_005545.3|[41582237]; 975: NM_005550 , "Homo sapiens kinesin family member C3 (KIFC3), mRNA", gi|19923320|ref|NM_005550.2|[19923320]; 976: NM_005560 , "Homo sapiens laminin, alpha 5 (LAMA5), mRNA", gi|21264601|ref|NM_005560.3|[21264601]; 977: NM_005563 , "Homo sapiens stathmin 1/oncoprotein 18 (STMN1), mRNA", gi|13518023|ref|NM_005563.2|[13518023]; 978: NM_005567 , "Homo sapiens lectin, galactoside-binding, soluble, 3 binding protein (LGALS3BP),", mRNA, gi|6006016|ref|NM_005567.2|[6006016]; 979: NM_005574 , "Homo sapiens LIM domain only 2 (rhombotin-like 1) (LMO2), mRNA", gi|6633806|ref|NM_005574.2|[6633806]; 980: NM_005575 , "Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA", gi|5031880|ref|NM_005575.1|[5031880]; 981: NM_005583 , "Homo sapiens lymphoblastic leukemia derived sequence 1 (LYL1), mRNA", gi|34147557|ref|NM_005583.3|[34147557]; 982: NM_005584 , "Homo sapiens mab-21-like 1 (C. elegans) (MAB21L1), mRNA", gi|18765719|ref|NM_005584.2|[18765719]; 983: NM_005608 , "Homo sapiens protein tyrosine phosphatase, receptor type, C-associated protein", "(PTPRCAP), mRNA", gi|5032004|ref|NM_005608.1|[5032004]; 984: NM_005620 , "Homo sapiens S100 calcium

binding protein A11 (calgizzarin) (S100A11), mRNA", gi|5032056|ref|NM_005620.1|[5032056]; 985: NM_005626 , "Homo sapiens splicing factor, arginine/serine-rich 4 (SFRS4), mRNA", gi|34147660|ref|NM_005626.3|[34147660]; 986: NM_005627 , "Homo sapiens serum/glucocorticoid regulated kinase (SGK), mRNA", gi|25168262|ref|NM_005627.2|[25168262]; 987: NM_005628 , "Homo sapiens solute carrier family 1 (neutral amino acid transporter), member 5", "(SLC1A5), mRNA", gi|5032092|ref|NM_005628.1|[5032092]; 988: NM_005632 , "Homo sapiens small optic lobes homolog (Drosophila) (SOLH), mRNA", gi|41406087|ref|NM_005632.2|[41406087]; 989: NM_005634 , "Homo sapiens SRY (sex determining region Y)-box 3 (SOX3), mRNA", gi|30061555|ref|NM_005634.2|[30061555]; 990: NM_005643 , "Homo sapiens TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated", "factor, 28kDa (TAF11), mRNA", gi|21269863|ref|NM_005643.2|[21269863]; 991: NM_005644 , "Homo sapiens TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated", "factor, 20kDa (TAF12), mRNA", gi|9943840|ref|NM_005644.2|[9943840]; 992: NM_005652 , "Homo sapiens telomeric repeat binding factor 2 (TERF2), mRNA", gi|21536372|ref|NM_005652.2|[21536372]; 993: NM_005655 , "Homo sapiens TGFB inducible early growth response (TIEG), mRNA", gi|5032176|ref|NM_005655.1|[5032176]; 994: NM_005657 , "Homo sapiens tumor protein p53 binding protein, 1 (TP53BP1), mRNA", gi|5032188|ref|NM_005657.1|[5032188]; 995: NM_005659 , "Homo sapiens ubiquitin fusion degradation 1-like (UFD1L), mRNA", gi|34222257|ref|NM_005659.3|[34222257]; 996: NM_005664 , "Homo sapiens makorin, ring finger protein, 3 (MKRN3), mRNA", gi|5032242|ref|NM_005664.1|[5032242]; 997: NM_005671 , "Homo sapiens reproduction 8 (D8S2298E), mRNA", gi|5031650|ref|NM_005671.1|[5031650]; 998: NM_005688 , "Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 5 (ABCC5),", mRNA, gi|5032100|ref|NM_005688.1|[5032100]; 999: NM_005690 , "Homo sapiens dynamin 1-like (DNM1L), transcript variant 3, mRNA", gi|6996008|ref|NM_005690.2|[6996008]; 1000: NM_005694 , "Homo sapiens COX17 homolog, cytochrome c oxidase assembly protein (yeast)", "(COX17), nuclear gene encoding mitochondrial protein, mRNA", gi|5031644|ref|NM_005694.1|[5031644]; 1001: NM_005697 , "Homo sapiens secretory carrier membrane protein 2 (SCAMP2), mRNA", gi|16445417|ref|NM_005697.3|[16445417]; 1002: NM_005698 , "Homo sapiens secretory carrier membrane protein 3 (SCAMP3), transcript variant", "1, mRNA", gi|16445418|ref|NM_005698.2|[16445418]; 1003: NM_005700 , "Homo sapiens dipeptidylpeptidase 3 (DPP3), transcript variant 1, mRNA", gi|18491023|ref|NM_005700.2|[18491023]; 1004: NM_005705 , "Homo sapiens pan-hematopoietic expression (PHEMX), transcript variant 2, mRNA", gi|37595533|ref|NM_005705.3|[37595533]; 1005: NM_005706 , "Homo sapiens tumor suppressing subtransferable candidate 4 (TSSC4), mRNA", gi|21071005|ref|NM_005706.2|[21071005]; 1006: NM_005713 , "Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) binding protein", "(COL4A3BP), transcript variant 1, mRNA", gi|5031716|ref|NM_005713.1|[5031716]; 1007: NM_005714 , "Homo sapiens potassium channel, subfamily K, member 7 (KCNK7), transcript", "variant C, mRNA", gi|5031820|ref|NM_005714.1|[5031820]; 1008: NM_005716 , Homo sapiens regulator of G-protein signalling 19 interacting protein 1, "(RGS19IP1), transcript variant 1, mRNA", gi|42544147|ref|NM_005716.2|[42544147]; 1009: NM_005717 , "Homo sapiens actin related protein 2/3 complex, subunit 5, 16kDa (ARPC5), mRNA", gi|23238212|ref|NM_005717.2|[23238212]; 1010: NM_005719 , "Homo sapiens actin related

protein 2/3 complex, subunit 3, 21kDa (ARPC3), mRNA", gi|23397667|ref|NM_005719.2|[23397667]; 1011: NM_005726 , "Homo sapiens Ts translation elongation factor, mitochondrial (TSFM), mRNA", gi|21361279|ref|NM_005726.2|[21361279]; 1012: NM_005727 , "Homo sapiens tetraspan 1 (TSPAN-1), mRNA", gi|21264577|ref|NM_005727.2|[21264577]; 1013: NM_005738 , "Homo sapiens ADP-ribosylation factor-like 4 (ARL4), mRNA", gi|5031602|ref|NM_005738.1|[5031602]; 1014: NM_005740 , "Homo sapiens dynein, axonemal, light polypeptide 4 (DNAL4), mRNA", gi|5031666|ref|NM_005740.1|[5031666]; 1015: NM_005745 , "Homo sapiens B-cell receptor-associated protein 31 (BCAP31), mRNA", gi|32171185|ref|NM_005745.5|[32171185]; 1016: NM_005755 , "Homo sapiens Epstein-Barr virus induced gene 3 (EBI3), mRNA", gi|14577916|ref|NM_005755.2|[14577916]; 1017: NM_005756 , "Homo sapiens G protein-coupled receptor 64 (GPR64), mRNA", gi|5031732|ref|NM_005756.1|[5031732]; 1018: NM_005764 , "Homo sapiens membrane-associated protein 17 (MAP17), mRNA", gi|41152089|ref|NM_005764.3|[41152089]; 1019: NM_005770 , "Homo sapiens small EDRK-rich factor 2 (SERF2), mRNA", gi|42475556|ref|NM_005770.3|[42475556]; 1020: NM_005772 , "Homo sapiens RNA terminal phosphate cyclase-like 1 (RCL1), mRNA", gi|21361284|ref|NM_005772.2|[21361284]; 1021: NM_005780 , "Homo sapiens lipoma HMGIC fusion partner (LHFP), mRNA", gi|5031864|ref|NM_005780.1|[5031864]; 1022: NM_005787 , "Homo sapiens asparagine-linked glycosylation 3 homolog (yeast,", "alpha-1,3-mannosyltransferase) (ALG3), mRNA", gi|39725713|ref|NM_005787.3|[39725713]; 1023: NM_005792 , "Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA", gi|5031918|ref|NM_005792.1|[5031918]; 1024: NM_005796 , "Homo sapiens nuclear transport factor 2 (NUTF2), mRNA", gi|5031984|ref|NM_005796.1|[5031984]; 1025: NM_005798 , "Homo sapiens ret finger protein 2 (RFP2), transcript variant 1, mRNA", gi|16445410|ref|NM_005798.2|[16445410]; 1026: NM_005805 , "Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 14", "(PSMD14), mRNA", gi|42734423|ref|NM_005805.2|[42734423]; 1027: NM_005833 , "Homo sapiens Rab9 effector p40 (RAB9P40), mRNA", gi|33695108|ref|NM_005833.2|[33695108]; 1028: NM_005835 , "Homo sapiens solute carrier family 17 (sodium phosphate), member 2 (SLC17A2),", mRNA, gi|5031954|ref|NM_005835.1|[5031954]; 1029: NM_005836 , "Homo sapiens translational inhibitor protein p14.5 (UK114), mRNA", gi|5032214|ref|NM_005836.1|[5032214]; 1030: NM_005842 , "Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA", gi|22209007|ref|NM_005842.2|[22209007]; 1031: NM_005845 , "Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4),", mRNA, gi|34452699|ref|NM_005845.2|[34452699]; 1032: NM_005850 , "Homo sapiens splicing factor 3b, subunit 4, 49kDa (SF3B4), mRNA", gi|23111059|ref|NM_005850.3|[23111059]; 1033: NM_005851 , "Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R), mRNA", gi|39725675|ref|NM_005851.3|[39725675]; 1034: NM_005853 , "Homo sapiens iroquois homeobox protein 5 (IRX5), mRNA", gi|42415493|ref|NM_005853.3|[42415493]; 1035: NM_005856 , "Homo sapiens receptor (calcitonin) activity modifying protein 3 (RAMP3), mRNA", gi|5032022|ref|NM_005856.1|[5032022]; 1036: NM_005857 , "Homo sapiens zinc metalloproteinase (STE24 homolog, yeast) (ZMPSTE24), mRNA", gi|18379365|ref|NM_005857.2|[18379365]; 1037: NM_005860 , "Homo sapiens follistatin-like 3 (secreted glycoprotein) (FSTL3), mRNA", gi|5031700|ref|NM_005860.1|[5031700]; 1038: NM_005861 , "Homo sapiens STIP1 homology and U-Box containing protein 1 (STUB1), mRNA", gi|5031962|ref|NM_005861.1|[5031962]; 1039: NM_005873 , "Homo sapiens regulator

of G-protein signalling 19 (RGS19), mRNA", gi|5031704|ref|NM_005873.1|[5031704]; 1040: NM_005876 , "Homo sapiens aortic preferentially expressed protein 1 (APEG1), mRNA", gi|37577150|ref|NM_005876.3|[37577150]; 1041: NM_005879 , "Homo sapiens TRAF interacting protein (TRIP), mRNA", gi|40807468|ref|NM_005879.2|[40807468]; 1042: NM_005881 , "Homo sapiens branched chain alpha-ketoacid dehydrogenase kinase (BCKDK), mRNA", gi|5031608|ref|NM_005881.1|[5031608]; 1043: NM_005882 , "Homo sapiens macrophage erythroblast attacher (MAEA), mRNA", gi|9257203|ref|NM_005882.2|[9257203]; 1044: NM_005891 , Homo sapiens acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A, "thiolase) (ACAT2), mRNA", gi|5174388|ref|NM_005891.1|[5174388]; 1045: NM_005895 , "Homo sapiens golgi autoantigen, golgin subfamily a, 3 (GOLGA3), mRNA", gi|30089939|ref|NM_005895.2|[30089939]; 1046: NM_005900 , "Homo sapiens MAD, mothers against decapentaplegic homolog 1 (Drosophila)", "(MADH1), mRNA", gi|5174508|ref|NM_005900.1|[5174508]; 1047: NM_005904 , "Homo sapiens MAD, mothers against decapentaplegic homolog 7 (Drosophila)", "(MADH7), mRNA", gi|5174516|ref|NM_005904.1|[5174516]; 1048: NM_005908 , "Homo sapiens mannosidase, beta A, lysosomal (MANBA), mRNA", gi|24797157|ref|NM_005908.2|[24797157]; 1049: NM_005909 , "Homo sapiens microtubule-associated protein 1B (MAP1B), transcript variant 1,", mRNA, gi|14165457|ref|NM_005909.2|[14165457]; 1050: NM_005912 , "Homo sapiens melanocortin 4 receptor (MC4R), mRNA", gi|5174532|ref|NM_005912.1|[5174532]; 1051: NM_005915 , "Homo sapiens MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, S.", "pombe) (S. cerevisiae) (MCM6), mRNA", gi|33469920|ref|NM_005915.4|[33469920]; 1052: NM_005917 , "Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1), mRNA", gi|21735619|ref|NM_005917.2|[21735619]; 1053: NM_005953 , "Homo sapiens metallothionein 2A (MT2A), mRNA", gi|31543214|ref|NM_005953.2|[31543214]; 1054: NM_005956 , "Homo sapiens methylenetetrahydrofolate dehydrogenase (NADP+ dependent),", "methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase", "(MTHFD1), mRNA", gi|13699867|ref|NM_005956.2|[13699867]; 1055: NM_005958 , "Homo sapiens melatonin receptor 1A (MTNR1A), mRNA", gi|14141171|ref|NM_005958.2|[14141171]; 1056: NM_005965 , "Homo sapiens myosin, light polypeptide kinase (MYLK), transcript variant 6, mRNA", gi|16950600|ref|NM_005965.2|[16950600]; 1057: NM_005975 , "Homo sapiens PTK6 protein tyrosine kinase 6 (PTK6), mRNA", gi|27886594|ref|NM_005975.2|[27886594]; 1058: NM_005984 , Homo sapiens solute carrier family 25 (mitochondrial carrier; citrate, "transporter), member 1 (SLC25A1), mRNA", gi|21389314|ref|NM_005984.1|[21389314]; 1059: NM_005985 , "Homo sapiens snail homolog 1 (Drosophila) (SNAI1), mRNA", gi|18765740|ref|NM_005985.2|[18765740]; 1060: NM_005996 , "Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA", gi|18375606|ref|NM_005996.2|[18375606]; 1061: NM_005997 , "Homo sapiens transcription factor-like 1 (TCFL1), mRNA", gi|5174714|ref|NM_005997.1|[5174714]; 1062: NM_006002 , Homo sapiens ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase), "(UCHL3), mRNA", gi|37059734|ref|NM_006002.3|[37059734]; 1063: NM_006003 , "Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1", "(UQCRFS1), mRNA", gi|5174742|ref|NM_006003.1|[5174742]; 1064: NM_006004 , "Homo sapiens ubiquinol-cytochrome c reductase hinge protein (UQCRH), mRNA", gi|5174744|ref|NM_006004.1|[5174744]; 1065: NM_006010 , "Homo sapiens arginine-rich, mutated in early stage tumors (ARMET), mRNA", gi|5174392|ref|NM_006010.1|[5174392];

1066: NM_006011 , "Homo sapiens sialyltransferase 8B (alpha-2, 8-sialyltransferase) (SIAT8B), mRNA", gi|28373096|ref|NM_006011.2|[28373096]; 1067: NM_006012 , "Homo sapiens ClpP caseinolytic protease, ATP-dependent, proteolytic subunit", "homolog (E. coli) (CLPP), nuclear gene encoding mitochondrial protein, mRNA", gi|5174418|ref|NM_006012.1|[5174418]; 1068: NM_006017 , "Homo sapiens prominin 1 (PROM1), mRNA", gi|5174386|ref|NM_006017.1|[5174386]; 1069: NM_006020 , "Homo sapiens alkB, alkylation repair homolog (E. coli) (ALKBH), mRNA", gi|5174384|ref|NM_006020.1|[5174384]; 1070: NM_006023 , "Homo sapiens chromosome 10 open reading frame 7 (C10orf7), mRNA", gi|5174422|ref|NM_006023.1|[5174422]; 1071: NM_006035 , "Homo sapiens CDC42 binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA", gi|16357473|ref|NM_006035.2|[16357473]; 1072: NM_006037 , "Homo sapiens histone deacetylase 4 (HDAC4), mRNA", gi|13259519|ref|NM_006037.2|[13259519]; 1073: NM_006041 , "Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1),", mRNA, gi|5174466|ref|NM_006041.1|[5174466]; 1074: NM_006042 , "Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1),", mRNA, gi|5174464|ref|NM_006042.1|[5174464]; 1075: NM_006056 , "Homo sapiens G protein-coupled receptor 66 (GPR66), mRNA", gi|24432088|ref|NM_006056.2|[24432088]; 1076: NM_006061 , "Homo sapiens cysteine-rich secretory protein 3 (CRISP3), mRNA", gi|5174674|ref|NM_006061.1|[5174674]; 1077: NM_006067 , "Homo sapiens neighbor of COX4 (NOC4), mRNA", gi|34147520|ref|NM_006067.3|[34147520]; 1078: NM_006070 , "Homo sapiens TRK-fused gene (TFG), mRNA", gi|34147663|ref|NM_006070.3|[34147663]; 1079: NM_006080 , "Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain,", "secreted, (semaphorin) 3A (SEMA3A), mRNA", gi|5174672|ref|NM_006080.1|[5174672]; 1080: NM_006084 , "Homo sapiens interferon-stimulated transcription factor 3, gamma 48kDa (ISGF3G),", mRNA, gi|25282406|ref|NM_006084.3|[25282406]; 1081: NM_006089 , "Homo sapiens sex comb on midleg-like 2 (Drosophila) (SCML2), mRNA", gi|5174668|ref|NM_006089.1|[5174668]; 1082: NM_006090 , "Homo sapiens choline/ethanolaminephosphotransferase (CEPT1), mRNA", gi|21735567|ref|NM_006090.2|[21735567]; 1083: NM_006091 , "Homo sapiens coronin, actin binding protein, 2B (CORO2B), mRNA", gi|24307902|ref|NM_006091.1|[24307902]; 1084: NM_006094 , "Homo sapiens deleted in liver cancer 1 (DLC1), transcript variant 2, mRNA", gi|33188436|ref|NM_006094.3|[33188436]; 1085: NM_006096 , "Homo sapiens N-myc downstream regulated gene 1 (NDRG1), mRNA", gi|37655182|ref|NM_006096.2|[37655182]; 1086: NM_006097 , "Homo sapiens myosin, light polypeptide 9, regulatory (MYL9), transcript variant", "1, mRNA", gi|31563522|ref|NM_006097.3|[31563522]; 1087: NM_006101 , "Homo sapiens kinetochore associated 2 (KNTC2), mRNA", gi|5174456|ref|NM_006101.1|[5174456]; 1088: NM_006103 , "Homo sapiens WAP four-disulfide core domain 2 (WFDC2), transcript variant 1,", mRNA, gi|18379363|ref|NM_006103.2|[18379363]; 1089: NM_006114 , Homo sapiens translocase of outer mitochondrial membrane 40 homolog (yeast), "(TOMM40), mRNA", gi|5174722|ref|NM_006114.1|[5174722]; 1090: NM_006119 , "Homo sapiens fibroblast growth factor 8 (androgen-induced) (FGF8), transcript", "variant B, mRNA", gi|15147351|ref|NM_006119.2|[15147351]; 1091: NM_006122 , "Homo sapiens mannosidase, alpha, class 2A, member 2 (MAN2A2), mRNA", gi|5540099|ref|NM_006122.1|[5540099]; 1092: NM_006133 , "Homo sapiens chromosome 11 open reading frame 11 (C11orf11), mRNA", gi|27262631|ref|NM_006133.1|[27262631]; 1093: NM_006135 , "Homo sapiens capping protein (actin filament) muscle Z-line, alpha 1 (CAPZA1),", mRNA,

gi|5453596|ref|NM_006135.1|[5453596]; 1094: NM_006148 , "Homo sapiens LIM and SH3 protein 1 (LASP1), mRNA", gi|5453709|ref|NM_006148.1|[5453709]; 1095: NM_006156 , "Homo sapiens neural precursor cell expressed, developmentally down-regulated 8", "(NEDD8), mRNA", gi|5453759|ref|NM_006156.1|[5453759]; 1096: NM_006157 , "Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA", gi|5453763|ref|NM_006157.1|[5453763]; 1097: NM_006164 , "Homo sapiens nuclear factor (erythroid-derived 2)-like 2 (NFE2L2), mRNA", gi|20149575|ref|NM_006164.2|[20149575]; 1098: NM_006168 , "Homo sapiens NK6 transcription factor related, locus 1 (Drosophila) (NKX6-1),", mRNA, gi|5453787|ref|NM_006168.1|[5453787]; 1099: NM_006172 , "Homo sapiens natriuretic peptide precursor A (NPPA), mRNA", gi|23510318|ref|NM_006172.1|[23510318]; 1100: NM_006181 , "Homo sapiens netrin 2-like (chicken) (NTN2L), mRNA", gi|5453809|ref|NM_006181.1|[5453809]; 1101: NM_006194 , "Homo sapiens paired box gene 9 (PAX9), mRNA", gi|7242166|ref|NM_006194.1|[7242166]; 1102: NM_006195 , "Homo sapiens pre-B-cell leukemia transcription factor 3 (PBX3), mRNA", gi|24475894|ref|NM_006195.2|[24475894]; 1103: NM_006196 , "Homo sapiens poly(rC) binding protein 1 (PCBP1), mRNA", gi|14141164|ref|NM_006196.2|[14141164]; 1104: NM_006204 , "Homo sapiens phosphodiesterase 6C, cGMP-specific, cone, alpha prime (PDE6C),", mRNA, gi|21361307|ref|NM_006204.2|[21361307]; 1105: NM_006205 , "Homo sapiens phosphodiesterase 6H, cGMP-specific, cone, gamma (PDE6H), mRNA", gi|5453867|ref|NM_006205.1|[5453867]; 1106: NM_006221 , Homo sapiens protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1, "(PIN1), mRNA", gi|5453897|ref|NM_006221.1|[5453897]; 1107: NM_006228 , "Homo sapiens prepronociceptin (PNOC), mRNA", gi|11079650|ref|NM_006228.2|[11079650]; 1108: NM_006232 , "Homo sapiens polymerase (RNA) II (DNA directed) polypeptide H (POLR2H), mRNA", gi|14589952|ref|NM_006232.2|[14589952]; 1109: NM_006236 , "Homo sapiens POU domain, class 3, transcription factor 3 (POU3F3), mRNA", gi|5453935|ref|NM_006236.1|[5453935]; 1110: NM_006240 , "Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1),", "transcript variant 1, mRNA", gi|23312379|ref|NM_006240.2|[23312379]; 1111: NM_006246 , "Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform", "(PPP2R5E), mRNA", gi|31083295|ref|NM_006246.2|[31083295]; 1112: NM_006254 , "Homo sapiens protein kinase C, delta (PRKCD), mRNA", gi|31377781|ref|NM_006254.2|[31377781]; 1113: NM_006259 , "Homo sapiens protein kinase, cGMP-dependent, type II (PRKG2), mRNA", gi|5453977|ref|NM_006259.1|[5453977]; 1114: NM_006261 , "Homo sapiens prophet of Pit1, paired-like homeodomain transcription factor", "(PROP1), mRNA", gi|40254838|ref|NM_006261.2|[40254838]; 1115: NM_006262 , "Homo sapiens peripherin (PRPH), mRNA", gi|21264344|ref|NM_006262.2|[21264344]; 1116: NM_006263 , "Homo sapiens proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)", "(PSME1), transcript variant 1, mRNA", gi|30581139|ref|NM_006263.2|[30581139]; 1117: NM_006270 , "Homo sapiens related RAS viral (r-ras) oncogene homolog (RRAS), mRNA", gi|20127497|ref|NM_006270.2|[20127497]; 1118: NM_006280 , "Homo sapiens signal sequence receptor, delta (translocon-associated protein", "delta) (SSR4), mRNA", gi|5454089|ref|NM_006280.1|[5454089]; 1119: NM_006284 , "Homo sapiens TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated", "factor, 30kDa (TAF10), mRNA", gi|21166374|ref|NM_006284.2|[21166374]; 1120: NM_006285 , "Homo sapiens testis-specific kinase 1 (TESK1), mRNA", gi|5454109|ref|NM_006285.1|[5454109]; 1121: NM_006289 , "Homo sapiens talin 1 (TLN1), mRNA", gi|16753232|ref|NM_006289.2|[16753232]; 1122:

NM_006292 , "Homo sapiens tumor susceptibility gene 101 (TSG101), mRNA", gi|18765712|ref|NM_006292.2|[18765712]; 1123: NM_006298 , "Homo sapiens zinc finger protein 192 (ZNF192), mRNA", gi|5454177|ref|NM_006298.1|[5454177]; 1124: NM_006302 , "Homo sapiens glucosidase I (GCS1), mRNA", gi|5453661|ref|NM_006302.1|[5453661]; 1125: NM_006315 , "Homo sapiens ring finger protein 3 (RNF3), mRNA", gi|34305288|ref|NM_006315.3|[34305288]; 1126: NM_006329 , "Homo sapiens fibulin 5 (FBLN5), mRNA", gi|19743802|ref|NM_006329.2|[19743802]; 1127: NM_006331 , "Homo sapiens C2f protein (C2F), mRNA", gi|31652261|ref|NM_006331.3|[31652261]; 1128: NM_006333 , "Homo sapiens nuclear DNA-binding protein (C1D), transcript variant 1, mRNA", gi|27894371|ref|NM_006333.2|[27894371]; 1129: NM_006338 , "Homo sapiens leucine rich repeat neuronal 5 (LRRN5), transcript variant 1, mRNA", gi|42544230|ref|NM_006338.2|[42544230]; 1130: NM_006342 , "Homo sapiens transforming, acidic coiled-coil containing protein 3 (TACC3), mRNA", gi|5454101|ref|NM_006342.1|[5454101]; 1131: NM_006344 , "Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin,", "superfamily member 13 (macrophage-derived) (CLECSF13), transcript variant 2,", mRNA, gi|5453683|ref|NM_006344.1|[5453683]; 1132: NM_006345 , "Homo sapiens solute carrier family 30 (zinc transporter), member 9 (SLC30A9),", mRNA, gi|7656945|ref|NM_006345.2|[7656945]; 1133: NM_006346 , "Homo sapiens progesterone-induced blocking factor 1 (PIBF1), mRNA", gi|5453889|ref|NM_006346.1|[5453889]; 1134: NM_006347 , "Homo sapiens peptidyl prolyl isomerase H (cyclophilin H) (PPIH), mRNA", gi|19224661|ref|NM_006347.2|[19224661]; 1135: NM_006356 , "Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d", "(ATP5H), mRNA", gi|5453558|ref|NM_006356.1|[5453558]; 1136: NM_006357 , "Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)", "(UBE2E3), transcript variant 1, mRNA", gi|33359695|ref|NM_006357.2|[33359695]; 1137: NM_006365 , "Homo sapiens transcriptional activator of the c-fos promoter (CROC4), mRNA", gi|5453624|ref|NM_006365.1|[5453624]; 1138: NM_006368 , "Homo sapiens cAMP responsive element binding protein 3 (CREB3), mRNA", gi|38327637|ref|NM_006368.4|[38327637]; 1139: NM_006370 , Homo sapiens vesicle transport through interaction with t-SNAREs homolog 1B, "(yeast) (VTI1B), mRNA", gi|5454165|ref|NM_006370.1|[5454165]; 1140: NM_006374 , "Homo sapiens serine/threonine kinase 25 (STE20 homolog, yeast) (STK25), mRNA", gi|34147665|ref|NM_006374.3|[34147665]; 1141: NM_006389 , "Homo sapiens hypoxia up-regulated 1 (HYOU1), mRNA", gi|13699861|ref|NM_006389.2|[13699861]; 1142: NM_006390 , "Homo sapiens importin 8 (IPO8), mRNA", gi|5453999|ref|NM_006390.1|[5453999]; 1143: NM_006395 , "Homo sapiens APG7 autophagy 7-like (S. cerevisiae) (APG7L), mRNA", gi|5453667|ref|NM_006395.1|[5453667]; 1144: NM_006396 , "Homo sapiens Sjogren's syndrome/scleroderma autoantigen 1 (SSSCA1), mRNA", gi|5453837|ref|NM_006396.1|[5453837]; 1145: NM_006397 , "Homo sapiens ribonuclease H2, large subunit (RNASEH2A), mRNA", gi|38455390|ref|NM_006397.2|[38455390]; 1146: NM_006399 , "Homo sapiens basic leucine zipper transcription factor, ATF-like (BATF), mRNA", gi|18375640|ref|NM_006399.2|[18375640]; 1147: NM_006408 , "Homo sapiens anterior gradient 2 homolog (Xenopus laevis) (AGR2), mRNA", gi|20070225|ref|NM_006408.2|[20070225]; 1148: NM_006422 , "Homo sapiens A kinase (PRKA) anchor protein 3 (AKAP3), mRNA", gi|21493040|ref|NM_006422.2|[21493040]; 1149: NM_006428 , "Homo sapiens mitochondrial ribosomal protein L28 (MRPL28), nuclear gene encoding", "mitochondrial protein, mRNA", gi|39812062|ref|NM_006428.3|[39812062]; 1150:

NM_006447 , "Homo sapiens ubiquitin specific protease 16 (USP16), mRNA", gi|5454155|ref|NM_006447.1|[5454155]; 1151: NM_006453 , "Homo sapiens transducin (beta)-like 3 (TBL3), mRNA", gi|19913368|ref|NM_006453.2|[19913368]; 1152: NM_006455 , "Homo sapiens synaptonemal complex protein SC65 (SC65), mRNA", gi|39812427|ref|NM_006455.2|[39812427]; 1153: NM_006465 , "Homo sapiens AT rich interactive domain 3B (BRIGHT- like) (ARID3B), mRNA", gi|5453637|ref|NM_006465.1|[5453637]; 1154: NM_006467 , "Homo sapiens polymerase (RNA) III (DNA directed) (32kD) (RPC32), mRNA", gi|5454017|ref|NM_006467.1|[5454017]; 1155: NM_006477 , "Homo sapiens RAS-related on chromosome 22 (RRP22), mRNA", gi|42476128|ref|NM_006477.2|[42476128]; 1156: NM_006479 , "Homo sapiens RAD51-interacting protein (PIR51), mRNA", gi|19923778|ref|NM_006479.2|[19923778]; 1157: NM_006492 , "Homo sapiens aristaless-like homeobox 3 (ALX3), mRNA", gi|5729727|ref|NM_006492.1|[5729727]; 1158: NM_006495 , "Homo sapiens ecotropic viral integration site 2B (EVI2B), mRNA", gi|20070234|ref|NM_006495.2|[20070234]; 1159: NM_006497 , "Homo sapiens hypermethylated in cancer 1 (HIC1), mRNA", gi|5729870|ref|NM_006497.1|[5729870]; 1160: NM_006502 , "Homo sapiens polymerase (DNA directed), eta (POLH), mRNA", gi|5729981|ref|NM_006502.1|[5729981]; 1161: NM_006503 , "Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4),", "transcript variant 1, mRNA", gi|24430156|ref|NM_006503.2|[24430156]; 1162: NM_006513 , "Homo sapiens seryl-tRNA synthetase (SARS), mRNA", gi|16306547|ref|NM_006513.2|[16306547]; 1163: NM_006515 , "Homo sapiens SET domain and mariner transposase fusion gene (SETMAR), mRNA", gi|5730038|ref|NM_006515.1|[5730038]; 1164: NM_006530 , "Homo sapiens glioma-amplified sequence-41 (GAS41), mRNA", gi|29337287|ref|NM_006530.2|[29337287]; 1165: NM_006531 , "Homo sapiens Probe hTg737 (polycystic kidney disease, autosomal recessive)", "(TG737), transcript variant 2, mRNA", gi|28329438|ref|NM_006531.2|[28329438]; 1166: NM_006537 , "Homo sapiens ubiquitin specific protease 3 (USP3), mRNA", gi|5730109|ref|NM_006537.1|[5730109]; 1167: NM_006538 , "Homo sapiens BCL2-like 11 (apoptosis facilitator) (BCL2L11), transcript variant", "6, mRNA", gi|5729739|ref|NM_006538.1|[5729739]; 1168: NM_006539 , "Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA", gi|22027545|ref|NM_006539.2|[22027545]; 1169: NM_006548 , "Homo sapiens IGF-II mRNA-binding protein 2 (IMP-2), mRNA", gi|34222220|ref|NM_006548.3|[34222220]; 1170: NM_006554 , "Homo sapiens metaxin 2 (MTX2), mRNA", gi|5729936|ref|NM_006554.1|[5729936]; 1171: NM_006556 , "Homo sapiens phosphomevalonate kinase (PMVK), mRNA", gi|20127505|ref|NM_006556.2|[20127505]; 1172: NM_006570 , "Homo sapiens Ras-related GTP binding A (RRAGA), mRNA", gi|34147579|ref|NM_006570.3|[34147579]; 1173: NM_006577 , "Homo sapiens UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1", "(B3GNT1), transcript variant 1, mRNA", gi|15451893|ref|NM_006577.3|[15451893]; 1174: NM_006582 , "Homo sapiens glucocorticoid modulatory element binding protein 1 (GMEB1),", "transcript variant 1, mRNA", gi|13435376|ref|NM_006582.2|[13435376]; 1175: NM_006584 , "Homo sapiens chaperonin containing TCP1, subunit 6B (zeta 2) (CCT6B), mRNA", gi|5729760|ref|NM_006584.1|[5729760]; 1176: NM_006585 , , ref|NM_006585.1|CCT8[6005726], This record was temporarily removed by RefSeq staff for additional review., , 1177: NM_006586 , "Homo sapiens trinucleotide repeat containing 5

(TNRC5), mRNA", gi|33942071|ref|NM_006586.2|[33942071]; 1178: NM_006589 , "Homo sapiens chromosome 1 open reading frame 2 (C1orf2), transcript variant 1,", mRNA, gi|38146115|ref|NM_006589.2|[38146115]; 1179: NM_006593 , "Homo sapiens T-box, brain, 1 (TBR1), mRNA", gi|22547231|ref|NM_006593.2|[22547231]; 1180: NM_006604 , "Homo sapiens ret finger protein-like 3 (RFPL3), mRNA", gi|5730012|ref|NM_006604.1|[5730012]; 1181: NM_006611 , "Homo sapiens killer cell lectin-like receptor subfamily A, member 1 (KLRA1),", mRNA, gi|5729898|ref|NM_006611.1|[5729898]; 1182: NM_006622 , "Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), mRNA", gi|5730054|ref|NM_006622.1|[5730054]; 1183: NM_006626 , "Homo sapiens zinc finger protein 482 (ZNF482), mRNA", gi|34222260|ref|NM_006626.3|[34222260]; 1184: NM_006627 , "Homo sapiens POP4 (processing of precursor , S. cerevisiae) homolog (POP4), mRNA", gi|5729985|ref|NM_006627.1|[5729985]; 1185: NM_006631 , "Homo sapiens zinc finger protein 266 (ZNF266), mRNA", gi|37622348|ref|NM_006631.2|[37622348]; 1186: NM_006633 , "Homo sapiens IQ motif containing GTPase activating protein 2 (IQGAP2), mRNA", gi|5729886|ref|NM_006633.1|[5729886]; 1187: NM_006638 , "Homo sapiens ribonuclease P1 (RNASEP1), mRNA", gi|5730016|ref|NM_006638.1|[5730016]; 1188: NM_006642 , "Homo sapiens serologically defined colon cancer antigen 8 (SDCCAG8), mRNA", gi|28269671|ref|NM_006642.1|[28269671]; 1189: NM_006654 , "Homo sapiens fibroblast growth factor receptor substrate 2 (FRS2), mRNA", gi|21314643|ref|NM_006654.2|[21314643]; 1190: NM_006664 , "Homo sapiens chemokine (C-C motif) ligand 27 (CCL27), mRNA", gi|22165428|ref|NM_006664.2|[22165428]; 1191: NM_006666 , "Homo sapiens RuvB-like 2 (E. coli) (RUVBL2), mRNA", gi|5730022|ref|NM_006666.1|[5730022]; 1192: NM_006670 , "Homo sapiens trophoblast glycoprotein (TPBG), mRNA", gi|34222307|ref|NM_006670.3|[34222307]; 1193: NM_006675 , "Homo sapiens transmembrane 4 superfamily member tetraspan NET-5 (NET-5), mRNA", gi|21264572|ref|NM_006675.2|[21264572]; 1194: NM_006697 , "Homo sapiens cisplatin resistance associated (CRA), mRNA", gi|5870890|ref|NM_006697.1|[5870890]; 1195: NM_006698 , "Homo sapiens bladder cancer associated protein (BLCAP), mRNA", gi|5729737|ref|NM_006698.1|[5729737]; 1196: NM_006702 , "Homo sapiens neuropathy target esterase (NTE), mRNA", gi|31543298|ref|NM_006702.2|[31543298]; 1197: NM_006715 , "Homo sapiens mannosidase, alpha, class 2C, member 1 (MAN2C1), mRNA", gi|6631092|ref|NM_006715.1|[6631092]; 1198: NM_006730 , "Homo sapiens deoxyribonuclease I-like 1 (DNASE1L1), mRNA", gi|5803006|ref|NM_006730.1|[5803006]; 1199: NM_006735 , "Homo sapiens homeo box A2 (HOXA2), mRNA", gi|37596298|ref|NM_006735.3|[37596298]; 1200: NM_006736 , "Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 2 (DNAJB2), mRNA", gi|34222304|ref|NM_006736.4|[34222304]; 1201: NM_006744 , "Homo sapiens retinol binding protein 4, plasma (RBP4), mRNA", gi|8400727|ref|NM_006744.2|[8400727]; 1202: NM_006745 , "Homo sapiens sterol-C4-methyl oxidase-like (SC4MOL), mRNA", gi|9257238|ref|NM_006745.2|[9257238]; 1203: NM_006747 , "Homo sapiens signal-induced proliferation-associated gene 1 (SIPA1), transcript", "variant 2, mRNA", gi|24497626|ref|NM_006747.2|[24497626]; 1204: NM_006749 , "Homo sapiens solute carrier family 20 (phosphate transporter), member 2", "(SLC20A2), mRNA", gi|34222154|ref|NM_006749.3|[34222154]; 1205: NM_006751 , "Homo sapiens sperm specific antigen 2 (SSFA2), mRNA", gi|34222128|ref|NM_006751.3|[34222128]; 1206: NM_006756 , "Homo sapiens transcription elongation factor A (SII), 1 (TCEA1), mRNA", gi|5803190|ref|NM_006756.1|[5803190]; 1207: NM_006759 , "Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA", gi|13027637|ref|NM_006759.2|[13027637]; 1208:

NM_006764 , "Homo sapiens interferon-related developmental regulator 2 (IFRD2), mRNA", gi|21361365|ref|NM_006764.2|[21361365]; 1209: NM_006777 , "Homo sapiens kaiso (ZNF-kaiso), mRNA", gi|41152068|ref|NM_006777.3|[41152068]; 1210: NM_006784 , "Homo sapiens WD repeat domain 3 (WDR3), mRNA", gi|5803220|ref|NM_006784.1|[5803220]; 1211: NM_006793 , "Homo sapiens peroxiredoxin 3 (PRDX3), nuclear gene encoding mitochondrial", "protein, transcript variant 1, mRNA", gi|32483378|ref|NM_006793.2|[32483378]; 1212: NM_006801 , Homo sapiens KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention, "receptor 1 (KDELR1), mRNA", gi|32307173|ref|NM_006801.2|[32307173]; 1213: NM_006802 , "Homo sapiens splicing factor 3a, subunit 3, 60kDa (SF3A3), mRNA", gi|5803166|ref|NM_006802.1|[5803166]; 1214: NM_006804 , "Homo sapiens START domain containing 3 (STARD3), mRNA", gi|31543656|ref|NM_006804.2|[31543656]; 1215: NM_006809 , "Homo sapiens translocase of outer mitochondrial membrane 34 (TOMM34), mRNA", gi|40807467|ref|NM_006809.4|[40807467]; 1216: NM_006813 , "Homo sapiens proline-rich nuclear receptor coactivator 1 (PNRC1), mRNA", gi|5802981|ref|NM_006813.1|[5802981]; 1217: NM_006816 , "Homo sapiens lectin, mannose-binding 2 (LMAN2), mRNA", gi|5803022|ref|NM_006816.1|[5803022]; 1218: NM_006817 , "Homo sapiens chromosome 12 open reading frame 8 (C12orf8), mRNA", gi|13124889|ref|NM_006817.2|[13124889]; 1219: NM_006818 , "Homo sapiens ALL1-fused gene from chromosome 1q (AF1Q), mRNA", gi|21626459|ref|NM_006818.2|[21626459]; 1220: NM_006824 , "Homo sapiens EBNA1 binding protein 2 (EBNA1BP2), mRNA", gi|5803110|ref|NM_006824.1|[5803110]; 1221: NM_006828 , "Homo sapiens helicase, ATP binding 1 (HELIC1), mRNA", gi|24307916|ref|NM_006828.1|[24307916]; 1222: NM_006830 , "Homo sapiens ubiquinol-cytochrome c reductase (6.4kD) subunit (UQCR), mRNA", gi|19923785|ref|NM_006830.2|[19923785]; 1223: NM_006831 , "Homo sapiens ATP/GTP-binding protein (HEAB), mRNA", gi|5803028|ref|NM_006831.1|[5803028]; 1224: NM_006837 , Homo sapiens COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis), "(COPS5), mRNA", gi|38027922|ref|NM_006837.2|[38027922]; 1225: NM_006839 , "Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA", gi|5803114|ref|NM_006839.1|[5803114]; 1226: NM_006841 , "Homo sapiens solute carrier family 38, member 3 (SLC38A3), mRNA", gi|40795668|ref|NM_006841.3|[40795668]; 1227: NM_006843 , "Homo sapiens serine dehydratase (SDS), mRNA", gi|33469957|ref|NM_006843.2|[33469957]; 1228: NM_006876 , "Homo sapiens UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6", "(B3GNT6), mRNA", gi|5802983|ref|NM_006876.1|[5802983]; 1229: NM_006886 , "Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon", "subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA", gi|21327678|ref|NM_006886.2|[21327678]; 1230: NM_006901 , "Homo sapiens myosin IXA (MYO9A), mRNA", gi|5902011|ref|NM_006901.1|[5902011]; 1231: NM_006913 , "Homo sapiens ring finger protein 5 (RNF5), mRNA", gi|34305290|ref|NM_006913.2|[34305290]; 1232: NM_006917 , "Homo sapiens retinoid X receptor, gamma (RXRG), mRNA", gi|21361386|ref|NM_006917.2|[21361386]; 1233: NM_006923 , "Homo sapiens stromal cell-derived factor 2 (SDF2), mRNA", gi|14141194|ref|NM_006923.2|[14141194]; 1234: NM_006928 , "Homo sapiens silver homolog (mouse) (SILV), mRNA", gi|42542384|ref|NM_006928.3|[42542384]; 1235: NM_006929 , "Homo sapiens superkiller viralicidic activity 2-like (S. cerevisiae) (SKIV2L),", mRNA, gi|20631986|ref|NM_006929.3|[20631986]; 1236: NM_006934 , "Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine),", "member 9 (SLC6A9), transcript variant 1,

mRNA", gi|5902093|ref|NM_006934.1|[5902093]; 1237: NM_006946 , "Homo sapiens spectrin, beta, non-erythrocytic 2 (SPTBN2), mRNA", gi|5902121|ref|NM_006946.1|[5902121]; 1238: NM_006949 , "Homo sapiens syntaxin binding protein 2 (STXBP2), mRNA", gi|5902127|ref|NM_006949.1|[5902127]; 1239: NM_006950 , "Homo sapiens synapsin I (SYN1), transcript variant Ia, mRNA", gi|19924098|ref|NM_006950.2|[19924098]; 1240: NM_006973 , "Homo sapiens zinc finger protein 32 (KOX 30) (ZNF32), mRNA", gi|24307924|ref|NM_006973.1|[24307924]; 1241: NM_006977 , "Homo sapiens zinc finger protein 46 (KUP) (ZNF46), mRNA", gi|40217848|ref|NM_006977.2|[40217848]; 1242: NM_006979 , "Homo sapiens solute carrier family 39 (zinc transporter), member 7 (SLC39A7),", mRNA, gi|5901935|ref|NM_006979.1|[5901935]; 1243: NM_006980 , "Homo sapiens transcription termination factor, mitochondrial (MTERF), nuclear", "gene encoding mitochondrial protein, mRNA", gi|14790134|ref|NM_006980.2|[14790134]; 1244: NM_006982 , "Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA", gi|5901917|ref|NM_006982.1|[5901917]; 1245: NM_006984 , "Homo sapiens claudin 10 (CLDN10), transcript variant 2, mRNA", gi|38570070|ref|NM_006984.3|[38570070]; 1246: NM_006987 , "Homo sapiens rabphilin 3A-like (without C2 domains) (RPH3AL), mRNA", gi|31543557|ref|NM_006987.2|[31543557]; 1247: NM_006988 , Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with, "thrombospondin type 1 motif, 1 (ADAMTS1), mRNA", gi|11038653|ref|NM_006988.2|[11038653]; 1248: NM_006992 , "Homo sapiens B7 gene (B7), transcript variant 2, mRNA", gi|42542401|ref|NM_006992.2|[42542401]; 1249: NM_006993 , "Homo sapiens nucleophosmin/nucleoplasmin, 3 (NPM3), mRNA", gi|6857817|ref|NM_006993.1|[6857817]; 1250: NM_006998 , "Homo sapiens secretagogin, EF-hand calcium binding protein (SCGN), mRNA", gi|15055536|ref|NM_006998.2|[15055536]; 1251: NM_007002 , "Homo sapiens adhesion regulating molecule 1 (ADRM1), transcript variant 1, mRNA", gi|28373191|ref|NM_007002.2|[28373191]; 1252: NM_007006 , "Homo sapiens cleavage and polyadenylation specific factor 5, 25 kDa (CPSF5),", mRNA, gi|5901925|ref|NM_007006.1|[5901925]; 1253: NM_007007 , "Homo sapiens cleavage and polyadenylation specific factor 6, 68kDa (CPSF6), mRNA", gi|5901927|ref|NM_007007.1|[5901927]; 1254: NM_007009 , "Homo sapiens zona pellucida binding protein (ZPBP), mRNA", gi|5902115|ref|NM_007009.1|[5902115]; 1255: NM_007019 , "Homo sapiens ubiquitin-conjugating enzyme E2C (UBE2C), transcript variant 1,", mRNA, gi|32967292|ref|NM_007019.2|[32967292]; 1256: NM_007022 , "Homo sapiens putative tumor suppressor 101F6 (101F6), mRNA", gi|31541779|ref|NM_007022.3|[31541779]; 1257: NM_007024 , "Homo sapiens placental protein 6 (PL6), mRNA", gi|40795669|ref|NM_007024.4|[40795669]; 1258: NM_007027 , "Homo sapiens topoisomerase (DNA) II binding protein (TOPBP1), mRNA", gi|20143948|ref|NM_007027.2|[20143948]; 1259: NM_007031 , "Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA", gi|5901979|ref|NM_007031.1|[5901979]; 1260: NM_007038 , Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with, "thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMTS5), mRNA", gi|5901887|ref|NM_007038.1|[5901887]; 1261: NM_007046 , "Homo sapiens elastin microfibril interfacer 1 (EMILIN1), mRNA", gi|5901943|ref|NM_007046.1|[5901943]; 1262: NM_007050 , "Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), transcript", "variant 2, mRNA", gi|19743928|ref|NM_007050.3|[19743928]; 1263: NM_007051 , "Homo sapiens Fas (TNFRSF6) associated factor 1 (FAF1), transcript variant 1,", mRNA, gi|19528653|ref|NM_007051.2|[19528653]; 1264: NM_007056 , "Homo sapiens splicing factor,

arginine/serine-rich 16", "(suppressor-of-white-apricot homolog, Drosophila) (SFRS16), mRNA", gi|5902129|ref|NM_007056.1|[5902129]; 1265: NM_007059 , "Homo sapiens kaptin (actin binding protein) (KPTN), mRNA", gi|5901993|ref|NM_007059.1|[5901993]; 1266: NM_007064 , Homo sapiens serine/threonine kinase with Dbl- and pleckstrin homology domains, "(TRAD), mRNA", gi|5902139|ref|NM_007064.1|[5902139]; 1267: NM_007065 , "Homo sapiens CDC37 cell division cycle 37 homolog (S. cerevisiae) (CDC37), mRNA", gi|39995072|ref|NM_007065.3|[39995072]; 1268: NM_007066 , "Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibitor gamma (PKIG),", "transcript variant 2, mRNA", gi|32483384|ref|NM_007066.3|[32483384]; 1269: NM_007069 , "Homo sapiens HRAS-like suppressor 3 (HRASLS3), mRNA", gi|5901975|ref|NM_007069.1|[5901975]; 1270: NM_007072 , "Homo sapiens HERV-H LTR-associating 2 (HHLA2), mRNA", gi|31542933|ref|NM_007072.2|[31542933]; 1271: NM_007076 , , ref|NM_007076.2|[42794619]; 1272: NM_007081 , "Homo sapiens RAB, member of RAS oncogene family-like 2B (RABL2B), mRNA", gi|5902039|ref|NM_007081.1|[5902039]; 1273: NM_007082 , "Homo sapiens RAB, member of RAS oncogene family-like 2A (RABL2A), transcript", "variant 2, mRNA", gi|7549818|ref|NM_007082.2|[7549818]; 1274: NM_007083 , Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 6, "(NUDT6), transcript variant 1, mRNA", gi|37594465|ref|NM_007083.3|[37594465]; 1275: NM_007107 , "Homo sapiens signal sequence receptor, gamma (translocon-associated protein", "gamma) (SSR3), mRNA", gi|28416942|ref|NM_007107.2|[28416942]; 1276: NM_007114 , "Homo sapiens TATA element modulatory factor 1 (TMF1), mRNA", gi|6005903|ref|NM_007114.1|[6005903]; 1277: NM_007117 , "Homo sapiens thyrotropin-releasing hormone (TRH), mRNA", gi|6005919|ref|NM_007117.1|[6005919]; 1278: NM_007130 , "Homo sapiens zinc finger protein 41 (ZNF41), transcript variant 1, mRNA", gi|23510456|ref|NM_007130.1|[23510456]; 1279: NM_007136 , "Homo sapiens zinc finger protein 80 (pT17) (ZNF80), mRNA", gi|6005981|ref|NM_007136.1|[6005981]; 1280: NM_007147 , "Homo sapiens zinc finger protein 175 (ZNF175), mRNA", gi|37594438|ref|NM_007147.2|[37594438]; 1281: NM_007149 , "Homo sapiens zinc finger protein 184 (Kruppel-like) (ZNF184), mRNA", gi|24307934|ref|NM_007149.1|[24307934]; 1282: NM_007152 , "Homo sapiens zinc finger protein 195 (ZNF195), mRNA", gi|6005973|ref|NM_007152.1|[6005973]; 1283: NM_007158 , "Homo sapiens NRAS-related gene (D1S155E), mRNA", gi|41282241|ref|NM_007158.3|[41282241]; 1284: NM_007180 , "Homo sapiens trehalase (brush-border membrane glycoprotein) (TREH), mRNA", gi|6005913|ref|NM_007180.1|[6005913]; 1285: NM_007191 , "Homo sapiens WNT inhibitory factor 1 (WIF1), mRNA", gi|18379354|ref|NM_007191.2|[18379354]; 1286: NM_007192 , "Homo sapiens suppressor of Ty 16 homolog (S. cerevisiae) (SUPT16H), mRNA", gi|19924176|ref|NM_007192.2|[19924176]; 1287: NM_007195 , "Homo sapiens polymerase (DNA directed) iota (POLI), mRNA", gi|6005847|ref|NM_007195.1|[6005847]; 1288: NM_007208 , "Homo sapiens mitochondrial ribosomal protein L3 (MRPL3), nuclear gene encoding", "mitochondrial protein, mRNA", gi|21265090|ref|NM_007208.2|[21265090]; 1289: NM_007211 , "Homo sapiens chromosome 12 open reading frame 2 (C12orf2), mRNA", gi|23503242|ref|NM_007211.2|[23503242]; 1290: NM_007212 , "Homo sapiens ring finger protein 2 (RNF2), mRNA", gi|34305287|ref|NM_007212.2|[34305287]; 1291: NM_007215 , "Homo sapiens polymerase (DNA directed), gamma 2, accessory subunit (POLG2), mRNA", gi|6005837|ref|NM_007215.1|[6005837]; 1292: NM_007216 , "Homo sapiens Hermansky-Pudlak syndrome 5 (HPS5), transcript variant 2, mRNA",

gi|31657126|ref|NM_007216.3|[31657126]; 1293: NM_007217 , "Homo sapiens programmed cell death 10 (PDCD10), transcript variant 1, mRNA", gi|22538790|ref|NM_007217.3|[22538790]; 1294: NM_007221 , "Homo sapiens polyamine-modulated factor 1 (PMF1), mRNA", gi|6005831|ref|NM_007221.1|[6005831]; 1295: NM_007229 , Homo sapiens protein kinase C and casein kinase substrate in neurons 2, "(PACSIN2), mRNA", gi|6005825|ref|NM_007229.1|[6005825]; 1296: NM_007231 , "Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14", "(SLC6A14), mRNA", gi|6005714|ref|NM_007231.1|[6005714]; 1297: NM_007234 , "Homo sapiens dynactin 3 (p22) (DCTN3), transcript variant 1, mRNA", gi|22165423|ref|NM_007234.3|[22165423]; 1298: NM_007235 , "Homo sapiens exportin, tRNA (nuclear export receptor for tRNAs) (XPOT), mRNA", gi|40217845|ref|NM_007235.3|[40217845]; 1299: NM_007246 , "Homo sapiens kelch-like 2, Mayven (Drosophila) (KLHL2), mRNA", gi|21359895|ref|NM_007246.2|[21359895]; 1300: NM_007252 , "Homo sapiens POU domain, class 6, transcription factor 2 (POU6F2), mRNA", gi|6005855|ref|NM_007252.1|[6005855]; 1301: NM_007254 , "Homo sapiens polynucleotide kinase 3'-phosphatase (PNKP), mRNA", gi|31543418|ref|NM_007254.2|[31543418]; 1302: NM_007262 , "Homo sapiens Parkinson disease (autosomal recessive, early onset) 7 (PARK7),", mRNA, gi|34222306|ref|NM_007262.3|[34222306]; 1303: NM_007263 , "Homo sapiens coatomer protein complex, subunit epsilon (COPE), transcript", "variant 1, mRNA", gi|40805821|ref|NM_007263.3|[40805821]; 1304: NM_007264 , "Homo sapiens adrenomedullin receptor (ADMR), mRNA", gi|6466448|ref|NM_007264.2|[6466448]; 1305: NM_007265 , "Homo sapiens suppressor of S. cerevisiae gcr2 (HSGT1), mRNA", gi|6005783|ref|NM_007265.1|[6005783]; 1306: NM_007270 , "Homo sapiens FK506 binding protein 9, 63 kDa (FKBP9), mRNA", gi|33469984|ref|NM_007270.2|[33469984]; 1307: NM_007273 , "Homo sapiens repressor of estrogen receptor activity (REA), mRNA", gi|31543548|ref|NM_007273.3|[31543548]; 1308: NM_007277 , "Homo sapiens SEC6-like 1 (S. cerevisiae) (SEC6L1), mRNA", gi|38148698|ref|NM_007277.3|[38148698]; 1309: NM_007278 , "Homo sapiens GABA(A) receptor-associated protein (GABARAP), mRNA", gi|6005763|ref|NM_007278.1|[6005763]; 1310: NM_007280 , "Homo sapiens Opa-interacting protein 5 (OIP5), mRNA", gi|24307928|ref|NM_007280.1|[24307928]; 1311: NM_007285 , "Homo sapiens GABA(A) receptor-associated protein-like 2 (GABARAPL2), mRNA", gi|27374999|ref|NM_007285.6|[27374999]; 1312: NM_007353 , "Homo sapiens guanine nucleotide binding protein (G protein) alpha 12 (GNA12),", mRNA, gi|42476110|ref|NM_007353.2|[42476110]; 1313: NM_007357 , "Homo sapiens component of oligomeric golgi complex 2 (COG2), mRNA", gi|6678675|ref|NM_007357.1|[6678675]; 1314: NM_007364 , "Homo sapiens integral type I protein (P24B), mRNA", gi|6679188|ref|NM_007364.1|[6679188]; 1315: NM_007365 , "Homo sapiens peptidyl arginine deiminase, type II (PADI2), mRNA", gi|15042936|ref|NM_007365.1|[15042936]; 1316: NM_007367 , "Homo sapiens RNA binding protein (autoantigenic, hnRNP-associated with lethal", "yellow) (RALY), transcript variant 2, mRNA", gi|21396479|ref|NM_007367.2|[21396479]; 1317: NM_007373 , "Homo sapiens soc-2 suppressor of clear homolog (C. elegans) (SHOC2), mRNA", gi|41281397|ref|NM_007373.2|[41281397]; 1318: NM_007374 , "Homo sapiens sine oculis homeobox homolog 6 (Drosophila) (SIX6), mRNA", gi|6677978|ref|NM_007374.1|[6677978]; 1319: NM_012083 , "Homo sapiens frequently rearranged in advanced T-cell lymphomas 2 (FRAT2), mRNA", gi|31317237|ref|NM_012083.2|[31317237]; 1320: NM_012086 , "Homo

sapiens general transcription factor IIIC, polypeptide 3, 102kDa (GTF3C3),", mRNA, gi|6912397|ref|NM_012086.1|[6912397]; 1321: NM_012087 , "Homo sapiens general transcription factor IIIC, polypeptide 5, 63kDa (GTF3C5),", mRNA, gi|6912401|ref|NM_012087.1|[6912401]; 1322: NM_012096 , "Homo sapiens adaptor protein containing pH domain, PTB domain and leucine zipper", "motif (APPL), mRNA", gi|6912241|ref|NM_012096.1|[6912241]; 1323: NM_012097 , "Homo sapiens ADP-ribosylation factor-like 5 (ARL5), transcript variant 1, mRNA", gi|29542733|ref|NM_012097.2|[29542733]; 1324: NM_012103 , "Homo sapiens ancient ubiquitous protein 1 (AUP1), transcript variant 1, mRNA", gi|32313582|ref|NM_012103.2|[32313582]; 1325: NM_012104 , "Homo sapiens beta-site APP-cleaving enzyme (BACE), transcript variant a, mRNA", gi|21040369|ref|NM_012104.2|[21040369]; 1326: NM_012105 , "Homo sapiens beta-site APP-cleaving enzyme 2 (BACE2), transcript variant a, mRNA", gi|21040358|ref|NM_012105.3|[21040358]; 1327: NM_012111 , "Homo sapiens AHA1, activator of heat shock 90kDa protein ATPase homolog 1", "(yeast) (AHSA1), mRNA", gi|6912279|ref|NM_012111.1|[6912279]; 1328: NM_012112 , "Homo sapiens TPX2, microtubule-associated protein homolog (Xenopus laevis)", "(TPX2), mRNA", gi|40354199|ref|NM_012112.4|[40354199]; 1329: NM_012124 , "Homo sapiens cysteine and histidine-rich domain (CHORD)-containing, zinc binding", "protein 1 (CHORDC1), mRNA", gi|6912303|ref|NM_012124.1|[6912303]; 1330: NM_012130 , "Homo sapiens claudin 14 (CLDN14), transcript variant 2, mRNA", gi|21536295|ref|NM_012130.2|[21536295]; 1331: NM_012133 , "Homo sapiens coatomer protein complex, subunit gamma 2 (COPG2), mRNA", gi|6912319|ref|NM_012133.1|[6912319]; 1332: NM_012139 , Homo sapiens deafness locus associated putative guanine nucleotide exchange, "factor (DELGEF), mRNA", gi|40548400|ref|NM_012139.2|[40548400]; 1333: NM_012144 , "Homo sapiens dynein, axonemal, intermediate polypeptide 1 (DNAI1), mRNA", gi|22212919|ref|NM_012144.2|[22212919]; 1334: NM_012152 , "Homo sapiens endothelial differentiation, lysophosphatidic acid", "G-protein-coupled receptor, 7 (EDG7), mRNA", gi|6912347|ref|NM_012152.1|[6912347]; 1335: NM_012160 , "Homo sapiens F-box and leucine-rich repeat protein 4 (FBXL4), mRNA", gi|21536437|ref|NM_012160.3|[21536437]; 1336: NM_012164 , "Homo sapiens F-box and WD-40 domain protein 2 (FBXW2), mRNA", gi|7549806|ref|NM_012164.2|[7549806]; 1337: NM_012168 , "Homo sapiens F-box only protein 2 (FBXO2), mRNA", gi|15812197|ref|NM_012168.2|[15812197]; 1338: NM_012170 , "Homo sapiens F-box only protein 22 (FBXO22), transcript variant 2, mRNA", gi|22547147|ref|NM_012170.2|[22547147]; 1339: NM_012177 , "Homo sapiens F-box only protein 5 (FBXO5), mRNA", gi|15812190|ref|NM_012177.2|[15812190]; 1340: NM_012179 , "Homo sapiens F-box only protein 7 (FBXO7), mRNA", gi|15812192|ref|NM_012179.2|[15812192]; 1341: NM_012182 , "Homo sapiens forkhead box B1 (FOXB1), mRNA", gi|11386194|ref|NM_012182.1|[11386194]; 1342: NM_012183 , "Homo sapiens forkhead box D3 (FOXD3), mRNA", gi|6912371|ref|NM_012183.1|[6912371]; 1343: NM_012191 , "Homo sapiens putative tumor suppressor (FUS2), mRNA", gi|6912379|ref|NM_012191.1|[6912379]; 1344: NM_012192 , "Homo sapiens fracture callus 1 homolog (rat) (FXC1), mRNA", gi|29837656|ref|NM_012192.2|[29837656]; 1345: NM_012198 , "Homo sapiens grancalcin, EF-hand calcium binding protein (GCA), mRNA", gi|21614521|ref|NM_012198.2|[21614521]; 1346: NM_012204 , "Homo sapiens general transcription factor IIIC, polypeptide 4, 90kDa (GTF3C4),", mRNA, gi|6912399|ref|NM_012204.1|[6912399]; 1347: NM_012222 , "Homo sapiens mutY homolog

(E. coli) (MUTYH), mRNA", gi|6912519|ref|NM_012222.1|[6912519]; 1348: NM_012237 , Homo sapiens sirtuin (silent mating type information regulation 2 homolog) 2 (S., "cerevisiae) (SIRT2), transcript variant 1, mRNA", gi|13775599|ref|NM_012237.2|[13775599]; 1349: NM_012242 , "Homo sapiens dickkopf homolog 1 (Xenopus laevis) (DKK1), mRNA", gi|7110718|ref|NM_012242.1|[7110718]; 1350: NM_012254 , "Homo sapiens solute carrier family 27 (fatty acid transporter), member 5", "(SLC27A5), mRNA", gi|13325056|ref|NM_012254.1|[13325056]; 1351: NM_012256 , "Homo sapiens zinc finger protein 212 (ZNF212), mRNA", gi|24797064|ref|NM_012256.2|[24797064]; 1352: NM_012259 , "Homo sapiens hairy/enhancer-of-split related with YRPW motif 2 (HEY2), mRNA", gi|6912413|ref|NM_012259.1|[6912413]; 1353: NM_012265 , "Homo sapiens chromosome 22 open reading frame 3 (C22orf3), mRNA", gi|11072100|ref|NM_012265.1|[11072100]; 1354: NM_012281 , "Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2", "(KCND2), mRNA", gi|27436982|ref|NM_012281.2|[27436982]; 1355: NM_012285 , "Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member", "4 (KCNH4), mRNA", gi|6912445|ref|NM_012285.1|[6912445]; 1356: NM_012289 , "Homo sapiens kelch-like ECH-associated protein 1 (KEAP1), mRNA", gi|22027641|ref|NM_012289.2|[22027641]; 1357: NM_012311 , "Homo sapiens KIN, antigenic determinant of recA protein homolog (mouse) (KIN),", mRNA, gi|40068516|ref|NM_012311.2|[40068516]; 1358: NM_012327 , "Homo sapiens phosphatidylinositol glycan, class N (PIGN), transcript variant 2,", mRNA, gi|34328903|ref|NM_012327.3|[34328903]; 1359: NM_012339 , "Homo sapiens transmembrane 4 superfamily member tetraspan NET-7 (NET-7), mRNA", gi|21264576|ref|NM_012339.2|[21264576]; 1360: NM_012342 , Homo sapiens BMP and activin membrane-bound inhibitor homolog (Xenopus laevis), "(BAMBI), mRNA", gi|6912533|ref|NM_012342.1|[6912533]; 1361: NM_012381 , "Homo sapiens origin recognition complex, subunit 3-like (yeast) (ORC3L),", "transcript variant 2, mRNA", gi|32483366|ref|NM_012381.2|[32483366]; 1362: NM_012392 , Homo sapiens PEF protein with a long N-terminal hydrophobic domain (peflin), "(PEF), mRNA", gi|6912581|ref|NM_012392.1|[6912581]; 1363: NM_012396 , "Homo sapiens pleckstrin homology-like domain, family A, member 3 (PHLDA3), mRNA", gi|6912589|ref|NM_012396.1|[6912589]; 1364: NM_012399 , "Homo sapiens phosphotidylinositol transfer protein, beta (PITPNB), mRNA", gi|19923401|ref|NM_012399.2|[19923401]; 1365: NM_012402 , Homo sapiens ADP-ribosylation factor interacting protein 2 (arfaptin 2), "(ARFIP2), mRNA", gi|38569401|ref|NM_012402.2|[38569401]; 1366: NM_012407 , "Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA", gi|7110696|ref|NM_012407.1|[7110696]; 1367: NM_012424 , "Homo sapiens ribosomal protein S6 kinase, 52kDa, polypeptide 1 (RPS6KC1), mRNA", gi|19923722|ref|NM_012424.2|[19923722]; 1368: NM_012425 , "Homo sapiens Ras suppressor protein 1 (RSU1), transcript variant 1, mRNA", gi|34577084|ref|NM_012425.3|[34577084]; 1369: NM_012427 , "Homo sapiens kallikrein 5 (KLK5), mRNA", gi|22208993|ref|NM_012427.3|[22208993]; 1370: NM_012430 , "Homo sapiens SEC22 vesicle trafficking protein-like 2 (S. cerevisiae) (SEC22L2),", mRNA, gi|14591918|ref|NM_012430.2|[14591918]; 1371: NM_012445 , "Homo sapiens spondin 2, extracellular matrix protein (SPON2), mRNA", gi|6912681|ref|NM_012445.1|[6912681]; 1372: NM_012448 , "Homo sapiens signal transducer and activator of transcription 5B (STAT5B), mRNA", gi|42519913|ref|NM_012448.3|[42519913]; 1373: NM_012450 , "Homo sapiens solute

carrier family 13 (sodium/sulfate symporters), member 4", "(SLC13A4), mRNA", gi|31795545|ref|NM_012450.2|[31795545]; 1374: NM_012451 , "Homo sapiens synaptogyrin 4 (SYNGR4), mRNA", gi|22035701|ref|NM_012451.2|[22035701]; 1375: NM_012456 , Homo sapiens translocase of inner mitochondrial membrane 10 homolog (yeast), "(TIMM10), mRNA", gi|6912707|ref|NM_012456.1|[6912707]; 1376: NM_012458 , Homo sapiens translocase of inner mitochondrial membrane 13 homolog (yeast), "(TIMM13), nuclear gene encoding mitochondrial protein, mRNA", gi|27436898|ref|NM_012458.2|[27436898]; 1377: NM_012459 , Homo sapiens translocase of inner mitochondrial membrane 8 homolog B (yeast), "(TIMM8B), mRNA", gi|6912711|ref|NM_012459.1|[6912711]; 1378: NM_012460 , Homo sapiens translocase of inner mitochondrial membrane 9 homolog (yeast), "(TIMM9), mRNA", gi|21359892|ref|NM_012460.2|[21359892]; 1379: NM_012461 , "Homo sapiens TERF1 (TRF1)-interacting nuclear factor 2 (TINF2), mRNA", gi|6912715|ref|NM_012461.1|[6912715]; 1380: NM_012481 , "Homo sapiens zinc finger protein, subfamily 1A, 3 (Aiolos) (ZNFN1A3), transcript", "variant 1, mRNA", gi|38045957|ref|NM_012481.3|[38045957]; 1381: NM_012482 , "Homo sapiens zinc finger protein 281 (ZNF281), mRNA", gi|40255235|ref|NM_012482.3|[40255235]; 1382: NM_013232 , "Homo sapiens programmed cell death 6 (PDCD6), mRNA", gi|22027539|ref|NM_013232.2|[22027539]; 1383: NM_013235 , "Homo sapiens nuclear RNase III Drosha (RNASE3L), mRNA", gi|21359821|ref|NM_013235.2|[21359821]; 1384: NM_013238 , "Homo sapiens DnaJ (Hsp40) homolog, subfamily D, member 1 (DNAJD1), mRNA", gi|7019452|ref|NM_013238.1|[7019452]; 1385: NM_013241 , "Homo sapiens formin homology 2 domain containing 1 (FHOD1), mRNA", gi|7019374|ref|NM_013241.1|[7019374]; 1386: NM_013242 , "Homo sapiens likely ortholog of mouse gene trap locus 3 (GTL3), mRNA", gi|42716281|ref|NM_013242.2|[42716281]; 1387: NM_013248 , "Homo sapiens NTF2-like export factor 1 (NXT1), mRNA", gi|20127526|ref|NM_013248.2|[20127526]; 1388: NM_013250 , "Homo sapiens zinc finger protein 215 (ZNF215), mRNA", gi|7019582|ref|NM_013250.1|[7019582]; 1389: NM_013254 , "Homo sapiens TANK-binding kinase 1 (TBK1), mRNA", gi|19743810|ref|NM_013254.2|[19743810]; 1390: NM_013256 , "Homo sapiens zinc finger protein 180 (HHZ168) (ZNF180), mRNA", gi|7019578|ref|NM_013256.1|[7019578]; 1391: NM_013260 , "Homo sapiens transcriptional regulator protein (HCNGP), mRNA", gi|21361710|ref|NM_013260.3|[21361710]; 1392: NM_013263 , "Homo sapiens bromodomain containing 7 (BRD7), mRNA", gi|41350211|ref|NM_013263.2|[41350211]; 1393: NM_013264 , "Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 25 (DDX25), mRNA", gi|21327696|ref|NM_013264.2|[21327696]; 1394: NM_013266 , "Homo sapiens catenin (cadherin-associated protein), alpha 3 (CTNNA3), mRNA", gi|7019570|ref|NM_013266.1|[7019570]; 1395: NM_013267 , "Homo sapiens liver mitochondrial glutaminase (GA), nuclear gene encoding", "mitochondrial protein, transcript variant 1, mRNA", gi|20336213|ref|NM_013267.2|[20336213]; 1396: NM_013270 , "Homo sapiens testes-specific protease 50 (TSP50), mRNA", gi|31543829|ref|NM_013270.2|[31543829]; 1397: NM_013274 , "Homo sapiens polymerase (DNA directed), lambda (POLL), mRNA", gi|38146101|ref|NM_013274.2|[38146101]; 1398: NM_013275 , "Homo sapiens ankyrin repeat domain 11 (ANKRD11), mRNA", gi|40786546|ref|NM_013275.3|[40786546]; 1399: NM_013283 , "Homo sapiens methionine adenosyltransferase II, beta (MAT2B), transcript variant", "1, mRNA", gi|33519456|ref|NM_013283.3|[33519456]; 1400: NM_013284 , "Homo sapiens polymerase

(DNA directed), mu (POLM), mRNA", gi|7019492|ref|NM_013284.1|[7019492]; 1401: NM_013285 , "Homo sapiens nucleolar GTPase (HUMAUANTIG), mRNA", gi|7019418|ref|NM_013285.1|[7019418]; 1402: NM_013286 , "Homo sapiens chromosome 3p21.1 gene sequence (HUMAGCGB), mRNA", gi|31712021|ref|NM_013286.2|[31712021]; 1403: NM_013301 , "Homo sapiens protein predicted by clone 23882 (HSU79303), mRNA", gi|9558742|ref|NM_013301.1|[9558742]; 1404: NM_013312 , "Homo sapiens hook homolog 2 (Drosophila) (HOOK2), mRNA", gi|7019410|ref|NM_013312.1|[7019410]; 1405: NM_013322 , "Homo sapiens sorting nexin 10 (SNX10), mRNA", gi|23111022|ref|NM_013322.2|[23111022]; 1406: NM_013324 , "Homo sapiens cytokine inducible SH2-containing protein (CISH), transcript", "variant 1, mRNA", gi|21614504|ref|NM_013324.4|[21614504]; 1407: NM_013326 , "Homo sapiens chromosome 18 open reading frame 8 (C18orf8), mRNA", gi|21361441|ref|NM_013326.2|[21361441]; 1408: NM_013330 , "Homo sapiens non-metastatic cells 7, protein expressed in", "(nucleoside-diphosphate kinase) (NME7), transcript variant 1, mRNA", gi|37574616|ref|NM_013330.3|[37574616]; 1409: NM_013333 , "Homo sapiens epsin 1 (EPN1), mRNA", gi|41350200|ref|NM_013333.2|[41350200]; 1410: NM_013335 , "Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA), mRNA", gi|31881778|ref|NM_013335.2|[31881778]; 1411: NM_013336 , "Homo sapiens Sec61 alpha 1 subunit (S. cerevisiae) (SEC61A1), mRNA", gi|14591931|ref|NM_013336.2|[14591931]; 1412: NM_013338 , "Homo sapiens asparagine-linked glycosylation 5 homolog (yeast,", "dolichyl-phosphate beta-glucosyltransferase) (ALG5), mRNA", gi|38176301|ref|NM_013338.3|[38176301]; 1413: NM_013339 , "Homo sapiens asparagine-linked glycosylation 6 homolog (yeast,", "alpha-1,3-glucosyltransferase) (ALG6), mRNA", gi|38026891|ref|NM_013339.2|[38026891]; 1414: NM_013341 , "Homo sapiens hypothetical protein PTD004 (PTD004), mRNA", gi|24431968|ref|NM_013341.2|[24431968]; 1415: NM_013342 , "Homo sapiens TCF3 (E2A) fusion partner (in childhood Leukemia) (TFPT), mRNA", gi|7019370|ref|NM_013342.1|[7019370]; 1416: NM_013343 , "Homo sapiens loss of heterozygosity, 3, chromosomal region 2, gene A (LOH3CR2A),", mRNA, gi|7106370|ref|NM_013343.1|[7106370]; 1417: NM_013345 , "Homo sapiens G protein-coupled receptor 132 (GPR132), mRNA", gi|30181231|ref|NM_013345.2|[30181231]; 1418: NM_013348 , "Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 14", "(KCNJ14), transcript variant 1, mRNA", gi|25777633|ref|NM_013348.2|[25777633]; 1419: NM_013366 , "Homo sapiens anaphase promoting complex subunit 2 (ANAPC2), mRNA", gi|41327747|ref|NM_013366.3|[41327747]; 1420: NM_013374 , "Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA", gi|22027537|ref|NM_013374.2|[22027537]; 1421: NM_013375 , "Homo sapiens activator of basal transcription 1 (ABT1), mRNA", gi|17572813|ref|NM_013375.2|[17572813]; 1422: NM_013380 , "Homo sapiens zinc finger protein 228 (ZNF228), mRNA", gi|34932234|ref|NM_013380.2|[34932234]; 1423: NM_013381 , "Homo sapiens thyrotropin-releasing hormone degrading ectoenzyme (TRHDE), mRNA", gi|7019560|ref|NM_013381.1|[7019560]; 1424: NM_013382 , "Homo sapiens protein-O-mannosyltransferase 2 (POMT2), mRNA", gi|32455270|ref|NM_013382.3|[32455270]; 1425: NM_013384 , "Homo sapiens LAG1 longevity assurance homolog 2 (S. cerevisiae) (LASS2),", "transcript variant 3, mRNA", gi|32455253|ref|NM_013384.3|[32455253]; 1426: NM_013386 , "Homo sapiens calcium-binding transporter (DKFZp586G0123), mRNA", gi|33598953|ref|NM_013386.2|[33598953]; 1427: NM_013387 , "Homo sapiens ubiquinol-cytochrome c reductase complex (7.2 kD) (HSPC051), mRNA", gi|41281884|ref|NM_013387.2|[41281884]; 1428: NM_013392 , "Homo sapiens nuclear receptor

binding protein (NRBP), mRNA", gi|7019332|ref|NM_013392.1|[7019332]; 1429: NM_013400 , "Homo sapiens replication initiator 1 (REPIN1), mRNA", gi|7019516|ref|NM_013400.1|[7019516]; 1430: NM_013403 , "Homo sapiens striatin, calmodulin binding protein 4 (STRN4), mRNA", gi|7019572|ref|NM_013403.1|[7019572]; 1431: NM_013441 , "Homo sapiens Down syndrome critical region gene 1-like 2 (DSCR1L2), mRNA", gi|38455419|ref|NM_013441.2|[38455419]; 1432: NM_013442 , "Homo sapiens stomatin (EPB72)-like 2 (STOML2), mRNA", gi|7305502|ref|NM_013442.1|[7305502]; 1433: NM_014012 , "Homo sapiens RAS (RAD and GEM)-like GTP-binding (REM), mRNA", gi|35493898|ref|NM_014012.4|[35493898]; 1434: NM_014020 , "Homo sapiens LR8 protein (LR8), mRNA", gi|21361500|ref|NM_014020.2|[21361500]; 1435: NM_014035 , "Homo sapiens sorting nexing 24 (SNX24), mRNA", gi|7662654|ref|NM_014035.1|[7662654]; 1436: NM_014038 , "Homo sapiens basic leucine zipper and W2 domains 2 (BZW2), mRNA", gi|7661743|ref|NM_014038.1|[7661743]; 1437: NM_014041 , "Homo sapiens signal peptidase 12kDa (SPC12), mRNA", gi|7661745|ref|NM_014041.1|[7661745]; 1438: NM_014044 , "Homo sapiens unc-50 homolog (C. elegans) (UNC50), mRNA", gi|37059764|ref|NM_014044.4|[37059764]; 1439: NM_014045 , "Homo sapiens low density lipoprotein receptor-related protein 10 (LRP10), mRNA", gi|32490558|ref|NM_014045.2|[32490558]; 1440: NM_014047 , "Homo sapiens HSPC023 protein (HSPC023), mRNA", gi|7661741|ref|NM_014047.1|[7661741]; 1441: NM_014048 , "Homo sapiens myocardin-related transcription factor B (MRTF-B), mRNA", gi|38569479|ref|NM_014048.3|[38569479]; 1442: NM_014051 , "Homo sapiens transmembrane protein 14A (TMEM14A), mRNA", gi|32261328|ref|NM_014051.2|[32261328]; 1443: NM_014055 , Homo sapiens carnitine deficiency-associated gene expressed in ventricle 1, "(CDV-1), mRNA", gi|32526900|ref|NM_014055.2|[32526900]; 1444: NM_014059 , "Homo sapiens response gene to complement 32 (RGC32), mRNA", gi|7662650|ref|NM_014059.1|[7662650]; 1445: NM_014060 , "Homo sapiens malignant T cell amplified sequence 1 (MCTS1), mRNA", gi|7662501|ref|NM_014060.1|[7662501]; 1446: NM_014065 , "Homo sapiens HT001 protein (HT001), mRNA", gi|33469986|ref|NM_014065.2|[33469986]; 1447: NM_014070 , "Homo sapiens chromosome 6 open reading frame 15 (C6orf15), mRNA", gi|7662666|ref|NM_014070.1|[7662666]; 1448: NM_014099 , , ref|NM_014099.1|[7662610], This record was temporarily removed by RefSeq staff for additional review., , 1449: NM_014109 , "Homo sapiens PRO2000 protein (PRO2000), mRNA", gi|24497617|ref|NM_014109.2|[24497617]; 1450: NM_014113 , "Homo sapiens PRO0038 protein (PRO0038), mRNA", gi|7662519|ref|NM_014113.1|[7662519]; 1451: NM_014117 , "Homo sapiens PRO0149 protein (PRO0149), mRNA", gi|38016918|ref|NM_014117.2|[38016918]; 1452: NM_014124 , , ref|NM_014124.1|[7662541], This record was temporarily removed by RefSeq staff for additional review., , 1453: NM_014133 , , ref|NM_014133.1|[7662573], This record was temporarily removed by RefSeq staff for additional review., , 1454: NM_014135 , , ref|NM_014135.1|[7662577], This record was temporarily removed by RefSeq staff for additional review., , 1455: NM_014140 , "Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of", "chromatin, subfamily a-like 1 (SMARCAL1), mRNA", gi|21071059|ref|NM_014140.2|[21071059]; 1456: NM_014144 , "Homo sapiens chromosome 11 open reading frame 21 (C11orf21), mRNA", gi|7662662|ref|NM_014144.1|[7662662]; 1457: NM_014145 , "Homo sapiens chromosome 20 open reading frame 30 (C20orf30), mRNA", gi|42476067|ref|NM_014145.3|[42476067]; 1458: NM_014155 , "Homo sapiens HSPC063 protein (HSPC063), mRNA",

gi|7661765|ref|NM_014155.1|[7661765]; 1459: NM_014161 , "Homo sapiens mitochondrial ribosomal protein L18 (MRPL18), nuclear gene encoding", "mitochondrial protein, mRNA", gi|21265079|ref|NM_014161.2|[21265079]; 1460: NM_014162 , "Homo sapiens HSPC072 protein (HSPC072), mRNA", gi|7661779|ref|NM_014162.1|[7661779]; 1461: NM_014164 , "Homo sapiens FXYD domain containing ion transport regulator 5 (FXYD5), mRNA", gi|21618360|ref|NM_014164.3|[21618360]; 1462: NM_014165 , "Homo sapiens chromosome 6 open reading frame 66 (C6orf66), mRNA", gi|7661785|ref|NM_014165.1|[7661785]; 1463: NM_014166 , "Homo sapiens vitamin D receptor interacting protein (VDRIP), mRNA", gi|40254874|ref|NM_014166.2|[40254874]; 1464: NM_014171 , "Homo sapiens postsynaptic protein CRIPT (CRIPT), mRNA", gi|41350204|ref|NM_014171.3|[41350204]; 1465: NM_014173 , "Homo sapiens HSPC142 protein (HSPC142), mRNA", gi|7661801|ref|NM_014173.1|[7661801]; 1466: NM_014174 , "Homo sapiens thymocyte protein thy28 (THY28), transcript variant 1, mRNA", gi|40806217|ref|NM_014174.2|[40806217]; 1467: NM_014179 , "Homo sapiens HSPC157 protein (HSPC157), mRNA", gi|7661813|ref|NM_014179.1|[7661813]; 1468: NM_014185 , , ref|NM_014185.1|[7661825], This record was replaced or removed. See revision history for details., , 1469: NM_014187 , "Homo sapiens HSPC171 protein (HSPC171), mRNA", gi|7661829|ref|NM_014187.1|[7661829]; 1470: NM_014191 , "Homo sapiens sodium channel, voltage gated, type VIII, alpha (SCN8A), mRNA", gi|7657543|ref|NM_014191.1|[7657543]; 1471: NM_014205 , "Homo sapiens chromosome 11 open reading frame 5 (C11orf5), mRNA", gi|42716303|ref|NM_014205.2|[42716303]; 1472: NM_014206 , "Homo sapiens chromosome 11 open reading frame 10 (C11orf10), mRNA", gi|7656933|ref|NM_014206.1|[7656933]; 1473: NM_014211 , "Homo sapiens gamma-aminobutyric acid (GABA) A receptor, pi (GABRP), mRNA", gi|7657105|ref|NM_014211.1|[7657105]; 1474: NM_014225 , "Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65),", "alpha isoform (PPP2R1A), mRNA", gi|32455242|ref|NM_014225.3|[32455242]; 1475: NM_014226 , "Homo sapiens renal tumor antigen (RAGE), mRNA", gi|7657497|ref|NM_014226.1|[7657497]; 1476: NM_014234 , "Homo sapiens hydroxysteroid (17-beta) dehydrogenase 8 (HSD17B8), mRNA", gi|20143980|ref|NM_014234.3|[20143980]; 1477: NM_014235 , "Homo sapiens ubiquitin-like 4 (UBL4), mRNA", gi|40254852|ref|NM_014235.2|[40254852]; 1478: NM_014236 , "Homo sapiens glyceronephosphate O-acyltransferase (GNPAT), mRNA", gi|7657133|ref|NM_014236.1|[7657133]; 1479: NM_014239 , "Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa", "(EIF2B2), mRNA", gi|7657057|ref|NM_014239.1|[7657057]; 1480: NM_014243 , Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with, "thrombospondin type 1 motif, 3 (ADAMTS3), mRNA", gi|21265036|ref|NM_014243.1|[21265036]; 1481: NM_014245 , "Homo sapiens ring finger protein 7 (RNF7), transcript variant 1, mRNA", gi|34304329|ref|NM_014245.2|[34304329]; 1482: NM_014248 , "Homo sapiens ring-box 1 (RBX1), mRNA", gi|22091459|ref|NM_014248.2|[22091459]; 1483: NM_014252 , Homo sapiens solute carrier family 25 (mitochondrial carrier; ornithine, "transporter) member 15 (SLC25A15), nuclear gene encoding mitochondrial protein,", mRNA, gi|7657584|ref|NM_014252.1|[7657584]; 1484: NM_014258 , "Homo sapiens synaptonemal complex protein 2 (SYCP2), mRNA", gi|38373672|ref|NM_014258.2|[38373672]; 1485: NM_014262 , "Homo sapiens leprecan-like 2 protein (LEPREL2), mRNA", gi|28466982|ref|NM_014262.2|[28466982]; 1486: NM_014273 , Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with, "thrombospondin type 1 motif, 6 (ADAMTS6),

mRNA", gi|21536389|ref|NM_014273.2|[21536389]; 1487: NM_014275 , "Homo sapiens mannosyl (alpha-1,3-)-glycoprotein", "beta-1,4-N-acetylglucosaminyltransferase, isoenzyme B (MGAT4B), transcript", "variant 1, mRNA", gi|16915933|ref|NM_014275.2|[16915933]; 1488: NM_014276 , Homo sapiens recombining binding protein suppressor of hairless, "(Drosophila)-like (RBPSUHL), mRNA", gi|34577080|ref|NM_014276.2|[34577080]; 1489: NM_014278 , "Homo sapiens heat shock protein (hsp110 family) (APG-1), mRNA", gi|31541940|ref|NM_014278.2|[31541940]; 1490: NM_014283 , "Homo sapiens chromosome 1 open reading frame 9 (C1orf9), mRNA", gi|29837653|ref|NM_014283.2|[29837653]; 1491: NM_014288 , "Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA", gi|27597074|ref|NM_014288.3|[27597074]; 1492: NM_014290 , "Homo sapiens tudor repeat associator with PCTAIRE 2 (PCTAIRE2BP), mRNA", gi|24307950|ref|NM_014290.1|[24307950]; 1493: NM_014296 , "Homo sapiens calpain 7 (CAPN7), mRNA", gi|41327720|ref|NM_014296.2|[41327720]; 1494: NM_014301 , "Homo sapiens nitrogen fixation cluster-like (NIFU), mRNA", gi|24307952|ref|NM_014301.1|[24307952]; 1495: NM_014302 , "Homo sapiens Sec61 gamma subunit (SEC61G), mRNA", gi|14591933|ref|NM_014302.2|[14591933]; 1496: NM_014303 , "Homo sapiens pescadillo homolog 1, containing BRCT domain (zebrafish) (PES1),", mRNA, gi|22091458|ref|NM_014303.2|[22091458]; 1497: NM_014305 , "Homo sapiens TDP-glucose 4,6-dehydratase (TGDS), mRNA", gi|7657640|ref|NM_014305.1|[7657640]; 1498: NM_014308 , "Homo sapiens phosphoinositide-3-kinase, regulatory subunit, polypeptide p101", "(P101-PI3K), mRNA", gi|7657432|ref|NM_014308.1|[7657432]; 1499: NM_014315 , "Homo sapiens kelch domain containing 2 (KLHDC2), mRNA", gi|7657300|ref|NM_014315.1|[7657300]; 1500: NM_014317 , "Homo sapiens trans-prenyltransferase (TPRT), mRNA", gi|11863164|ref|NM_014317.2|[11863164]; 1501: NM_014319 , "Homo sapiens integral inner nuclear membrane protein (MAN1), mRNA", gi|36287116|ref|NM_014319.3|[36287116]; 1502: NM_014322 , "Homo sapiens opsin 3 (encephalopsin, panopsin) (OPN3), mRNA", gi|7657070|ref|NM_014322.1|[7657070]; 1503: NM_014329 , "Homo sapiens autoantigen (RCD-8), mRNA", gi|21361430|ref|NM_014329.2|[21361430]; 1504: NM_014338 , "Homo sapiens phosphatidylserine decarboxylase (PISD), mRNA", gi|34147578|ref|NM_014338.3|[34147578]; 1505: NM_014342 , "Homo sapiens mitochondrial carrier homolog 2 (C. elegans) (MTCH2), nuclear gene", "encoding mitochondrial protein, mRNA", gi|40254847|ref|NM_014342.2|[40254847]; 1506: NM_014344 , "Homo sapiens four jointed box 1 (Drosophila) (FJX1), mRNA", gi|18765710|ref|NM_014344.2|[18765710]; 1507: NM_014348 , "Homo sapiens POM121 membrane glycoprotein-like 1 (rat) (POM121L1), mRNA", gi|7657468|ref|NM_014348.1|[7657468]; 1508: NM_014360 , "Homo sapiens NK2 transcription factor related, locus 8 (Drosophila) (NKX2-8),", mRNA, gi|31377776|ref|NM_014360.2|[31377776]; 1509: NM_014361 , "Homo sapiens contactin 5 (CNTN5), transcript variant 1, mRNA", gi|28373127|ref|NM_014361.2|[28373127]; 1510: NM_014364 , "Homo sapiens glyceraldehyde-3-phosphate dehydrogenase, spermatogenic (GAPDS),", mRNA, gi|34222311|ref|NM_014364.3|[34222311]; 1511: NM_014365 , "Homo sapiens heat shock 27kDa protein 8 (HSPB8), mRNA", gi|38016940|ref|NM_014365.2|[38016940]; 1512: NM_014366 , "Homo sapiens nucleostemin (NS), mRNA", gi|37497106|ref|NM_014366.3|[37497106]; 1513: NM_014368 , "Homo sapiens LIM homeobox 6 (LHX6), transcript variant 1, mRNA", gi|40549416|ref|NM_014368.2|[40549416]; 1514: NM_014372 , "Homo sapiens ring finger protein 11 (RNF11), mRNA", gi|34452682|ref|NM_014372.3|[34452682]; 1515: NM_014384 ,

"Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA", gi|7656848|ref|NM_014384.1|[7656848]; 1516: NM_014390 , "Homo sapiens staphylococcal nuclease domain containing 1 (SND1), mRNA", gi|7657430|ref|NM_014390.1|[7657430]; 1517: NM_014391 , "Homo sapiens ankyrin repeat domain 1 (cardiac muscle) (ANKRD1), mRNA", gi|38327521|ref|NM_014391.2|[38327521]; 1518: NM_014402 , "Homo sapiens low molecular mass ubiquinone-binding protein (9.5kD) (QP-C),", "nuclear gene encoding mitochondrial protein, mRNA", gi|27894387|ref|NM_014402.2|[27894387]; 1519: NM_014409 , "Homo sapiens TAF5-like RNA polymerase II, p300/CBP-associated factor", "(PCAF)-associated factor, 65kDa (TAF5L), mRNA", gi|21269865|ref|NM_014409.2|[21269865]; 1520: NM_014415 , "Homo sapiens zinc finger protein (ZNF-U69274), mRNA", gi|7657702|ref|NM_014415.1|[7657702]; 1521: NM_014421 , "Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), mRNA", gi|7657022|ref|NM_014421.1|[7657022]; 1522: NM_014426 , "Homo sapiens sorting nexin 5 (SNX5), transcript variant 2, mRNA", gi|23111045|ref|NM_014426.2|[23111045]; 1523: NM_014427 , "Homo sapiens copine VII (CPNE7), transcript variant 2, mRNA", gi|25141326|ref|NM_014427.3|[25141326]; 1524: NM_014429 , "Homo sapiens microrchidia homolog (mouse) (MORC), mRNA", gi|7657340|ref|NM_014429.1|[7657340]; 1525: NM_014430 , "Homo sapiens cell death-inducing DFFA-like effector b (CIDEB), mRNA", gi|7656978|ref|NM_014430.1|[7656978]; 1526: NM_014432 , "Homo sapiens interleukin 20 receptor, alpha (IL20RA), mRNA", gi|31083155|ref|NM_014432.2|[31083155]; 1527: NM_014437 , "Homo sapiens solute carrier family 39 (zinc transporter), member 1 (SLC39A1),", mRNA, gi|34147669|ref|NM_014437.3|[34147669]; 1528: NM_014440 , "Homo sapiens interleukin 1 family, member 6 (epsilon) (IL1F6), mRNA", gi|7657091|ref|NM_014440.1|[7657091]; 1529: NM_014453 , "Homo sapiens putative breast adenocarcinoma marker (32kD) (BC-2), transcript", "variant 1, mRNA", gi|38372936|ref|NM_014453.2|[38372936]; 1530: NM_014459 , "Homo sapiens protocadherin 17 (PCDH17), mRNA", gi|14589926|ref|NM_014459.2|[14589926]; 1531: NM_014462 , "Homo sapiens LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae)", "(LSM1), mRNA", gi|7657312|ref|NM_014462.1|[7657312]; 1532: NM_014466 , "Homo sapiens tektin 2 (testicular) (TEKT2), mRNA", gi|16507949|ref|NM_014466.2|[16507949]; 1533: NM_014471 , "Homo sapiens serine protease inhibitor, Kazal type 4 (SPINK4), mRNA", gi|7657452|ref|NM_014471.1|[7657452]; 1534: NM_014484 , "Homo sapiens molybdenum cofactor synthesis 3 (MOCS3), mRNA", gi|31652257|ref|NM_014484.3|[31652257]; 1535: NM_014504 , "Homo sapiens RAB guanine nucleotide exchange factor (GEF) 1 (RABGEF1), mRNA", gi|7657495|ref|NM_014504.1|[7657495]; 1536: NM_014505 , "Homo sapiens potassium large conductance calcium-activated channel, subfamily M,", "beta member 4 (KCNMB4), mRNA", gi|26051274|ref|NM_014505.4|[26051274]; 1537: NM_014506 , "Homo sapiens torsin family 1, member B (torsin B) (TOR1B), mRNA", gi|14149652|ref|NM_014506.1|[14149652]; 1538: NM_014507 , Homo sapiens malonyl-CoA:acyl carrier protein transacylase (malonyltransferase), "(MT), mRNA", gi|27477044|ref|NM_014507.1|[27477044]; 1539: NM_014517 , "Homo sapiens upstream binding protein 1 (LBP-1a) (UBP1), mRNA", gi|31543907|ref|NM_014517.2|[31543907]; 1540: NM_014520 , "Homo sapiens MYB binding protein (P160) 1a (MYBBP1A), mRNA", gi|7657350|ref|NM_014520.1|[7657350]; 1541: NM_014548 , "Homo sapiens tropomodulin 2 (neuronal) (TMOD2), mRNA", gi|40789262|ref|NM_014548.2|[40789262]; 1542: NM_014563 , "Homo sapiens spondyloepiphyseal dysplasia, late (SEDL), mRNA",

gi|38044279|ref|NM_014563.2|[38044279]; 1543: NM_014565 , "Homo sapiens olfactory receptor, family 1, subfamily A, member 1 (OR1A1), mRNA", gi|7657420|ref|NM_014565.1|[7657420]; 1544: NM_014571 , "Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEYL), mRNA", gi|19923414|ref|NM_014571.2|[19923414]; 1545: NM_014580 , "Homo sapiens solute carrier family 2, (facilitated glucose transporter) member 8", "(SLC2A8), mRNA", gi|21361448|ref|NM_014580.2|[21361448]; 1546: NM_014581 , "Homo sapiens odorant binding protein 2B (OBP2B), mRNA", gi|7657406|ref|NM_014581.1|[7657406]; 1547: NM_014588 , "Homo sapiens visual system homeobox 1 homolog, CHX10-like (zebrafish) (VSX1),", "transcript variant 1, mRNA", gi|40806214|ref|NM_014588.4|[40806214]; 1548: NM_014595 , "Homo sapiens 5', 3'-nucleotidase, cytosolic (NT5C), mRNA", gi|7657032|ref|NM_014595.1|[7657032]; 1549: NM_014602 , "Homo sapiens phosphoinositide-3-kinase, regulatory subunit 4, p150 (PIK3R4),", mRNA, gi|23943911|ref|NM_014602.1|[23943911]; 1550: NM_014606 , , ref|NM_014606.1|[7657151], This record was temporarily removed by RefSeq staff for additional review., , 1551: NM_014608 , "Homo sapiens cytoplasmic FMR1 interacting protein 1 (CYFIP1), mRNA", gi|24307968|ref|NM_014608.1|[24307968]; 1552: NM_014620 , "Homo sapiens homeo box C4 (HOXC4), transcript variant 1, mRNA", gi|24497537|ref|NM_014620.2|[24497537]; 1553: NM_014621 , "Homo sapiens homeo box D4 (HOXD4), mRNA", gi|23397671|ref|NM_014621.2|[23397671]; 1554: NM_014623 , "Homo sapiens male-enhanced antigen (MEA), mRNA", gi|7657325|ref|NM_014623.1|[7657325]; 1555: NM_014625 , "Homo sapiens nephrosis 2, idiopathic, steroid-resistant (podocin) (NPHS2), mRNA", gi|7657614|ref|NM_014625.1|[7657614]; 1556: NM_014628 , "Homo sapiens MAD2L1 binding protein (MAD2L1BP), mRNA", gi|7661917|ref|NM_014628.1|[7661917]; 1557: NM_014632 , "Homo sapiens flavoprotein oxidoreductase MICAL2 (MICAL2), mRNA", gi|41281417|ref|NM_014632.2|[41281417]; 1558: NM_014633 , Homo sapiens SH2 domain binding protein 1 (tetratricopeptide repeat containing), "(SH2BP1), mRNA", gi|41281407|ref|NM_014633.2|[41281407]; 1559: NM_014652 , "Homo sapiens importin 13 (IPO13), mRNA", gi|41281424|ref|NM_014652.2|[41281424]; 1560: NM_014657 , "Homo sapiens KIAA0406 gene product (KIAA0406), mRNA", gi|24307960|ref|NM_014657.1|[24307960]; 1561: NM_014662 , , ref|NM_014662.1|[7662221], This record was temporarily removed by RefSeq staff for additional review., , 1562: NM_014671 , , ref|NM_014671.1|[7661855], This record was temporarily removed by RefSeq staff for additional review., , 1563: NM_014674 , , ref|NM_014674.1|[7662001], This record was temporarily removed by RefSeq staff for additional review., , 1564: NM_014686 , , ref|NM_014686.1|[7662075], This record was temporarily removed by RefSeq staff for additional review., , 1565: NM_014700 , "Homo sapiens eferin (Rab11-FIP3), mRNA", gi|41281455|ref|NM_014700.2|[41281455]; 1566: NM_014708 , "Homo sapiens kinetochore associated 1 (KNTC1), mRNA", gi|41327744|ref|NM_014708.3|[41327744]; 1567: NM_014713 , "Homo sapiens lysosomal-associated protein transmembrane 4 alpha (LAPTM4A), mRNA", gi|41352690|ref|NM_014713.3|[41352690]; 1568: NM_014714 , "Homo sapiens KIAA0590 gene product (KIAA0590), mRNA", gi|41281446|ref|NM_014714.2|[41281446]; 1569: NM_014733 , "Homo sapiens zinc finger, FYVE domain containing 16 (ZFYVE16), mRNA", gi|41281465|ref|NM_014733.2|[41281465]; 1570: NM_014734 , "Homo sapiens KIAA0247 (KIAA0247), mRNA", gi|41281456|ref|NM_014734.2|[41281456]; 1571: NM_014738 , "Homo sapiens KIAA0195 gene product (KIAA0195), mRNA",

gi|41281472|ref|NM_014738.2|[41281472]; 1572: NM_014748 , "Homo sapiens sorting nexin 17 (SNX17), mRNA", gi|23238249|ref|NM_014748.2|[23238249]; 1573: NM_014753 , "Homo sapiens BMS1-like, ribosome assembly protein (yeast) (BMS1L), mRNA", gi|41281482|ref|NM_014753.2|[41281482]; 1574: NM_014754 , "Homo sapiens phosphatidylserine synthase 1 (PTDSS1), mRNA", gi|7662646|ref|NM_014754.1|[7662646]; 1575: NM_014757 , "Homo sapiens mastermind-like 1 (Drosophila) (MAML1), mRNA", gi|41350321|ref|NM_014757.3|[41350321]; 1576: NM_014760 , , ref|NM_014760.1|[7662007], This record was temporarily removed by RefSeq staff for additional review., , 1577: NM_014777 , , ref|NM_014777.1|[7661931], This record was temporarily removed by RefSeq staff for additional review., , 1578: NM_014783 , "Homo sapiens similar to human GTPase-activating protein (ARHGAP11A), mRNA", gi|40788020|ref|NM_014783.2|[40788020]; 1579: NM_014784 , "Homo sapiens Rho guanine nucleotide exchange factor (GEF) 11 (ARHGEF11),", "transcript variant 1, mRNA", gi|38026914|ref|NM_014784.2|[38026914]; 1580: NM_014785 , , ref|NM_014785.1|[7662029], This record was temporarily removed by RefSeq staff for additional review., , 1581: NM_014786 , "Homo sapiens Rho guanine nucleotide exchange factor (GEF) 17 (ARHGEF17), mRNA", gi|21361457|ref|NM_014786.2|[21361457]; 1582: NM_014791 , "Homo sapiens maternal embryonic leucine zipper kinase (MELK), mRNA", gi|41281490|ref|NM_014791.2|[41281490]; 1583: NM_014797 , , ref|NM_014797.1|[7662127], This record was temporarily removed by RefSeq staff for additional review., , 1584: NM_014805 , "Homo sapiens EPM2A (laforin) interacting protein 1 (EPM2AIP1), mRNA", gi|31982934|ref|NM_014805.2|[31982934]; 1585: NM_014813 , , ref|NM_014813.1|[7662319], This record was temporarily removed by RefSeq staff for additional review., , 1586: NM_014814 , "Homo sapiens proteasome regulatory particle subunit p44S10 (p44S10), mRNA", gi|7661913|ref|NM_014814.1|[7661913]; 1587: NM_014819 , "Homo sapiens praja 2, RING-H2 motif containing (PJA2), mRNA", gi|41281511|ref|NM_014819.2|[41281511]; 1588: NM_014821 , "Homo sapiens KIAA0317 (KIAA0317), mRNA", gi|42734314|ref|NM_014821.2|[42734314]; 1589: NM_014840 , , ref|NM_014840.1|[7662169], This record was temporarily removed by RefSeq staff for additional review., , 1590: NM_014845 , "Homo sapiens KIAA0274 (KIAA0274), mRNA", gi|36030904|ref|NM_014845.4|[36030904]; 1591: NM_014846 , "Homo sapiens KIAA0196 gene product (KIAA0196), mRNA", gi|41281517|ref|NM_014846.2|[41281517]; 1592: NM_014862 , "Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), mRNA", gi|41281514|ref|NM_014862.2|[41281514]; 1593: NM_014865 , "Homo sapiens chromosome condensation-related SMC-associated protein 1 (CNAP1),", mRNA, gi|41281520|ref|NM_014865.2|[41281520]; 1594: NM_014867 , , ref|NM_014867.1|[7662259], This record was temporarily removed by RefSeq staff for additional review., , 1595: NM_014872 , , ref|NM_014872.1|[7662073], This record was temporarily removed by RefSeq staff for additional review., , 1596: NM_014873 , , ref|NM_014873.1|[7661995], This record was temporarily removed by RefSeq staff for additional review., , 1597: NM_014875 , , ref|NM_014875.1|[7661877], This record was temporarily removed by RefSeq staff for additional review., , 1598: NM_014876 , "Homo sapiens KIAA0063 gene product (KIAA0063), mRNA", gi|34222319|ref|NM_014876.3|[34222319]; 1599: NM_014881 , "Homo sapiens DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae) (DCLRE1A),", mRNA, gi|42734318|ref|NM_014881.2|[42734318]; 1600: NM_014886 , "Homo sapiens TGF beta-inducible nuclear protein 1 (TINP1), mRNA", gi|21359901|ref|NM_014886.2|[21359901]; 1601: NM_014888 , "Homo sapiens family with sequence similarity 3, member C (FAM3C), mRNA",

gi|7661713|ref|NM_014888.1|[7661713]; 1602: NM_014889 , "Homo sapiens pitrilysin metalloproteinase 1 (PITRM1), mRNA", gi|41352060|ref|NM_014889.2|[41352060]; 1603: NM_014892 , , ref|NM_014892.1|[7662491], This record was temporarily removed by RefSeq staff for additional review., , 1604: NM_014901 , "Homo sapiens ring finger protein 44 (RNF44), mRNA", gi|42718018|ref|NM_014901.4|[42718018]; 1605: NM_014907 , "Homo sapiens FERM and PDZ domain containing 1 (FRMPD1), mRNA", gi|7662415|ref|NM_014907.1|[7662415]; 1606: NM_014910 , , ref|NM_014910.1|[7662479], This record was temporarily removed by RefSeq staff for additional review., , 1607: NM_014914 , "Homo sapiens centaurin, gamma 2 (CENTG2), mRNA", gi|41281554|ref|NM_014914.2|[41281554]; 1608: NM_014917 , , ref|NM_014917.1|[7662425], This record was temporarily removed by RefSeq staff for additional review., , 1609: NM_014935 , "Homo sapiens phosphoinositol 3-phosphate-binding protein-3 (PEPP3), mRNA", gi|37595547|ref|NM_014935.2|[37595547]; 1610: NM_014937 , "Homo sapiens inositol polyphosphate-5-phosphatase F (INPP5F), transcript variant", "1, mRNA", gi|38327540|ref|NM_014937.2|[38327540]; 1611: NM_014939 , "Homo sapiens KIAA1012 (KIAA1012), mRNA", gi|42476075|ref|NM_014939.2|[42476075]; 1612: NM_014940 , "Homo sapiens HSV-1 stimulation-related gene 1 (HSRG1), mRNA", gi|38016939|ref|NM_014940.2|[38016939]; 1613: NM_014949 , , ref|NM_014949.1|[7662371], This record was temporarily removed by RefSeq staff for additional review., , 1614: NM_014977 , "Homo sapiens apoptotic chromatin condensation inducer in the nucleus (ACINUS),", mRNA, gi|7662237|ref|NM_014977.1|[7662237]; 1615: NM_014992 , "Homo sapiens dishevelled associated activator of morphogenesis 1 (DAAM1), mRNA", gi|21071076|ref|NM_014992.1|[21071076]; 1616: NM_015029 , "Homo sapiens processing of precursors 1 (POP1), mRNA", gi|23097291|ref|NM_015029.1|[23097291]; 1617: NM_015039 , "Homo sapiens nicotinamide nucleotide adenylyltransferase 2 (NMNAT2), transcript", "variant 1, mRNA", gi|25141321|ref|NM_015039.2|[25141321]; 1618: NM_015050 , "Homo sapiens KIAA0082 (KIAA0082), mRNA", gi|24307982|ref|NM_015050.1|[24307982]; 1619: NM_015064 , "Homo sapiens Rab6-interacting protein 2 (ELKS), transcript variant alpha, mRNA", gi|38045899|ref|NM_015064.2|[38045899]; 1620: NM_015074 , "Homo sapiens kinesin family member 1B (KIF1B), transcript variant 1, mRNA", gi|41393562|ref|NM_015074.2|[41393562]; 1621: NM_015078 , "Homo sapiens Rho family guanine-nucleotide exchange factor (KIAA0861), mRNA", gi|31742504|ref|NM_015078.2|[31742504]; 1622: NM_015089 , "Homo sapiens p53-associated parkin-like cytoplasmic protein (PARC), mRNA", gi|24307990|ref|NM_015089.1|[24307990]; 1623: NM_015101 , "Homo sapiens chromosome 1 open reading frame 17 (C1orf17), mRNA", gi|16506819|ref|NM_015101.1|[16506819]; 1624: NM_015149 , "Homo sapiens RalGDS-like gene (RGL), mRNA", gi|20127535|ref|NM_015149.2|[20127535]; 1625: NM_015163 , "Homo sapiens tripartite motif-containing 9 (TRIM9), transcript variant 1, mRNA", gi|29543553|ref|NM_015163.3|[29543553]; 1626: NM_015169 , "Homo sapiens RRS1 ribosome biogenesis regulator homolog (S. cerevisiae) (RRS1),", mRNA, gi|34147329|ref|NM_015169.2|[34147329]; 1627: NM_015178 , "Homo sapiens Rho-related BTB domain containing 2 (RHOBTB2), mRNA", gi|14165285|ref|NM_015178.1|[14165285]; 1628: NM_015198 , "Homo sapiens cordon-bleu homolog (mouse) (COBL), mRNA", gi|31581523|ref|NM_015198.2|[31581523]; 1629: NM_015216 , "Homo sapiens KIAA0433 protein (KIAA0433), mRNA", gi|41281582|ref|NM_015216.2|[41281582]; 1630: NM_015254 , "Homo sapiens kinesin family member 13B (KIF13B), mRNA",

gi|13194196|ref|NM_015254.1|[13194196]; 1631: NM_015292 , Homo sapiens likely ortholog of mouse membrane bound C2 domain containing, "protein (MBC2), mRNA", gi|14149679|ref|NM_015292.1|[14149679]; 1632: NM_015308 , "Homo sapiens formin binding protein 4 (FNBP4), mRNA", gi|24308032|ref|NM_015308.1|[24308032]; 1633: NM_015316 , "Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 13B", "(PPP1R13B), mRNA", gi|18699719|ref|NM_015316.1|[18699719]; 1634: NM_015318 , "Homo sapiens rho/rac guanine nucleotide exchange factor (GEF) 18 (ARHGEF18),", mRNA, gi|41327768|ref|NM_015318.2|[41327768]; 1635: NM_015331 , "Homo sapiens nicastrin (NCSTN), mRNA", gi|24638432|ref|NM_015331.1|[24638432]; 1636: NM_015339 , "Homo sapiens activity-dependent neuroprotector (ADNP), transcript variant 1,", mRNA, gi|31563504|ref|NM_015339.2|[31563504]; 1637: NM_015341 , "Homo sapiens barren homolog (Drosophila) (BRRN1), mRNA", gi|25121986|ref|NM_015341.2|[25121986]; 1638: NM_015343 , "Homo sapiens dullard homolog (Xenopus laevis) (DULLARD), mRNA", gi|34222318|ref|NM_015343.3|[34222318]; 1639: NM_015358 , "Homo sapiens zinc finger, CW-type with coiled-coil domain 3 (ZCWCC3), mRNA", gi|28872811|ref|NM_015358.1|[28872811]; 1640: NM_015362 , , ref|NM_015362.3|[44662829]; 1641: NM_015368 , "Homo sapiens pannexin 1 (PANX1), mRNA", gi|39995063|ref|NM_015368.3|[39995063]; 1642: NM_015372 , "Homo sapiens hypothetical protein HSN44A4A (HSN44A4A), mRNA", gi|7661723|ref|NM_015372.1|[7661723]; 1643: NM_015376 , , ref|NM_015376.1|[7662333], This record was temporarily removed by RefSeq staff for additional review., , 1644: NM_015388 , "Homo sapiens chromosome 6 open reading frame 109 (C6orf109), mRNA", gi|7661641|ref|NM_015388.1|[7661641]; 1645: NM_015393 , "Homo sapiens DKFZP564O0823 protein (DKFZP564O0823), mRNA", gi|7661631|ref|NM_015393.1|[7661631]; 1646: NM_015399 , "Homo sapiens breast cancer metastasis suppressor 1 (BRMS1), mRNA", gi|24475631|ref|NM_015399.2|[24475631]; 1647: NM_015407 , "Homo sapiens DKFZP564O243 protein (DKFZP564O243), mRNA", gi|34147328|ref|NM_015407.3|[34147328]; 1648: NM_015414 , "Homo sapiens ribosomal protein L36 (RPL36), transcript variant 2, mRNA", gi|16117793|ref|NM_015414.2|[16117793]; 1649: NM_015416 , "Homo sapiens cervical cancer 1 protooncogene (HCCR1), mRNA", gi|21166356|ref|NM_015416.2|[21166356]; 1650: NM_015439 , "Homo sapiens chromosome 6 open reading frame 80 (C6orf80), mRNA", gi|31083115|ref|NM_015439.2|[31083115]; 1651: NM_015480 , "Homo sapiens poliovirus receptor-related 3 (PVRL3), mRNA", gi|11386198|ref|NM_015480.1|[11386198]; 1652: NM_015484 , "Homo sapiens GCIP-interacting protein p29 (P29), mRNA", gi|7661635|ref|NM_015484.1|[7661635]; 1653: NM_015485 , "Homo sapiens RWD domain containing 3 (RWDD3), mRNA", gi|21361481|ref|NM_015485.2|[21361481]; 1654: NM_015490 , "Homo sapiens SEC31-like 2 (S. cerevisiae) (SEC31L2), transcript variant 1, mRNA", gi|38149839|ref|NM_015490.3|[38149839]; 1655: NM_015509 , "Homo sapiens DKFZP566B183 protein (DKFZP566B183), mRNA", gi|31542527|ref|NM_015509.2|[31542527]; 1656: NM_015510 , "Homo sapiens DKFZP566O084 protein (DKFZp566O084), mRNA", gi|23065521|ref|NM_015510.3|[23065521]; 1657: NM_015511 , "Homo sapiens chromosome 20 open reading frame 4 (C20orf4), mRNA", gi|18034689|ref|NM_015511.2|[18034689]; 1658: NM_015513 , "Homo sapiens cysteine-rich with EGF-like domains 1 (CRELD1), mRNA", gi|22095396|ref|NM_015513.2|[22095396]; 1659: NM_015517 , Homo sapiens MBD2 (methyl-CpG-binding protein)-interacting zinc finger protein, "(MIZF), transcript variant 1, mRNA",

gi|39725947|ref|NM_015517.3|[39725947]; 1660: NM_015527 , "Homo sapiens DKFZP434P1750 protein (DKFZP434P1750), mRNA", gi|21361484|ref|NM_015527.2|[21361484]; 1661: NM_015533 , "Homo sapiens DKFZP586B1621 protein (DKFZP586B1621), mRNA", gi|20149620|ref|NM_015533.2|[20149620]; 1662: NM_015535 , "Homo sapiens DNA polymerase-transactivated protein 6 (DNAPTP6), mRNA", gi|7661597|ref|NM_015535.1|[7661597]; 1663: NM_015540 , "Homo sapiens DKFZP727M111 protein (DKFZP727M111), mRNA", gi|24430138|ref|NM_015540.2|[24430138]; 1664: NM_015558 , Homo sapiens synovial sarcoma translocation gene on chromosome 18-like 1, "(SS18L1), transcript variant 2, mRNA", gi|39777611|ref|NM_015558.3|[39777611]; 1665: NM_015570 , "Homo sapiens autism susceptibility candidate 2 (AUTS2), mRNA", gi|17864089|ref|NM_015570.1|[17864089]; 1666: NM_015582 , "Homo sapiens DKFZP564B147 protein (DKFZP564B147), mRNA", gi|7661599|ref|NM_015582.1|[7661599]; 1667: NM_015584 , "Homo sapiens polymerase (DNA-directed), delta interacting protein 2 (POLDIP2),", mRNA, gi|30089946|ref|NM_015584.2|[30089946]; 1668: NM_015603 , "Homo sapiens coiled-coil domain containing 9 (CCDC9), mRNA", gi|7661689|ref|NM_015603.1|[7661689]; 1669: NM_015604 , "Homo sapiens WD repeat domain 21 (WDR21), transcript variant 1, mRNA", gi|31317287|ref|NM_015604.2|[31317287]; 1670: NM_015623 , , ref|NM_015623.2|[32306520], This record was temporarily removed by RefSeq staff for additional review., , 1671: NM_015646 , "Homo sapiens RAP1B, member of RAS oncogene family (RAP1B), mRNA", gi|34222320|ref|NM_015646.3|[34222320]; 1672: NM_015649 , "Homo sapiens interferon regulatory factor 2 binding protein 1 (IRF2BP1), mRNA", gi|24308114|ref|NM_015649.1|[24308114]; 1673: NM_015653 , "Homo sapiens DKFZP566F0546 protein (DKFZP566F0546), mRNA", gi|13124762|ref|NM_015653.1|[13124762]; 1674: NM_015654 , "Homo sapiens DKFZP564C103 protein (DKFZP564C103), mRNA", gi|34222325|ref|NM_015654.3|[34222325]; 1675: NM_015691 , "Homo sapiens KIAA1280 protein (KIAA1280), mRNA", gi|38570148|ref|NM_015691.2|[38570148]; 1676: NM_015699 , , ref|NM_015699.1|[7661559], This record was temporarily removed by RefSeq staff for additional review., , 1677: NM_015702 , "Homo sapiens hypothetical protein CL25022 (CL25022), mRNA", gi|7661547|ref|NM_015702.1|[7661547]; 1678: NM_015710 , "Homo sapiens glioma tumor suppressor candidate region gene 2 (GLTSCR2), mRNA", gi|21359905|ref|NM_015710.2|[21359905]; 1679: NM_015714 , "Homo sapiens putative lymphocyte G0/G1 switch gene (G0S2), mRNA", gi|20070269|ref|NM_015714.2|[20070269]; 1680: NM_015715 , "Homo sapiens phospholipase A2, group III (PLA2G3), mRNA", gi|7657125|ref|NM_015715.1|[7657125]; 1681: NM_015722 , "Homo sapiens calcyon protein (CALCYON), mRNA", gi|9257200|ref|NM_015722.2|[9257200]; 1682: NM_015855 , "Homo sapiens Wilms tumor associated protein (WIT-1), mRNA", gi|19743572|ref|NM_015855.2|[19743572]; 1683: NM_015859 , "Homo sapiens general transcription factor IIA, 1, 19/37kDa (GTF2A1), transcript", "variant 1, mRNA", gi|42476103|ref|NM_015859.2|[42476103]; 1684: NM_015865 , "Homo sapiens solute carrier family 14 (urea transporter), member 1 (Kidd blood", "group) (SLC14A1), mRNA", gi|7706676|ref|NM_015865.1|[7706676]; 1685: NM_015871 , "Homo sapiens zinc finger protein (ZT86), mRNA", gi|21359908|ref|NM_015871.2|[21359908]; 1686: NM_015884 , "Homo sapiens membrane-bound transcription factor protease, site 2 (MBTPS2), mRNA", gi|7706692|ref|NM_015884.1|[7706692]; 1687: NM_015885 , "Homo sapiens pre-mRNA

cleavage complex II protein Pcf11 (PCF11), mRNA", gi|33620744|ref|NM_015885.2|[33620744]; 1688: NM_015889 , "Homo sapiens PC2 (positive cofactor 2, multiprotein complex)", "glutamine/Q-rich-associated protein (PCQAP), mRNA", gi|21312133|ref|NM_015889.2|[21312133]; 1689: NM_015894 , "Homo sapiens stathmin-like 3 (STMN3), mRNA", gi|14670374|ref|NM_015894.2|[14670374]; 1690: NM_015895 , "Homo sapiens geminin, DNA replication inhibitor (GMNN), mRNA", gi|41393571|ref|NM_015895.3|[41393571]; 1691: NM_015901 , Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 13, "(NUDT13), mRNA", gi|34330151|ref|NM_015901.3|[34330151]; 1692: NM_015918 , "Homo sapiens RNase MRP/RNase P protein-like (POP5), transcript variant 1, mRNA", gi|38016924|ref|NM_015918.3|[38016924]; 1693: NM_015920 , "Homo sapiens ribosomal protein S27-like (RPS27L), mRNA", gi|18490988|ref|NM_015920.2|[18490988]; 1694: NM_015921 , "Homo sapiens chromosome 6 open reading frame 82 (C6orf82), mRNA", gi|7706243|ref|NM_015921.1|[7706243]; 1695: NM_015925 , "Homo sapiens liver-specific bHLH-Zip transcription factor (LISCH7), mRNA", gi|34916060|ref|NM_015925.3|[34916060]; 1696: NM_015926 , "Homo sapiens putative secreted protein ZSIG11 (ZSIG11), mRNA", gi|34147580|ref|NM_015926.3|[34147580]; 1697: NM_015927 , "Homo sapiens transforming growth factor beta 1 induced transcript 1 (TGFB1I1),", mRNA, gi|34147679|ref|NM_015927.3|[34147679]; 1698: NM_015929 , "Homo sapiens lipoyltransferase 1 (LIPT1), transcript variant 1, mRNA", gi|21729874|ref|NM_015929.2|[21729874]; 1699: NM_015932 , "Homo sapiens chromosome 13 open reading frame 12 (C13orf12), mRNA", gi|21361533|ref|NM_015932.2|[21361533]; 1700: NM_015937 , "Homo sapiens phosphatidylinositol glycan, class T (PIGT), mRNA", gi|23397652|ref|NM_015937.2|[23397652]; 1701: NM_015938 , "Homo sapiens CGI-07 protein (CGI-07), mRNA", gi|19923795|ref|NM_015938.2|[19923795]; 1702: NM_015941 , "Homo sapiens ATPase, H+ transporting, lysosomal 50/57kD V1 subunit H (ATP6V1H),", mRNA, gi|7706261|ref|NM_015941.1|[7706261]; 1703: NM_015942 , "Homo sapiens CGI-12 protein (CGI-12), mRNA", gi|34147675|ref|NM_015942.3|[34147675]; 1704: NM_015945 , "Homo sapiens solute carrier family 35, member C2 (SLC35C2), transcript variant", "2, mRNA", gi|34335287|ref|NM_015945.10|[34335287]; 1705: NM_015947 , "Homo sapiens CGI-18 protein (CGI-18), mRNA", gi|7705601|ref|NM_015947.1|[7705601]; 1706: NM_015950 , "Homo sapiens mitochondrial ribosomal protein L2 (MRPL2), nuclear gene encoding", "mitochondrial protein, mRNA", gi|41872659|ref|NM_015950.3|[41872659]; 1707: NM_015953 , "Homo sapiens nitric oxide synthase interacting protein (NOSIP), mRNA", gi|34147607|ref|NM_015953.3|[34147607]; 1708: NM_015956 , "Homo sapiens mitochondrial ribosomal protein L4 (MRPL4), nuclear gene encoding", "mitochondrial protein, transcript variant 1, mRNA", gi|22547135|ref|NM_015956.2|[22547135]; 1709: NM_015959 , "Homo sapiens thioredoxin-related transmembrane protein 2 (TMX2), mRNA", gi|7705725|ref|NM_015959.1|[7705725]; 1710: NM_015960 , "Homo sapiens CGI-32 protein (CGI-32), mRNA", gi|7705727|ref|NM_015960.1|[7705727]; 1711: NM_015962 , "Homo sapiens chromosome 14 open reading frame 111 (C14orf111), mRNA", gi|7705729|ref|NM_015962.1|[7705729]; 1712: NM_015964 , "Homo sapiens brain specific protein (CGI-38), mRNA", gi|7706275|ref|NM_015964.1|[7706275]; 1713: NM_015965 , "Homo sapiens cell death-regulatory protein GRIM19 (GRIM19), mRNA", gi|21361821|ref|NM_015965.3|[21361821]; 1714: NM_015971 , "Homo sapiens mitochondrial ribosomal protein S7 (MRPS7), nuclear gene encoding", "mitochondrial protein, mRNA",

gi|16554617|ref|NM_015971.2|[16554617]; 1715: NM_015972 , "Homo sapiens polymerase (RNA) I polypeptide D, 16kDa (POLR1D), mRNA", gi|7705739|ref|NM_015972.1|[7705739]; 1716: NM_015974 , "Homo sapiens crystallin, lambda 1 (CRYL1), mRNA", gi|7705743|ref|NM_015974.1|[7705743]; 1717: NM_015976 , "Homo sapiens sorting nexin 7 (SNX7), transcript variant 1, mRNA", gi|23111053|ref|NM_015976.2|[23111053]; 1718: NM_015982 , "Homo sapiens germ cell specific Y-box binding protein (YBX2), mRNA", gi|7705750|ref|NM_015982.1|[7705750]; 1719: NM_015986 , "Homo sapiens cytokine receptor-like factor 3 (CRLF3), mRNA", gi|27764872|ref|NM_015986.2|[27764872]; 1720: NM_015991 , "Homo sapiens complement component 1, q subcomponent, alpha polypeptide (C1QA),", mRNA, gi|7705752|ref|NM_015991.1|[7705752]; 1721: NM_015997 , "Homo sapiens CGI-41 protein (CGI-41), mRNA", gi|21361524|ref|NM_015997.2|[21361524]; 1722: NM_015999 , "Homo sapiens adiponectin receptor 1 (ADIPOR1), mRNA", gi|21361518|ref|NM_015999.2|[21361518]; 1723: NM_016004 , "Homo sapiens chromosome 20 open reading frame 9 (C20orf9), mRNA", gi|7705768|ref|NM_016004.1|[7705768]; 1724: NM_016011 , "Homo sapiens nuclear receptor binding factor 1 (CGI-63), mRNA", gi|7705776|ref|NM_016011.1|[7705776]; 1725: NM_016013 , "Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor", "1 (NDUFAF1), mRNA", gi|7705778|ref|NM_016013.1|[7705778]; 1726: NM_016015 , "Homo sapiens leucine carboxyl methyltransferase 1 (LCMT1), mRNA", gi|15082255|ref|NM_016015.2|[15082255]; 1727: NM_016020 , "Homo sapiens transcription factor B1, mitochondrial (TFB1M), mRNA", gi|7705784|ref|NM_016020.1|[7705784]; 1728: NM_016022 , Homo sapiens likely ortholog of C. elegans anterior pharynx defective 1A, "(APH-1A), mRNA", gi|7705786|ref|NM_016022.1|[7705786]; 1729: NM_016027 , "Homo sapiens lactamase, beta 2 (LACTB2), mRNA", gi|7705792|ref|NM_016027.1|[7705792]; 1730: NM_016028 , "Homo sapiens CGI-85 protein (CGI-85), transcript variant 2, mRNA", gi|27477098|ref|NM_016028.3|[27477098]; 1731: NM_016033 , "Homo sapiens CGI-90 protein (CGI-90), mRNA", gi|7705802|ref|NM_016033.1|[7705802]; 1732: NM_016045 , "Homo sapiens chromosome 20 open reading frame 45 (C20orf45), mRNA", gi|7705609|ref|NM_016045.1|[7705609]; 1733: NM_016046 , "Homo sapiens exosomal core protein CSL4 (CSL4), mRNA", gi|22035626|ref|NM_016046.2|[22035626]; 1734: NM_016049 , "Homo sapiens chromosome 14 open reading frame 122 (C14orf122), mRNA", gi|34222327|ref|NM_016049.3|[34222327]; 1735: NM_016052 , "Homo sapiens CGI-115 protein (CGI-115), mRNA", gi|31542299|ref|NM_016052.2|[31542299]; 1736: NM_016053 , "Homo sapiens CGI-116 protein (CGI-116), mRNA", gi|7705621|ref|NM_016053.1|[7705621]; 1737: NM_016055 , "Homo sapiens mitochondrial ribosomal protein L48 (MRPL48), nuclear gene encoding", "mitochondrial protein, mRNA", gi|38788229|ref|NM_016055.3|[38788229]; 1738: NM_016056 , "Homo sapiens CGI-119 protein (CGI-119), mRNA", gi|7706334|ref|NM_016056.1|[7706334]; 1739: NM_016062 , "Homo sapiens CGI-128 protein (CGI-128), mRNA", gi|7706342|ref|NM_016062.1|[7706342]; 1740: NM_016065 , "Homo sapiens mitochondrial ribosomal protein S16 (MRPS16), nuclear gene encoding", "mitochondrial protein, mRNA", gi|16554612|ref|NM_016065.2|[16554612]; 1741: NM_016067 , "Homo sapiens mitochondrial ribosomal protein S18C (MRPS18C), nuclear gene", "encoding mitochondrial protein, mRNA", gi|7705629|ref|NM_016067.1|[7705629]; 1742: NM_016069 , Homo sapiens mitochondria-associated protein involved in granulocyte-macrophage, "colony-stimulating factor signal transduction (Magmas), nuclear gene encoding", "mitochondrial protein, mRNA", gi|27363460|ref|NM_016069.8|[27363460]; 1743: NM_016071 , "Homo

sapiens mitochondrial ribosomal protein S33 (MRPS33), nuclear gene encoding", "mitochondrial protein, transcript variant 1, mRNA", gi|16950595|ref|NM_016071.2|[16950595]; 1744: NM_016072 , "Homo sapiens CGI-141 protein (CGI-141), mRNA", gi|19923443|ref|NM_016072.2|[19923443]; 1745: NM_016079 , "Homo sapiens neuroendocrine differentiation factor (NEDF), mRNA", gi|7706352|ref|NM_016079.1|[7706352]; 1746: NM_016080 , "Homo sapiens CGI-150 protein (CGI-150), mRNA", gi|34850073|ref|NM_016080.2|[34850073]; 1747: NM_016082 , "Homo sapiens CDK5 regulatory subunit associated protein 1 (CDK5RAP1), transcript", "variant 2, mRNA", gi|28872783|ref|NM_016082.3|[28872783]; 1748: NM_016086 , "Homo sapiens map kinase phosphatase-like protein MK-STYX (MK-STYX), mRNA", gi|32481212|ref|NM_016086.2|[32481212]; 1749: NM_016087 , "Homo sapiens wingless-type MMTV integration site family, member 16 (WNT16),", "transcript variant 2, mRNA", gi|17402913|ref|NM_016087.2|[17402913]; 1750: NM_016090 , "Homo sapiens RNA binding motif protein 7 (RBM7), mRNA", gi|31543547|ref|NM_016090.2|[31543547]; 1751: NM_016091 , "Homo sapiens eukaryotic translation initiation factor 3, subunit 6 interacting", "protein (EIF3S6IP), mRNA", gi|7705432|ref|NM_016091.1|[7705432]; 1752: NM_016095 , "Homo sapiens DNA replication complex GINS protein PSF2 (Pfs2), mRNA", gi|7706366|ref|NM_016095.1|[7706366]; 1753: NM_016097 , "Homo sapiens HSPC039 protein (HSPC039), mRNA", gi|32261311|ref|NM_016097.2|[32261311]; 1754: NM_016099 , "Homo sapiens golgi autoantigen, golgin subfamily a, 7 (GOLGA7), mRNA", gi|7705820|ref|NM_016099.1|[7705820]; 1755: NM_016101 , "Homo sapiens comparative gene identification transcript 37 (CGI-37), mRNA", gi|40538791|ref|NM_016101.2|[40538791]; 1756: NM_016102 , "Homo sapiens tripartite motif-containing 17 (TRIM17), mRNA", gi|7705824|ref|NM_016102.1|[7705824]; 1757: NM_016103 , "Homo sapiens SAR1a gene homolog 2 (S. cerevisiae) (SARA2), mRNA", gi|38176155|ref|NM_016103.2|[38176155]; 1758: NM_016106 , "Homo sapiens sec1 family domain containing 1 (SCFD1), transcript variant 1, mRNA", gi|33469965|ref|NM_016106.2|[33469965]; 1759: NM_016127 , "Homo sapiens hypothetical protein MGC8721 (MGC8721), mRNA", gi|42476192|ref|NM_016127.4|[42476192]; 1760: NM_016133 , "Homo sapiens insulin induced gene 2 (INSIG2), mRNA", gi|38327532|ref|NM_016133.2|[38327532]; 1761: NM_016139 , "Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 2 (CHCHD2),", mRNA, gi|32307179|ref|NM_016139.2|[32307179]; 1762: NM_016142 , "Homo sapiens hydroxysteroid (17-beta) dehydrogenase 12 (HSD17B12), mRNA", gi|7705854|ref|NM_016142.1|[7705854]; 1763: NM_016145 , "Homo sapiens PTD008 protein (PTD008), mRNA", gi|7706664|ref|NM_016145.1|[7706664]; 1764: NM_016148 , "Homo sapiens SH3 and multiple ankyrin repeat domains 1 (SHANK1), mRNA", gi|11968151|ref|NM_016148.1|[11968151]; 1765: NM_016158 , "Homo sapiens erythrocyte transmembrane protein (LOC51145), mRNA", gi|7705856|ref|NM_016158.1|[7705856]; 1766: NM_016183 , "Homo sapiens chromosome 1 open reading frame 33 (C1orf33), mRNA", gi|18490986|ref|NM_016183.2|[18490986]; 1767: NM_016185 , "Homo sapiens hematological and neurological expressed 1 (HN1), mRNA", gi|7705876|ref|NM_016185.1|[7705876]; 1768: NM_016187 , "Homo sapiens bridging integrator 2 (BIN2), mRNA", gi|7705295|ref|NM_016187.1|[7705295]; 1769: NM_016195 , "Homo sapiens M-phase phosphoprotein 1 (MPHOSPH1), mRNA", gi|7705347|ref|NM_016195.1|[7705347]; 1770: NM_016200 , "Homo sapiens LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)", "(LSM8), mRNA", gi|21314665|ref|NM_016200.2|[21314665]; 1771: NM_016202 , "Homo sapiens zinc finger

protein 580 (ZNF580), mRNA", gi|7705880|ref|NM_016202.1|[7705880]; 1772: NM_016203 , "Homo sapiens protein kinase, AMP-activated, gamma 2 non-catalytic subunit", "(PRKAG2), mRNA", gi|33186924|ref|NM_016203.2|[33186924]; 1773: NM_016206 , "Homo sapiens colon carcinoma related protein (LOC51159), mRNA", gi|7705882|ref|NM_016206.1|[7705882]; 1774: NM_016209 , "Homo sapiens unknown (LOC51693), mRNA", gi|7706428|ref|NM_016209.1|[7706428]; 1775: NM_016210 , "Homo sapiens g20 protein (LOC51161), mRNA", gi|31543080|ref|NM_016210.2|[31543080]; 1776: NM_016216 , "Homo sapiens debranching enzyme homolog 1 (S. cerevisiae) (DBR1), mRNA", gi|7705890|ref|NM_016216.1|[7705890]; 1777: NM_016223 , Homo sapiens protein kinase C and casein kinase substrate in neurons 3, "(PACSIN3), mRNA", gi|34147484|ref|NM_016223.3|[34147484]; 1778: NM_016229 , "Homo sapiens cytochrome b5 reductase b5R.2 (CYB5R2), mRNA", gi|7706442|ref|NM_016229.1|[7706442]; 1779: NM_016230 , "Homo sapiens NADPH cytochrome B5 oxidoreductase (NCB5OR), mRNA", gi|21314659|ref|NM_016230.2|[21314659]; 1780: NM_016231 , "Homo sapiens nemo like kinase (NLK), mRNA", gi|42734431|ref|NM_016231.2|[42734431]; 1781: NM_016245 , "Homo sapiens dehydrogenase/reductase (SDR family) member 8 (DHRS8), mRNA", gi|7705904|ref|NM_016245.1|[7705904]; 1782: NM_016246 , "Homo sapiens dehydrogenase/reductase (SDR family) member 10 (DHRS10), mRNA", gi|7705906|ref|NM_016246.1|[7705906]; 1783: NM_016255 , "Homo sapiens family with sequence similarity 8, member A1 (FAM8A1), mRNA", gi|7705267|ref|NM_016255.1|[7705267]; 1784: NM_016256 , Homo sapiens N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase, "(NAGPA), mRNA", gi|7705908|ref|NM_016256.1|[7705908]; 1785: NM_016258 , "Homo sapiens high-glucose-regulated protein 8 (HGRG8), mRNA", gi|7705410|ref|NM_016258.1|[7705410]; 1786: NM_016260 , "Homo sapiens zinc finger protein, subfamily 1A, 2 (Helios) (ZNFN1A2), mRNA", gi|7705910|ref|NM_016260.1|[7705910]; 1787: NM_016265 , "Homo sapiens zinc finger protein 325 (ZNF325), mRNA", gi|7706464|ref|NM_016265.1|[7706464]; 1788: NM_016286 , "Homo sapiens dicarbonyl/L-xylulose reductase (DCXR), mRNA", gi|41350203|ref|NM_016286.2|[41350203]; 1789: NM_016287 , "Homo sapiens HP1-BP74 (HP1-BP74), mRNA", gi|7705416|ref|NM_016287.1|[7705416]; 1790: NM_016289 , "Homo sapiens MO25 protein (MO25), mRNA", gi|19745179|ref|NM_016289.2|[19745179]; 1791: NM_016304 , "Homo sapiens chromosome 15 open reading frame 15 (C15orf15), mRNA", gi|18491027|ref|NM_016304.2|[18491027]; 1792: NM_016308 , "Homo sapiens UMP-CMP kinase (UMP-CMPK), mRNA", gi|7706496|ref|NM_016308.1|[7706496]; 1793: NM_016310 , "Homo sapiens polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa", "(POLR3K), mRNA", gi|14589957|ref|NM_016310.2|[14589957]; 1794: NM_016316 , "Homo sapiens REV1-like (yeast) (REV1L), mRNA", gi|7706680|ref|NM_016316.1|[7706680]; 1795: NM_016319 , Homo sapiens COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis), "(COPS7A), mRNA", gi|7705329|ref|NM_016319.1|[7705329]; 1796: NM_016324 , "Homo sapiens zinc finger protein 274 (ZNF274), transcript variant ZNF274b, mRNA", gi|19743797|ref|NM_016324.2|[19743797]; 1797: NM_016332 , "Homo sapiens selenoprotein X, 1 (SEPX1), mRNA", gi|7706510|ref|NM_016332.1|[7706510]; 1798: NM_016337 , "Homo sapiens Enah/Vasp-like (EVL), mRNA", gi|7706686|ref|NM_016337.1|[7706686]; 1799: NM_016354 , "Homo sapiens solute carrier organic anion transporter family, member 4A1", "(SLCO4A1), mRNA", gi|39777593|ref|NM_016354.3|[39777593]; 1800: NM_016355 , "Homo sapiens DEAD (Asp-

Glu-Ala-Asp) box polypeptide 47 (DDX47), transcript", "variant 1, mRNA", gi|41327774|ref|NM_016355.3|[41327774]; 1801: NM_016358 , "Homo sapiens iroquois homeobox protein 4 (IRX4), mRNA", gi|7705554|ref|NM_016358.1|[7705554]; 1802: NM_016364 , "Homo sapiens dual specificity phosphatase 13 (DUSP13), mRNA", gi|20149630|ref|NM_016364.2|[20149630]; 1803: NM_016368 , "Homo sapiens myo-inositol 1-phosphate synthase A1 (ISYNA1), mRNA", gi|21902536|ref|NM_016368.3|[21902536]; 1804: NM_016371 , "Homo sapiens hydroxysteroid (17-beta) dehydrogenase 7 (HSD17B7), mRNA", gi|7705420|ref|NM_016371.1|[7705420]; 1805: NM_016372 , "Homo sapiens seven transmembrane domain orphan receptor (TPRA40), mRNA", gi|7705964|ref|NM_016372.1|[7705964]; 1806: NM_016397 , "Homo sapiens TH1-like (Drosophila) (TH1L), transcript variant 2, mRNA", gi|39812483|ref|NM_016397.2|[39812483]; 1807: NM_016400 , "Homo sapiens Huntingtin interacting protein K (HYPK), mRNA", gi|21361540|ref|NM_016400.2|[21361540]; 1808: NM_016404 , "Homo sapiens hypothetical protein HSPC152 (HSPC152), mRNA", gi|7705476|ref|NM_016404.1|[7705476]; 1809: NM_016406 , "Homo sapiens hypothetical protein HSPC155 (HSPC155), mRNA", gi|7705480|ref|NM_016406.1|[7705480]; 1810: NM_016407 , "Homo sapiens chromosome 20 open reading frame 43 (C20orf43), mRNA", gi|7705482|ref|NM_016407.1|[7705482]; 1811: NM_016412 , "Homo sapiens insulin-like growth factor 2, antisense (IGF2AS), mRNA", gi|7705972|ref|NM_016412.1|[7705972]; 1812: NM_016422 , "Homo sapiens ring finger protein 141 (RNF141), mRNA", gi|38045936|ref|NM_016422.3|[38045936]; 1813: NM_016423 , "Homo sapiens zinc finger protein 219 (ZNF219), mRNA", gi|7705974|ref|NM_016423.1|[7705974]; 1814: NM_016433 , "Homo sapiens glycolipid transfer protein (GLTP), mRNA", gi|20357594|ref|NM_016433.2|[20357594]; 1815: NM_016447 , "Homo sapiens membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)", "(MPP6), mRNA", gi|21361597|ref|NM_016447.2|[21361597]; 1816: NM_016448 , "Homo sapiens RA-regulated nuclear matrix-associated protein (RAMP), mRNA", gi|7705575|ref|NM_016448.1|[7705575]; 1817: NM_016453 , "Homo sapiens SH3 protein interacting with Nck, 90 kDa (AF3P21), transcript", "variant 1, mRNA", gi|37577149|ref|NM_016453.2|[37577149]; 1818: NM_016508 , "Homo sapiens cyclin-dependent kinase-like 3 (CDKL3), mRNA", gi|17017984|ref|NM_016508.2|[17017984]; 1819: NM_016526 , "Homo sapiens blocked early in transport 1 homolog (S. cerevisiae) like (BET1L),", mRNA, gi|34365798|ref|NM_016526.3|[34365798]; 1820: NM_016527 , "Homo sapiens hydroxyacid oxidase 2 (long chain) (HAO2), mRNA", gi|7705392|ref|NM_016527.1|[7705392]; 1821: NM_016530 , "Homo sapiens RAB8B, member RAS oncogene family (RAB8B), mRNA", gi|7706562|ref|NM_016530.1|[7706562]; 1822: NM_016539 , Homo sapiens sirtuin (silent mating type information regulation 2 homolog) 6 (S., "cerevisiae) (SIRT6), mRNA", gi|7706709|ref|NM_016539.1|[7706709]; 1823: NM_016545 , "Homo sapiens immediate early response 5 (IER5), mRNA", gi|16554598|ref|NM_016545.2|[16554598]; 1824: NM_016551 , "Homo sapiens transmembrane 7 superfamily member 3 (TM7SF3), mRNA", gi|7706574|ref|NM_016551.1|[7706574]; 1825: NM_016557 , "Homo sapiens chemokine (C-C motif) receptor-like 1 (CCRL1), transcript variant", "2, mRNA", gi|30795218|ref|NM_016557.2|[30795218]; 1826: NM_016558 , "Homo sapiens SCAN domain containing 1 (SCAND1), transcript variant 1, mRNA", gi|15967154|ref|NM_016558.2|[15967154]; 1827: NM_016559 , "Homo sapiens Pex5p-related protein (PEX5R), mRNA", gi|7706670|ref|NM_016559.1|[7706670]; 1828: NM_016561 , "Homo sapiens bifunctional apoptosis regulator (BFAR), mRNA",

gi|7706090|ref|NM_016561.1|[7706090]; 1829: NM_016567 , "Homo sapiens BRCA2 and CDKN1A interacting protein (BCCIP), transcript variant A,", mRNA, gi|17402869|ref|NM_016567.2|[17402869]; 1830: NM_016570 , "Homo sapiens PTX1 protein (PTX1), mRNA", gi|7706104|ref|NM_016570.1|[7706104]; 1831: NM_016573 , "Homo sapiens Gem-interacting protein (GMIP), mRNA", gi|7706106|ref|NM_016573.1|[7706106]; 1832: NM_016576 , "Homo sapiens guanosine monophosphate reductase 2 (GMPR2), mRNA", gi|20070275|ref|NM_016576.2|[20070275]; 1833: NM_016581 , Homo sapiens likely ortholog of mouse signaling intermediate in Toll, "pathway-evolutionarily conserved (SITPEC), mRNA", gi|20149632|ref|NM_016581.2|[20149632]; 1834: NM_016593 , "Homo sapiens cytochrome P450, family 39, subfamily A, polypeptide 1 (CYP39A1),", mRNA, gi|32313586|ref|NM_016593.3|[32313586]; 1835: NM_016602 , "Homo sapiens G protein-coupled receptor 2 (GPR2), mRNA", gi|7705315|ref|NM_016602.1|[7705315]; 1836: NM_016611 , "Homo sapiens potassium channel, subfamily K, member 4 (KCNK4), transcript", "variant 1, mRNA", gi|15718764|ref|NM_016611.2|[15718764]; 1837: NM_016614 , "Homo sapiens TRAF and TNF receptor associated protein (TTRAP), mRNA", gi|23510347|ref|NM_016614.2|[23510347]; 1838: NM_016617 , "Homo sapiens hypothetical protein BM-002 (BM-002), mRNA", gi|7705299|ref|NM_016617.1|[7705299]; 1839: NM_016621 , "Homo sapiens BRAF35/HDAC2 complex (80 kDa) (BHC80), mRNA", gi|19923461|ref|NM_016621.2|[19923461]; 1840: NM_016625 , "Homo sapiens BM-011 protein (MGC12197), mRNA", gi|38488726|ref|NM_016625.2|[38488726]; 1841: NM_016627 , "Homo sapiens hypothetical protein LOC51321 (LOC51321), mRNA", gi|42476207|ref|NM_016627.2|[42476207]; 1842: NM_016630 , "Homo sapiens acid cluster protein 33 (ACP33), mRNA", gi|42544234|ref|NM_016630.3|[42544234]; 1843: NM_016639 , "Homo sapiens tumor necrosis factor receptor superfamily, member 12A (TNFRSF12A),", mRNA, gi|7706185|ref|NM_016639.1|[7706185]; 1844: NM_016647 , "Homo sapiens mesenchymal stem cell protein DSCD75 (LOC51337), mRNA", gi|7706199|ref|NM_016647.1|[7706199]; 1845: NM_016651 , "Homo sapiens dapper homolog 1, antagonist of beta-catenin (xenopus) (DACT1),", mRNA, gi|38569506|ref|NM_016651.4|[38569506]; 1846: NM_016831 , "Homo sapiens period homolog 3 (Drosophila) (PER3), mRNA", gi|8567387|ref|NM_016831.1|[8567387]; 1847: NM_016937 , "Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA", gi|8393994|ref|NM_016937.1|[8393994]; 1848: NM_016940 , "Homo sapiens chromosome 21 open reading frame 6 (C21orf6), mRNA", gi|8393017|ref|NM_016940.1|[8393017]; 1849: NM_016948 , "Homo sapiens par-6 partitioning defective 6 homolog alpha (C.elegans) (PARD6A),", mRNA, gi|8394416|ref|NM_016948.1|[8394416]; 1850: NM_017412 , "Homo sapiens frizzled homolog 3 (Drosophila) (FZD3), mRNA", gi|22035685|ref|NM_017412.2|[22035685]; 1851: NM_017414 , "Homo sapiens ubiquitin specific protease 18 (USP18), mRNA", gi|32313609|ref|NM_017414.2|[32313609]; 1852: NM_017422 , "Homo sapiens calmodulin-like 5 (CALML5), mRNA", gi|38327636|ref|NM_017422.3|[38327636]; 1853: NM_017426 , "Homo sapiens nucleoporin 54kDa (NUP54), mRNA", gi|26051236|ref|NM_017426.2|[26051236]; 1854: NM_017429 , "Homo sapiens beta-carotene 15,15'-monooxygenase 1 (BCMO1), mRNA", gi|8393364|ref|NM_017429.1|[8393364]; 1855: NM_017435 , "Homo sapiens solute carrier organic anion transporter family, member 1C1", "(SLCO1C1), mRNA", gi|21361594|ref|NM_017435.2|[21361594]; 1856: NM_017443 , "Homo sapiens polymerase (DNA directed), epsilon 3 (p17 subunit) (POLE3), mRNA",

gi|31543422|ref|NM_017443.3|[31543422]; 1857: NM_017495 , "Homo sapiens RNA-binding region (RNP1, RRM) containing 1 (RNPC1), transcript", "variant 1, mRNA", gi|34577106|ref|NM_017495.4|[34577106]; 1858: NM_017542 , "Homo sapiens pogo transposable element with KRAB domain (POGK), mRNA", gi|22027479|ref|NM_017542.3|[22027479]; 1859: NM_017559 , "Homo sapiens hypothetical protein DKFZp434H2215 (DKFZp434H2215), mRNA", gi|8922137|ref|NM_017559.1|[8922137]; 1860: NM_017566 , "Homo sapiens hypothetical protein DKFZp434G0522 (DKFZp434G0522), mRNA", gi|21314674|ref|NM_017566.2|[21314674]; 1861: NM_017571 , "Homo sapiens hypothetical protein LOC55580 (LOC55580), mRNA", gi|8923837|ref|NM_017571.1|[8923837]; 1862: NM_017578 , "Homo sapiens ropporin, rhophilin associated protein 1 (ROPN1), mRNA", gi|21359919|ref|NM_017578.2|[21359919]; 1863: NM_017582 , "Homo sapiens ubiquitin-conjugating enzyme E2Q (putative) (UBE2Q), mRNA", gi|38045949|ref|NM_017582.5|[38045949]; 1864: NM_017589 , "Homo sapiens B-cell translocation gene 4 (BTG4), mRNA", gi|28872723|ref|NM_017589.2|[28872723]; 1865: NM_017596 , , ref|NM_017596.1|[8922142], This record was temporarily removed by RefSeq staff for additional review., , 1866: NM_017606 , "Homo sapiens hypothetical protein DKFZp434K1210 (DKFZp434K1210), mRNA", gi|40254896|ref|NM_017606.2|[40254896]; 1867: NM_017610 , "Homo sapiens ring finger protein 111 (RNF111), mRNA", gi|37595552|ref|NM_017610.6|[37595552]; 1868: NM_017623 , "Homo sapiens cyclin M3 (CNNM3), transcript variant 1, mRNA", gi|40068048|ref|NM_017623.3|[40068048]; 1869: NM_017624 , "Homo sapiens hypothetical protein FLJ20019 (FLJ20019), mRNA", gi|8923025|ref|NM_017624.1|[8923025]; 1870: NM_017629 , "Homo sapiens eukaryotic translation initiation factor 2C, 4 (EIF2C4), mRNA", gi|29029592|ref|NM_017629.2|[29029592]; 1871: NM_017630 , "Homo sapiens chromosome 14 open reading frame 113 (C14orf113), mRNA", gi|8923035|ref|NM_017630.1|[8923035]; 1872: NM_017631 , "Homo sapiens hypothetical protein FLJ20035 (FLJ20035), mRNA", gi|37059778|ref|NM_017631.3|[37059778]; 1873: NM_017632 , Homo sapiens collaborates/cooperates with ARF (alternate reading frame) protein, "(CARF), mRNA", gi|8923039|ref|NM_017632.1|[8923039]; 1874: NM_017633 , "Homo sapiens chromosome 6 open reading frame 37 (C6orf37), mRNA", gi|8923041|ref|NM_017633.1|[8923041]; 1875: NM_017634 , "Homo sapiens potassium channel tetramerisation domain containing 9 (KCTD9), mRNA", gi|39753958|ref|NM_017634.2|[39753958]; 1876: NM_017636 , "Homo sapiens transient receptor potential cation channel, subfamily M, member 4", "(TRPM4), mRNA", gi|21314670|ref|NM_017636.2|[21314670]; 1877: NM_017645 , "Homo sapiens family with sequence similarity 29, member A (FAM29A), mRNA", gi|31377561|ref|NM_017645.3|[31377561]; 1878: NM_017647 , "Homo sapiens FtsJ homolog 3 (E. coli) (FTSJ3), mRNA", gi|17017990|ref|NM_017647.2|[17017990]; 1879: NM_017654 , "Homo sapiens FLJ20073 protein (FLJ20073), mRNA", gi|38201705|ref|NM_017654.2|[38201705]; 1880: NM_017655 , "Homo sapiens PDZ domain protein GIPC2 (GIPC2), mRNA", gi|41393578|ref|NM_017655.4|[41393578]; 1881: NM_017657 , "Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA", gi|31377757|ref|NM_017657.2|[31377757]; 1882: NM_017659 , "Homo sapiens hypothetical protein FLJ20084 (FLJ20084), mRNA", gi|8923091|ref|NM_017659.1|[8923091]; 1883: NM_017665 , "Homo sapiens zinc finger, CCHC domain containing 10 (ZCCHC10), mRNA", gi|8923105|ref|NM_017665.1|[8923105]; 1884: NM_017668 , "Homo sapiens nudE nuclear

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NM_018303 , "Homo sapiens SEC5-like 1 (S. cerevisiae) (SEC5L1), mRNA", gi|30581133|ref|NM_018303.4|[30581133]; 2061: NM_018308 , "Homo sapiens acyl-Coenzyme A oxidase-like (ACOXL), mRNA", gi|8922839|ref|NM_018308.1|[8922839]; 2062: NM_018314 , "Homo sapiens ubiquitin-conjugating enzyme E2-like (UEV3), mRNA", gi|23943813|ref|NM_018314.2|[23943813]; 2063: NM_018317 , "Homo sapiens hypothetical protein FLJ11082 (FLJ11082), mRNA", gi|8922855|ref|NM_018317.1|[8922855]; 2064: NM_018319 , "Homo sapiens tyrosyl-DNA phosphodiesterase 1 (TDP1), mRNA", gi|20127585|ref|NM_018319.2|[20127585]; 2065: NM_018320 , "Homo sapiens ring finger protein 121 (RNF121), transcript variant 1, mRNA", gi|37588863|ref|NM_018320.3|[37588863]; 2066: NM_018327 , "Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA", gi|8922874|ref|NM_018327.1|[8922874]; 2067: NM_018329 , "Homo sapiens hypothetical protein FLJ11117 (FLJ11117), mRNA", gi|8922878|ref|NM_018329.1|[8922878]; 2068: NM_018338 , "Homo sapiens hypothetical protein FLJ11142 (FLJ11142), mRNA", gi|31377845|ref|NM_018338.2|[31377845]; 2069: NM_018350 , , ref|NM_018350.1|[8922918], This record was temporarily removed by RefSeq staff for additional review., , 2070: NM_018353 , "Homo sapiens chromosome 14 open reading frame 106 (C14orf106), mRNA", gi|42415491|ref|NM_018353.3|[42415491]; 2071: NM_018354 , "Homo sapiens chromosome 20 open reading frame 46 (C20orf46), mRNA", gi|8922926|ref|NM_018354.1|[8922926]; 2072: NM_018356 , "Homo sapiens hypothetical protein FLJ11193 (FLJ11193), mRNA", gi|8922930|ref|NM_018356.1|[8922930]; 2073: NM_018357 , "Homo sapiens acheron (FLJ11196), transcript variant 1, mRNA", gi|37537709|ref|NM_018357.2|[37537709]; 2074: NM_018360 , "Homo sapiens chromosome X open reading frame 15 (CXorf15), mRNA", gi|8922939|ref|NM_018360.1|[8922939]; 2075: NM_018368 , "Homo sapiens chromosome 6 open reading frame 209 (C6orf209), mRNA", gi|31542670|ref|NM_018368.2|[31542670]; 2076: NM_018372 , "Homo sapiens receptor-interacting factor 1 (RIF1), mRNA", gi|31377732|ref|NM_018372.2|[31377732]; 2077: NM_018374 , "Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA", gi|40254892|ref|NM_018374.2|[40254892]; 2078: NM_018375 , "Homo sapiens solute carrier family 39 (zinc transporter), member 9 (SLC39A9),", mRNA, gi|40254927|ref|NM_018375.2|[40254927]; 2079: NM_018378 , "Homo sapiens F-box and leucine-rich repeat protein 8 (FBXL8), mRNA", gi|22547145|ref|NM_018378.2|[22547145]; 2080: NM_018379 , "Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA", gi|31377840|ref|NM_018379.2|[31377840]; 2081: NM_018383 , "Homo sapiens WD repeat domain 33 (WDR33), mRNA", gi|19923528|ref|NM_018383.2|[19923528]; 2082: NM_018386 , "Homo sapiens hypothetical protein FLJ11305 (FLJ11305), mRNA", gi|8922986|ref|NM_018386.1|[8922986]; 2083: NM_018388 , "Homo sapiens muscleblind-like 3 (Drosophila) (MBNL3), mRNA", gi|19387843|ref|NM_018388.2|[19387843]; 2084: NM_018389 , "Homo sapiens solute carrier family 35, member C1 (SLC35C1), mRNA", gi|37059730|ref|NM_018389.3|[37059730]; 2085: NM_018398 , "Homo sapiens calcium channel, voltage-dependent, alpha 2/delta 3 subunit", "(CACNA2D3), mRNA", gi|8923764|ref|NM_018398.1|[8923764]; 2086: NM_018403 , "Homo sapiens transcription factor SMIF (HSA275986), mRNA", gi|8923766|ref|NM_018403.1|[8923766]; 2087: NM_018410 , "Homo sapiens hypothetical protein DKFZp762E1312 (DKFZp762E1312), mRNA", gi|21361746|ref|NM_018410.2|[21361746]; 2088: NM_018418 , "Homo sapiens spermatogenesis associated 7 (SPATA7), mRNA", gi|13384599|ref|NM_018418.1|[13384599]; 2089: NM_018419 , "Homo sapiens SRY (sex determining region Y)-box 18 (SOX18), mRNA",

gi|31077201|ref|NM_018419.2|[31077201]; 2090: NM_018422 , "Homo sapiens hypothetical protein DKFZp761K1423 (DKFZp761K1423), mRNA", gi|8922171|ref|NM_018422.1|[8922171]; 2091: NM_018428 , "Homo sapiens hepatocellular carcinoma-associated antigen 66 (HCA66), mRNA", gi|8923721|ref|NM_018428.1|[8923721]; 2092: NM_018431 , "Homo sapiens docking protein 5 (DOK5), transcript variant 1, mRNA", gi|29544725|ref|NM_018431.2|[29544725]; 2093: NM_018433 , "Homo sapiens jumonji domain containing 1 (JMJD1), mRNA", gi|20357521|ref|NM_018433.2|[20357521]; 2094: NM_018441 , "Homo sapiens peroxisomal trans-2-enoyl-CoA reductase (PECR), mRNA", gi|19923816|ref|NM_018441.2|[19923816]; 2095: NM_018444 , "Homo sapiens protein phosphatase 2C, magnesium-dependent, catalytic subunit", "(PPM2C), mRNA", gi|8923959|ref|NM_018444.1|[8923959]; 2096: NM_018452 , "Homo sapiens chromosome 6 open reading frame 35 (C6orf35), mRNA", gi|24431986|ref|NM_018452.2|[24431986]; 2097: NM_018453 , "Homo sapiens chromosome 14 open reading frame 11 (C14orf11), mRNA", gi|30425545|ref|NM_018453.2|[30425545]; 2098: NM_018457 , "Homo sapiens DKFZp564J157 protein (DKFZP564J157), mRNA", gi|35250772|ref|NM_018457.2|[35250772]; 2099: NM_018459 , , ref|NM_018459.1|[8922103], This record was replaced or removed. See revision history for details., , 2100: NM_018464 , "Homo sapiens chromosome 10 open reading frame 70 (C10orf70), mRNA", gi|8923929|ref|NM_018464.1|[8923929]; 2101: NM_018465 , "Homo sapiens chromosome 9 open reading frame 46 (C9orf46), mRNA", gi|8923931|ref|NM_018465.1|[8923931]; 2102: NM_018469 , "Homo sapiens uncharacterized hypothalamus protein HT008 (HT008), mRNA", gi|38679908|ref|NM_018469.3|[38679908]; 2103: NM_018473 , "Homo sapiens thioesterase superfamily member 2 (THEM2), mRNA", gi|40549423|ref|NM_018473.2|[40549423]; 2104: NM_018474 , "Homo sapiens chromosome 20 open reading frame 19 (C20orf19), mRNA", gi|32189414|ref|NM_018474.2|[32189414]; 2105: NM_018478 , "Homo sapiens chromosome 20 open reading frame 35 (C20orf35), mRNA", gi|8923782|ref|NM_018478.1|[8923782]; 2106: NM_018480 , "Homo sapiens uncharacterized hypothalamus protein HT007 (HT007), mRNA", gi|32189381|ref|NM_018480.2|[32189381]; 2107: NM_018484 , "Homo sapiens solute carrier family 22 (organic anion/cation transporter), member", "11 (SLC22A11), mRNA", gi|24497483|ref|NM_018484.2|[24497483]; 2108: NM_018487 , "Homo sapiens hepatocellular carcinoma-associated antigen 112 (HCA112), mRNA", gi|32484986|ref|NM_018487.2|[32484986]; 2109: NM_018489 , "Homo sapiens ash1 (absent, small, or homeotic)-like (Drosophila) (ASH1L), mRNA", gi|8922080|ref|NM_018489.1|[8922080]; 2110: NM_018557 , Homo sapiens low density lipoprotein-related protein 1B (deleted in tumors), "(LRP1B), mRNA", gi|9055269|ref|NM_018557.1|[9055269]; 2111: NM_018569 , "Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA", gi|21361756|ref|NM_018569.2|[21361756]; 2112: NM_018584 , "Homo sapiens calcium/calmodulin-dependent protein kinase II (CaMKIINalpha), mRNA", gi|31324542|ref|NM_018584.4|[31324542]; 2113: NM_018589 , "Homo sapiens chromosome 14 open reading frame 116 (C14orf116), mRNA", gi|20127573|ref|NM_018589.2|[20127573]; 2114: NM_018590 , "Homo sapiens chondroitin sulfate GalNAcT-2 (GALNACT-2), mRNA", gi|24429591|ref|NM_018590.3|[24429591]; 2115: NM_018602 , "Homo sapiens DnaJ (Hsp40) homolog, subfamily A, member 4 (DNAJA4), mRNA", gi|33354248|ref|NM_018602.2|[33354248]; 2116: NM_018622 , "Homo sapiens presenilin associated, rhomboid-like (PSARL), mRNA", gi|20127651|ref|NM_018622.3|[20127651]; 2117: NM_018640 , "Homo sapiens neuronal specific transcription factor DAT1 (DAT1), mRNA",

gi|41350202|ref|NM_018640.3|[41350202]; 2118: NM_018641 , "Homo sapiens carbohydrate (chondroitin 4) sulfotransferase 12 (CHST12), mRNA", gi|20070291|ref|NM_018641.2|[20070291]; 2119: NM_018644 , "Homo sapiens beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)", "(B3GAT1), transcript variant 1, mRNA", gi|16905508|ref|NM_018644.2|[16905508]; 2120: NM_018648 , "Homo sapiens nucleolar protein family A, member 3 (H/ACA small nucleolar RNPs)", "(NOLA3), mRNA", gi|15011920|ref|NM_018648.2|[15011920]; 2121: NM_018649 , "Homo sapiens H2A histone family, member Y2 (H2AFY2), mRNA", gi|8923919|ref|NM_018649.1|[8923919]; 2122: NM_018650 , "Homo sapiens MAP/microtubule affinity-regulating kinase 1 (MARK1), mRNA", gi|33589842|ref|NM_018650.2|[33589842]; 2123: NM_018654 , "Homo sapiens G protein-coupled receptor, family C, group 5, member D (GPRC5D),", mRNA, gi|8923704|ref|NM_018654.1|[8923704]; 2124: NM_018674 , "Homo sapiens amiloride-sensitive cation channel 4, pituitary (ACCN4), transcript", "variant 1, mRNA", gi|33519441|ref|NM_018674.3|[33519441]; 2125: NM_018687 , "Homo sapiens hepatocellular carcinoma-associated gene TD26 (LOC55908), mRNA", gi|33667073|ref|NM_018687.3|[33667073]; 2126: NM_018688 , "Homo sapiens bridging integrator 3 (BIN3), mRNA", gi|39725693|ref|NM_018688.3|[39725693]; 2127: NM_018695 , "Homo sapiens erbb2 interacting protein (ERBB2IP), mRNA", gi|8923908|ref|NM_018695.1|[8923908]; 2128: NM_018696 , "Homo sapiens elaC homolog 1 (E. coli) (ELAC1), mRNA", gi|8922121|ref|NM_018696.1|[8922121]; 2129: NM_018697 , Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial), "(LANCL2), mRNA", gi|19923550|ref|NM_018697.2|[19923550]; 2130: NM_018704 , "Homo sapiens hypothetical protein DKFZp547A023 (DKFZp547A023), mRNA", gi|24308178|ref|NM_018704.1|[24308178]; 2131: NM_018705 , , ref|NM_018705.1|[8922152], This record was temporarily removed by RefSeq staff for additional review., , 2132: NM_018722 , "Homo sapiens BWRT protein (HSA404617), mRNA", gi|10190657|ref|NM_018722.1|[10190657]; 2133: NM_018723 , "Homo sapiens ataxin 2-binding protein 1 (A2BP1), transcript variant 4, mRNA", gi|22538402|ref|NM_018723.2|[22538402]; 2134: NM_018725 , "Homo sapiens interleukin 17 receptor B (IL17RB), transcript variant 1, mRNA", gi|27477073|ref|NM_018725.2|[27477073]; 2135: NM_018845 , "Homo sapiens stromal cell protein (LOC55974), mRNA", gi|10047123|ref|NM_018845.1|[10047123]; 2136: NM_018897 , "Homo sapiens dynein, axonemal, heavy polypeptide 7 (DNAH7), mRNA", gi|17864091|ref|NM_018897.1|[17864091]; 2137: NM_018943 , "Homo sapiens tubulin, alpha 8 (TUBA8), mRNA", gi|9507214|ref|NM_018943.1|[9507214]; 2138: NM_018945 , "Homo sapiens phosphodiesterase 7B (PDE7B), mRNA", gi|40255306|ref|NM_018945.2|[40255306]; 2139: NM_018947 , "Homo sapiens cytochrome c, somatic (CYCS), nuclear gene encoding mitochondrial", "protein, mRNA", gi|34328939|ref|NM_018947.4|[34328939]; 2140: NM_018957 , "Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA", gi|15147251|ref|NM_018957.2|[15147251]; 2141: NM_018959 , "Homo sapiens DAZ associated protein 1 (DAZAP1), transcript variant 2, mRNA", gi|25470885|ref|NM_018959.2|[25470885]; 2142: NM_018967 , "Homo sapiens syntrophin, gamma 1 (SNTG1), mRNA", gi|9507162|ref|NM_018967.1|[9507162]; 2143: NM_018973 , "Homo sapiens dolichyl-phosphate mannosyltransferase polypeptide 3 (DPM3),", "transcript variant 1, mRNA", gi|24430133|ref|NM_018973.3|[24430133]; 2144: NM_018975 , "Homo sapiens telomeric repeat binding factor 2, interacting protein (TERF2IP),", mRNA, gi|9507032|ref|NM_018975.1|[9507032]; 2145: NM_018982 , "Homo sapiens hypothetical

protein DJ167A19.1 (DJ167A19.1), mRNA", gi|40538797|ref|NM_018982.3|[40538797]; 2146: NM_018983 , "Homo sapiens nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)", "(NOLA1), transcript variant 1, mRNA", gi|15011914|ref|NM_018983.2|[15011914]; 2147: NM_018990 , "Homo sapiens chromosome X open reading frame 9 (CXorf9), mRNA", gi|40254885|ref|NM_018990.2|[40254885]; 2148: NM_018992 , "Homo sapiens potassium channel tetramerisation domain containing 5 (KCTD5), mRNA", gi|9506650|ref|NM_018992.1|[9506650]; 2149: NM_018993 , "Homo sapiens Ras and Rab interactor 2 (RIN2), mRNA", gi|35493905|ref|NM_018993.2|[35493905]; 2150: NM_019002 , "Homo sapiens ETAA16 protein (ETAA16), mRNA", gi|37059813|ref|NM_019002.2|[37059813]; 2151: NM_019006 , "Homo sapiens protein associated with PRK1 (AWP1), mRNA", gi|21359917|ref|NM_019006.2|[21359917]; 2152: NM_019008 , , ref|NM_019008.4|[42766427]; 2153: NM_019009 , "Homo sapiens toll interacting protein (TOLLIP), mRNA", gi|21361618|ref|NM_019009.2|[21361618]; 2154: NM_019014 , "Homo sapiens polymerase (RNA) I polypeptide B, 128kDa (POLR1B), mRNA", gi|33469940|ref|NM_019014.2|[33469940]; 2155: NM_019020 , "Homo sapiens TBC1 domain family, member 16 (TBC1D16), mRNA", gi|33563375|ref|NM_019020.2|[33563375]; 2156: NM_019021 , "Homo sapiens hypothetical protein FLJ20010 (FLJ20010), mRNA", gi|9506646|ref|NM_019021.1|[9506646]; 2157: NM_019023 , "Homo sapiens hypothetical protein FLJ10640 (FLJ10640), mRNA", gi|9506614|ref|NM_019023.1|[9506614]; 2158: NM_019033 , "Homo sapiens hypothetical protein FLJ11235 (FLJ11235), mRNA", gi|9506642|ref|NM_019033.1|[9506642]; 2159: NM_019040 , "Homo sapiens elongation protein 4 homolog (S. cerevisiae) (ELP4), mRNA", gi|21361628|ref|NM_019040.2|[21361628]; 2160: NM_019045 , "Homo sapiens similar to rab11-binding protein (DKFZp686L20145), mRNA", gi|32526902|ref|NM_019045.2|[32526902]; 2161: NM_019055 , "Homo sapiens roundabout homolog 4, magic roundabout (Drosophila) (ROBO4), mRNA", gi|17511434|ref|NM_019055.4|[17511434]; 2162: NM_019056 , "Homo sapiens neuronal protein 17.3 (P17.3), mRNA", gi|20127560|ref|NM_019056.2|[20127560]; 2163: NM_019059 , Homo sapiens translocase of outer mitochondrial membrane 7 homolog (yeast), "(TOMM7), mRNA", gi|9506858|ref|NM_019059.1|[9506858]; 2164: NM_019063 , "Homo sapiens echinoderm microtubule associated protein like 4 (EML4), mRNA", gi|19923496|ref|NM_019063.2|[19923496]; 2165: NM_019064 , "Homo sapiens sidekick homolog 2 (chicken) (SDK2), mRNA", gi|21735576|ref|NM_019064.2|[21735576]; 2166: NM_019069 , "Homo sapiens WD repeat domain 5B (WDR5B), mRNA", gi|42544246|ref|NM_019069.3|[42544246]; 2167: NM_019074 , "Homo sapiens delta-like 4 (Drosophila) (DLL4), mRNA", gi|31881762|ref|NM_019074.2|[31881762]; 2168: NM_019081 , "Homo sapiens limkain b1 (LKAP), transcript variant 2, mRNA", gi|34878696|ref|NM_019081.2|[34878696]; 2169: NM_019082 , "Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 56 (DDX56), mRNA", gi|9506930|ref|NM_019082.1|[9506930]; 2170: NM_019083 , "Homo sapiens hypothetical protein FLJ10287 (FLJ10287), mRNA", gi|11024703|ref|NM_019083.1|[11024703]; 2171: NM_019088 , "Homo sapiens hypothetical protein F23149_1 (PD2), mRNA", gi|42476168|ref|NM_019088.2|[42476168]; 2172: NM_019096 , "Homo sapiens GTP binding protein 2 (GTPBP2), mRNA", gi|19923498|ref|NM_019096.2|[19923498]; 2173: NM_019102 , "Homo sapiens homeo box A5 (HOXA5), mRNA", gi|24497516|ref|NM_019102.2|[24497516]; 2174: NM_019103 , "Homo sapiens hypothetical protein LOC55954 (LOC55954), mRNA", gi|9506862|ref|NM_019103.1|[9506862]; 2175: NM_019104 , "Homo sapiens protein F25965

(F25965), mRNA", gi|28144915|ref|NM_019104.1|[28144915]; 2176: NM_019112 , "Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 7 (ABCA7),", "transcript variant 1, mRNA", gi|15451836|ref|NM_019112.2|[15451836]; 2177: NM_019613 , "Homo sapiens hypothetical protein 628 (LOC56270), mRNA", gi|19923554|ref|NM_019613.2|[19923554]; 2178: NM_019843 , Homo sapiens eukaryotic translation initiation factor 4E nuclear import factor 1, "(EIF4ENIF1), mRNA", gi|10947034|ref|NM_019843.2|[10947034]; 2179: NM_019845 , "Homo sapiens candidate mediator of the p53-dependent G2 arrest (REPRIMO), mRNA", gi|9790192|ref|NM_019845.1|[9790192]; 2180: NM_019848 , "Homo sapiens solute carrier family 10 (sodium/bile acid cotransporter family),", "member 3 (SLC10A3), mRNA", gi|10938005|ref|NM_019848.2|[10938005]; 2181: NM_019851 , "Homo sapiens fibroblast growth factor 20 (FGF20), mRNA", gi|9789946|ref|NM_019851.1|[9789946]; 2182: NM_019852 , "Homo sapiens methyltransferase like 3 (METTL3), mRNA", gi|21361826|ref|NM_019852.2|[21361826]; 2183: NM_019857 , "Homo sapiens CTP synthase II (CTPS2), transcript variant 1, mRNA", gi|28559082|ref|NM_019857.3|[28559082]; 2184: NM_019887 , "Homo sapiens diablo homolog (Drosophila) (DIABLO), nuclear gene encoding", "mitochondrial protein, transcript variant 1, mRNA", gi|42544195|ref|NM_019887.3|[42544195]; 2185: NM_020062 , "Homo sapiens SLC2A4 regulator (SLC2A4RG), mRNA", gi|39777592|ref|NM_020062.3|[39777592]; 2186: NM_020120 , "Homo sapiens UDP-glucose ceramide glucosyltransferase-like 1 (UGCGL1), mRNA", gi|9910279|ref|NM_020120.1|[9910279]; 2187: NM_020121 , "Homo sapiens UDP-glucose ceramide glucosyltransferase-like 2 (UGCGL2), mRNA", gi|11386200|ref|NM_020121.2|[11386200]; 2188: NM_020123 , "Homo sapiens SM-11044 binding protein (SMBP), mRNA", gi|33859832|ref|NM_020123.2|[33859832]; 2189: NM_020126 , "Homo sapiens sphingosine kinase 2 (SPHK2), mRNA", gi|21361698|ref|NM_020126.3|[21361698]; 2190: NM_020127 , "Homo sapiens tuftelin 1 (TUFT1), mRNA", gi|9910595|ref|NM_020127.1|[9910595]; 2191: NM_020130 , "Homo sapiens chromosome 8 open reading frame 4 (C8orf4), mRNA", gi|21359931|ref|NM_020130.2|[21359931]; 2192: NM_020133 , Homo sapiens 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic, "acid acyltransferase, delta) (AGPAT4), mRNA", gi|9910391|ref|NM_020133.1|[9910391]; 2193: NM_020135 , "Homo sapiens Werner helicase interacting protein 1 (WRNIP1), transcript variant", "1, mRNA", gi|18426901|ref|NM_020135.2|[18426901]; 2194: NM_020142 , "Homo sapiens NADH:ubiquinone oxidoreductase MLRQ subunit homolog (LOC56901),", mRNA, gi|34147589|ref|NM_020142.3|[34147589]; 2195: NM_020144 , "Homo sapiens poly(A) polymerase beta (testis specific) (PAPOLB), mRNA", gi|37202113|ref|NM_020144.3|[37202113]; 2196: NM_020147 , "Homo sapiens THAP domain containing 10 (THAP10), mRNA", gi|31543086|ref|NM_020147.2|[31543086]; 2197: NM_020151 , "Homo sapiens START domain containing 7 (STARD7), transcript variant 1, mRNA", gi|21450854|ref|NM_020151.2|[21450854]; 2198: NM_020154 , "Homo sapiens chromosome 15 hypothetical ATG/GTP binding protein (LOC56851), mRNA", gi|9910345|ref|NM_020154.1|[9910345]; 2199: NM_020156 , Homo sapiens core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta, "1,3-galactosyltransferase (C1GALT1), mRNA", gi|9910143|ref|NM_020156.1|[9910143]; 2200: NM_020169 , "Homo sapiens latexin protein (LXN), mRNA", gi|21359932|ref|NM_020169.2|[21359932]; 2201: NM_020170 , "Homo sapiens hypothetical protein from EUROIMAGE 2021883 (LOC56926), mRNA", gi|24308184|ref|NM_020170.1|[24308184]; 2202: NM_020184 , "Homo sapiens cyclin M4

(CNNM4), mRNA", gi|41350205|ref|NM_020184.2|[41350205]; 2203: NM_020186 , "Homo sapiens ACN9 homolog (S. cerevisiae) (ACN9), mRNA", gi|9910179|ref|NM_020186.1|[9910179]; 2204: NM_020188 , "Homo sapiens DC13 protein (DC13), mRNA", gi|42476040|ref|NM_020188.2|[42476040]; 2205: NM_020189 , "Homo sapiens DC6 protein (DC6), mRNA", gi|34222364|ref|NM_020189.4|[34222364]; 2206: NM_020191 , "Homo sapiens mitochondrial ribosomal protein S22 (MRPS22), nuclear gene encoding", "mitochondrial protein, mRNA", gi|16554602|ref|NM_020191.2|[16554602]; 2207: NM_020194 , "Homo sapiens GL004 protein (GL004), mRNA", gi|31377606|ref|NM_020194.4|[31377606]; 2208: NM_020195 , "Homo sapiens chromosome 14 open reading frame 124 (C14orf124), mRNA", gi|9910257|ref|NM_020195.1|[9910257]; 2209: NM_020196 , "Homo sapiens XPA binding protein 2 (XAB2), mRNA", gi|9910259|ref|NM_020196.1|[9910259]; 2210: NM_020198 , "Homo sapiens GK001 protein (GK001), mRNA", gi|9910241|ref|NM_020198.1|[9910241]; 2211: NM_020224 , , ref|NM_020224.1|[9910203], This record was temporarily removed by RefSeq staff for additional review., , 2212: NM_020226 , "Homo sapiens PR domain containing 8 (PRDM8), mRNA", gi|41349479|ref|NM_020226.2|[41349479]; 2213: NM_020228 , "Homo sapiens PR domain containing 10 (PRDM10), transcript variant 1, mRNA", gi|41349457|ref|NM_020228.2|[41349457]; 2214: NM_020229 , "Homo sapiens PR domain containing 11 (PRDM11), mRNA", gi|41349465|ref|NM_020229.2|[41349465]; 2215: NM_020230 , "Homo sapiens peter pan homolog (Drosophila) (PPAN), mRNA", gi|41872679|ref|NM_020230.3|[41872679]; 2216: NM_020231 , "Homo sapiens x 010 protein (MDS010), mRNA", gi|34303962|ref|NM_020231.3|[34303962]; 2217: NM_020232 , "Homo sapiens hepatocellular carcinoma susceptibility protein (HCCA3), mRNA", gi|39725705|ref|NM_020232.3|[39725705]; 2218: NM_020233 , "Homo sapiens x 006 protein (MDS006), mRNA", gi|37059747|ref|NM_020233.3|[37059747]; 2219: NM_020234 , "Homo sapiens x 009 protein (MDS009), mRNA", gi|34222368|ref|NM_020234.3|[34222368]; 2220: NM_020239 , "Homo sapiens small protein effector 1 of Cdc42 (SPEC1), mRNA", gi|12965169|ref|NM_020239.2|[12965169]; 2221: NM_020243 , Homo sapiens translocase of outer mitochondrial membrane 22 homolog (yeast), "(TOMM22), mRNA", gi|39725679|ref|NM_020243.3|[39725679]; 2222: NM_020247 , "Homo sapiens chaperone, ABC1 activity of bc1 complex like (S. pombe) (CABC1),", mRNA, gi|34147521|ref|NM_020247.3|[34147521]; 2223: NM_020249 , Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with, "thrombospondin type 1 motif, 9 (ADAMTS9), transcript variant 3, mRNA", gi|33624884|ref|NM_020249.2|[33624884]; 2224: NM_020307 , "Homo sapiens cyclin L1 (CCNL1), mRNA", gi|9945319|ref|NM_020307.1|[9945319]; 2225: NM_020309 , Homo sapiens solute carrier family 17 (sodium-dependent inorganic phosphate, "cotransporter), member 7 (SLC17A7), mRNA", gi|9945321|ref|NM_020309.1|[9945321]; 2226: NM_020310 , "Homo sapiens MAX binding protein (MNT), mRNA", gi|9945317|ref|NM_020310.1|[9945317]; 2227: NM_020319 , "Homo sapiens hypothetical protein DKFZp564O043 (DKFZP564O043), mRNA", gi|28461128|ref|NM_020319.1|[28461128]; 2228: NM_020354 , "Homo sapiens ectonucleoside triphosphate diphosphohydrolase 7 (ENTPD7), mRNA", gi|9966820|ref|NM_020354.1|[9966820]; 2229: NM_020357 , "Homo sapiens PEST-containing nuclear protein (PCNP), mRNA", gi|9966826|ref|NM_020357.1|[9966826]; 2230: NM_020363 , "Homo sapiens deleted in azoospermia 2 (DAZ2), mRNA", gi|11036659|ref|NM_020363.1|[11036659]; 2231: NM_020367 , "Homo sapiens chromosome 12

open reading frame 6 (C12orf6), mRNA", gi|20127593|ref|NM_020367.2|[20127593]; 2232: NM_020371 , "Homo sapiens apoptosis, caspase activation inhibitor (AVEN), mRNA", gi|9966840|ref|NM_020371.1|[9966840]; 2233: NM_020375 , "Homo sapiens chromosome 12 open reading frame 5 (C12orf5), mRNA", gi|9966848|ref|NM_020375.1|[9966848]; 2234: NM_020379 , "Homo sapiens mannosidase, alpha, class 1C, member 1 (MAN1C1), mRNA", gi|9966902|ref|NM_020379.1|[9966902]; 2235: NM_020380 , "Homo sapiens AF15q14 protein (AF15Q14), mRNA", gi|24475852|ref|NM_020380.2|[24475852]; 2236: NM_020381 , "Homo sapiens chromosome 6 open reading frame 210 (C6orf210), mRNA", gi|29893561|ref|NM_020381.2|[29893561]; 2237: NM_020387 , "Homo sapiens RAB25, member RAS oncogene family (RAB25), mRNA", gi|9966860|ref|NM_020387.1|[9966860]; 2238: NM_020397 , "Homo sapiens calcium/calmodulin-dependent protein kinase ID (CAMK1D), mRNA", gi|9966874|ref|NM_020397.1|[9966874]; 2239: NM_020401 , "Homo sapiens nuclear pore complex protein (NUP107), mRNA", gi|9966880|ref|NM_020401.1|[9966880]; 2240: NM_020410 , "Homo sapiens ATPase type 13A (ATP13A), mRNA", gi|9966896|ref|NM_020410.1|[9966896]; 2241: NM_020418 , "Homo sapiens poly(rC) binding protein 4 (PCBP4), transcript variant 1, mRNA", gi|14670367|ref|NM_020418.2|[14670367]; 2242: NM_020423 , "Homo sapiens ezrin-binding partner PACE-1 (PACE-1), transcript variant 1, mRNA", gi|27363466|ref|NM_020423.4|[27363466]; 2243: NM_020424 , "Homo sapiens hypothetical protein A-211C6.1 (LOC57149), mRNA", gi|19923825|ref|NM_020424.2|[19923825]; 2244: NM_020433 , "Homo sapiens junctophilin 2 (JPH2), transcript variant 1, mRNA", gi|29893810|ref|NM_020433.3|[29893810]; 2245: NM_020453 , "Homo sapiens ATPase, Class V, type 10D (ATP10D), mRNA", gi|28466988|ref|NM_020453.2|[28466988]; 2246: NM_020465 , "Homo sapiens NDRG family member 4 (NDRG4), mRNA", gi|14165263|ref|NM_020465.1|[14165263]; 2247: NM_020466 , "Homo sapiens hypothetical protein dJ122O8.2 (DJ122O8.2), mRNA", gi|20070310|ref|NM_020466.3|[20070310]; 2248: NM_020529 , Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells, "inhibitor, alpha (NFKBIA), mRNA", gi|10092618|ref|NM_020529.1|[10092618]; 2249: NM_020533 , "Homo sapiens mucolipin 1 (MCOLN1), mRNA", gi|10092596|ref|NM_020533.1|[10092596]; 2250: NM_020549 , "Homo sapiens choline acetyltransferase (CHAT), transcript variant M, mRNA", gi|11038626|ref|NM_020549.2|[11038626]; 2251: NM_020638 , "Homo sapiens fibroblast growth factor 23 (FGF23), mRNA", gi|15055547|ref|NM_020638.2|[15055547]; 2252: NM_020639 , "Homo sapiens ankyrin repeat domain 3 (ANKRD3), mRNA", gi|41327753|ref|NM_020639.2|[41327753]; 2253: NM_020640 , "Homo sapiens RP42 homolog (RP42), mRNA", gi|36030882|ref|NM_020640.2|[36030882]; 2254: NM_020642 , "Homo sapiens chromosome 11 open reading frame 17 (C11orf17), transcript variant", "2, mRNA", gi|21361869|ref|NM_020642.2|[21361869]; 2255: NM_020644 , "Homo sapiens chromosome 11 open reading frame 15 (C11orf15), mRNA", gi|11034854|ref|NM_020644.1|[11034854]; 2256: NM_020645 , "Homo sapiens nuclear receptor interacting protein 3 (NRIP3), mRNA", gi|11034818|ref|NM_020645.1|[11034818]; 2257: NM_020648 , "Homo sapiens twisted gastrulation homolog 1 (Drosophila) (TWSG1), mRNA", gi|21314788|ref|NM_020648.3|[21314788]; 2258: NM_020649 , "Homo sapiens chromobox homolog 8 (Pc class homolog, Drosophila) (CBX8), mRNA", gi|10190681|ref|NM_020649.1|[10190681]; 2259: NM_020655 , "Homo sapiens junctophilin 3 (JPH3), mRNA", gi|21704282|ref|NM_020655.2|[21704282]; 2260: NM_020669 , ,

ref|NM_020669.1|[10190709], This record was temporarily removed by RefSeq staff for additional review., , 2261: NM_020673 , "Homo sapiens RAB22A, member RAS oncogene family (RAB22A), mRNA", gi|34577103|ref|NM_020673.2|[34577103]; 2262: NM_020685 , "Homo sapiens HT021 (HT021), mRNA", gi|34222336|ref|NM_020685.3|[34222336]; 2263: NM_020710 , "Homo sapiens KIAA1185 protein (KIAA1185), mRNA", gi|24308206|ref|NM_020710.1|[24308206]; 2264: NM_020826 , "Homo sapiens synaptotagmin XIII (SYT13), mRNA", gi|24308232|ref|NM_020826.1|[24308232]; 2265: NM_020836 , "Homo sapiens brain-enriched guanylate kinase-associated protein (KIAA1446), mRNA", gi|34147339|ref|NM_020836.2|[34147339]; 2266: NM_020858 , "Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain,", "(semaphorin) 6D (SEMA6D), transcript variant 1, mRNA", gi|24234728|ref|NM_020858.1|[24234728]; 2267: NM_020892 , "Homo sapiens deltex homolog 2 (Drosophila) (DTX2), mRNA", gi|24308252|ref|NM_020892.1|[24308252]; 2268: NM_020898 , "Homo sapiens KIAA1536 protein (KIAA1536), mRNA", gi|14149741|ref|NM_020898.1|[14149741]; 2269: NM_020904 , "Homo sapiens pleckstrin homology domain containing, family A (phosphoinositide", "binding specific) member 4 (PLEKHA4), mRNA", gi|10190743|ref|NM_020904.1|[10190743]; 2270: NM_020982 , , ref|NM_020982.2|[44680149]; 2271: NM_020998 , "Homo sapiens macrophage stimulating 1 (hepatocyte growth factor-like) (MST1),", mRNA, gi|31543211|ref|NM_020998.2|[31543211]; 2272: NM_020999 , "Homo sapiens neurogenin 3 (NEUROG3), mRNA", gi|10337610|ref|NM_020999.1|[10337610]; 2273: NM_021018 , "Homo sapiens histone 1, H3f (HIST1H3F), mRNA", gi|21396497|ref|NM_021018.2|[21396497]; 2274: NM_021025 , "Homo sapiens T-cell leukemia, homeobox 3 (TLX3), mRNA", gi|10440563|ref|NM_021025.1|[10440563]; 2275: NM_021062 , "Homo sapiens histone 1, H2bb (HIST1H2BB), mRNA", gi|19924303|ref|NM_021062.2|[19924303]; 2276: NM_021070 , "Homo sapiens latent transforming growth factor beta binding protein 3 (LTBP3),", mRNA, gi|18497287|ref|NM_021070.2|[18497287]; 2277: NM_021077 , "Homo sapiens neuromedin B (NMB), mRNA", gi|24475648|ref|NM_021077.2|[24475648]; 2278: NM_021080 , "Homo sapiens disabled homolog 1 (Drosophila) (DAB1), mRNA", gi|33350927|ref|NM_021080.3|[33350927]; 2279: NM_021081 , "Homo sapiens growth hormone releasing hormone (GHRH), mRNA", gi|30581161|ref|NM_021081.3|[30581161]; 2280: NM_021098 , "Homo sapiens calcium channel, voltage-dependent, alpha 1H subunit (CACNA1H),", mRNA, gi|10864076|ref|NM_021098.1|[10864076]; 2281: NM_021100 , "Homo sapiens NFS1 nitrogen fixation 1 (S. cerevisiae) (NFS1), nuclear gene", "encoding mitochondrial protein, transcript variant 1, mRNA", gi|32307131|ref|NM_021100.3|[32307131]; 2282: NM_021104 , "Homo sapiens ribosomal protein L41 (RPL41), mRNA", gi|10863874|ref|NM_021104.1|[10863874]; 2283: NM_021126 , "Homo sapiens mercaptopyruvate sulfurtransferase (MPST), mRNA", gi|23510449|ref|NM_021126.3|[23510449]; 2284: NM_021133 , "Homo sapiens ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)", "(RNASEL), mRNA", gi|30795246|ref|NM_021133.2|[30795246]; 2285: NM_021134 , "Homo sapiens mitochondrial ribosomal protein L23 (MRPL23), nuclear gene encoding", "mitochondrial protein, mRNA", gi|27436903|ref|NM_021134.2|[27436903]; 2286: NM_021147 , "Homo sapiens uracil-DNA glycosylase 2 (UNG2), mRNA", gi|10863950|ref|NM_021147.1|[10863950]; 2287: NM_021149 , "Homo sapiens coactosin-like 1 (Dictyostelium) (COTL1), mRNA", gi|23510452|ref|NM_021149.2|[23510452]; 2288: NM_021158 , "Homo sapiens chromosome 20 open reading frame 97 (C20orf97), mRNA", gi|41327717|ref|NM_021158.3|[41327717]; 2289:

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gi|12232384|ref|NM_022730.1|[12232384]; 2404: NM_022746 , "Homo sapiens hypothetical protein FLJ22390 (FLJ22390), mRNA", gi|33285009|ref|NM_022746.2|[33285009]; 2405: NM_022750 , "Homo sapiens zinc finger CCCH type domain containing 1 (ZC3HDC1), mRNA", gi|12232412|ref|NM_022750.1|[12232412]; 2406: NM_022754 , "Homo sapiens sideroflexin 1 (SFXN1), mRNA", gi|40255158|ref|NM_022754.4|[40255158]; 2407: NM_022756 , "Homo sapiens hypothetical protein FLJ11730 (FLJ11730), mRNA", gi|40255019|ref|NM_022756.3|[40255019]; 2408: NM_022761 , "Homo sapiens chromosome 11 open reading frame 1 (C11orf1), mRNA", gi|12232430|ref|NM_022761.1|[12232430]; 2409: NM_022762 , "Homo sapiens hypothetical protein FLJ22318 (FLJ22318), mRNA", gi|34147687|ref|NM_022762.3|[34147687]; 2410: NM_022765 , Homo sapiens NEDD9 interacting protein with calponin homology and LIM domains, "(NICAL), mRNA", gi|20127615|ref|NM_022765.2|[20127615]; 2411: NM_022766 , "Homo sapiens ceramide kinase (CERK), transcript variant 1, mRNA", gi|32967301|ref|NM_022766.4|[32967301]; 2412: NM_022776 , "Homo sapiens oxysterol binding protein-like 11 (OSBPL11), mRNA", gi|23111058|ref|NM_022776.3|[23111058]; 2413: NM_022781 , "Homo sapiens ring finger protein 38 (RNF38), transcript variant 1, mRNA", gi|37577174|ref|NM_022781.3|[37577174]; 2414: NM_022784 , "Homo sapiens hypothetical protein FLJ12476 (FLJ12476), mRNA", gi|12232474|ref|NM_022784.1|[12232474]; 2415: NM_022785 , "Homo sapiens CAP-binding protein complex interacting protein 1 (FLJ23588),", "transcript variant 1, mRNA", gi|38570106|ref|NM_022785.2|[38570106]; 2416: NM_022819 , "Homo sapiens phospholipase A2, group IIF (PLA2G2F), mRNA", gi|12383057|ref|NM_022819.1|[12383057]; 2417: NM_022834 , "Homo sapiens von Willebrand factor A domain-related protein (WARP), transcript", "variant 1, mRNA", gi|40068484|ref|NM_022834.3|[40068484]; 2418: NM_022836 , "Homo sapiens DNA cross-link repair 1B (PSO2 homolog, S. cerevisiae) (DCLRE1B),", mRNA, gi|24431998|ref|NM_022836.2|[24431998]; 2419: NM_022840 , "Homo sapiens methyltransferase like 4 (METTL4), mRNA", gi|38505223|ref|NM_022840.2|[38505223]; 2420: NM_022897 , "Homo sapiens RAN binding protein 17 (RANBP17), mRNA", gi|22095364|ref|NM_022897.2|[22095364]; 2421: NM_022898 , "Homo sapiens B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B), transcript", "variant 2, mRNA", gi|12597634|ref|NM_022898.1|[12597634]; 2422: NM_022899 , "Homo sapiens ARP8 actin-related protein 8 homolog (yeast) (ACTR8), mRNA", gi|39812114|ref|NM_022899.3|[39812114]; 2423: NM_022903 , "Homo sapiens hypothetical protein FLJ12800 (FLJ12800), mRNA", gi|33285012|ref|NM_022903.2|[33285012]; 2424: NM_022908 , "Homo sapiens hypothetical protein FLJ12442 (FLJ12442), mRNA", gi|12597652|ref|NM_022908.1|[12597652]; 2425: NM_022911 , "Homo sapiens solute carrier family 26, member 6 (SLC26A6), transcript variant 1,", mRNA, gi|20336275|ref|NM_022911.2|[20336275]; 2426: NM_022914 , "Homo sapiens hypothetical protein 24432 (24432), mRNA", gi|12597658|ref|NM_022914.1|[12597658]; 2427: NM_022917 , "Homo sapiens nucleolar protein family 6 (RNA-associated) (NOL6), transcript", "variant alpha, mRNA", gi|39777587|ref|NM_022917.4|[39777587]; 2428: NM_023008 , "Homo sapiens hypothetical protein FLJ12949 (FLJ12949), transcript variant 1,", mRNA, gi|30410782|ref|NM_023008.2|[30410782]; 2429: NM_023039 , "Homo sapiens ankyrin repeat, family A (RFXANK-like), 2 (ANKRA2), mRNA", gi|21362082|ref|NM_023039.2|[21362082]; 2430: NM_023067 , "Homo sapiens forkhead box L2 (FOXL2), mRNA", gi|42716284|ref|NM_023067.2|[42716284]; 2431: NM_023071 , "Homo sapiens spermatogenesis associated, serine-rich 2 (SPATS2), mRNA",

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phosphatidylglycerophosphate synthase (PGS1), mRNA", gi|21314623|ref|NM_024419.2|[21314623]; 2490: NM_024491 , "Homo sapiens p10-binding protein (BITE), mRNA", gi|13346499|ref|NM_024491.1|[13346499]; 2491: NM_024504 , "Homo sapiens PR domain containing 14 (PRDM14), mRNA", gi|41349468|ref|NM_024504.2|[41349468]; 2492: NM_024505 , "Homo sapiens NADPH oxidase, EF hand calcium-binding domain 5 (NOX5), mRNA", gi|20127623|ref|NM_024505.2|[20127623]; 2493: NM_024506 , "Homo sapiens galactosidase, beta 1-like (GLB1L), mRNA", gi|40255042|ref|NM_024506.3|[40255042]; 2494: NM_024507 , "Homo sapiens kringle containing transmembrane protein 2 (KREMEN2), transcript", "variant 2, mRNA", gi|27437002|ref|NM_024507.2|[27437002]; 2495: NM_024512 , "Homo sapiens leucine rich repeat containing 2 (LRRC2), mRNA", gi|14719432|ref|NM_024512.2|[14719432]; 2496: NM_024523 , "Homo sapiens GRIP and coiled-coil domain-containing 1 (GCC1), mRNA", gi|34305454|ref|NM_024523.5|[34305454]; 2497: NM_024525 , "Homo sapiens tetratricopeptide repeat domain 13 (TTC13), mRNA", gi|31377702|ref|NM_024525.2|[31377702]; 2498: NM_024526 , "Homo sapiens EPS8-like 3 (EPS8L3), transcript variant 3, mRNA", gi|21071013|ref|NM_024526.2|[21071013]; 2499: NM_024536 , "Homo sapiens chondroitin polymerizing factor (CHPF), mRNA", gi|34222219|ref|NM_024536.4|[34222219]; 2500: NM_024537 , "Homo sapiens hypothetical protein FLJ12118 (FLJ12118), mRNA", gi|13375694|ref|NM_024537.1|[13375694]; 2501: NM_024540 , "Homo sapiens mitochondrial ribosomal protein L24 (MRPL24), nuclear gene encoding", "mitochondrial protein, transcript variant 2, mRNA", gi|22035587|ref|NM_024540.2|[22035587]; 2502: NM_024544 , "Homo sapiens hypothetical protein FLJ12875 (FLJ12875), mRNA", gi|13375704|ref|NM_024544.1|[13375704]; 2503: NM_024546 , "Homo sapiens chromosome 13 open reading frame 7 (C13orf7), mRNA", gi|21362045|ref|NM_024546.2|[21362045]; 2504: NM_024551 , "Homo sapiens adiponectin receptor 2 (ADIPOR2), mRNA", gi|38261972|ref|NM_024551.2|[38261972]; 2505: NM_024554 , "Homo sapiens piggyBac transposable element derived 5 (PGBD5), mRNA", gi|25777747|ref|NM_024554.2|[25777747]; 2506: NM_024565 , "Homo sapiens hypothetical protein FLJ14166 (FLJ14166), mRNA", gi|40018623|ref|NM_024565.4|[40018623]; 2507: NM_024570 , "Homo sapiens hypothetical protein FLJ11712 (FLJ11712), mRNA", gi|13375741|ref|NM_024570.1|[13375741]; 2508: NM_024572 , Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide, "N-acetylgalactosaminyltransferase 14 (GalNAc-T14) (GALNT14), mRNA", gi|13375743|ref|NM_024572.1|[13375743]; 2509: NM_024573 , "Homo sapiens chromosome 6 open reading frame 211 (C6orf211), mRNA", gi|13375745|ref|NM_024573.1|[13375745]; 2510: NM_024580 , "Homo sapiens hypothetical protein FLJ13119 (FLJ13119), mRNA", gi|40255246|ref|NM_024580.3|[40255246]; 2511: NM_024583 , "Homo sapiens secernin 3 (SCRN3), mRNA", gi|38504670|ref|NM_024583.2|[38504670]; 2512: NM_024584 , "Homo sapiens hypothetical protein FLJ13646 (FLJ13646), mRNA", gi|39979625|ref|NM_024584.2|[39979625]; 2513: NM_024585 , "Homo sapiens hypothetical protein FLJ22160 (FLJ22160), mRNA", gi|20149678|ref|NM_024585.2|[20149678]; 2514: NM_024587 , "Homo sapiens hypothetical protein FLJ22353 (FLJ22353), mRNA", gi|42734433|ref|NM_024587.2|[42734433]; 2515: NM_024589 , "Homo sapiens leucine zipper domain protein (FLJ22386), mRNA", gi|13375778|ref|NM_024589.1|[13375778]; 2516: NM_024590 , "Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA", gi|40254961|ref|NM_024590.2|[40254961]; 2517: NM_024594 , "Homo sapiens pantothenate kinase 3 (PANK3), mRNA",

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like 1 (CTNNBL1), mRNA", gi|29570786|ref|NM_030877.3|[29570786]; 2693: NM_030907 , "Homo sapiens hypothetical protein MGC10731 (MGC10731), mRNA", gi|34147392|ref|NM_030907.2|[34147392]; 2694: NM_030917 , "Homo sapiens FIP1 like 1 (S. cerevisiae) (FIP1L1), mRNA", gi|40254977|ref|NM_030917.2|[40254977]; 2695: NM_030926 , "Homo sapiens integral membrane protein 2C (ITM2C), mRNA", gi|31560867|ref|NM_030926.3|[31560867]; 2696: NM_030927 , "Homo sapiens tetraspanin similar to TM4SF9 (DC-TM4F2), mRNA", gi|13569888|ref|NM_030927.1|[13569888]; 2697: NM_030954 , "Homo sapiens hypothetical protein DKFZp564A022 (DKFZP564A022), mRNA", gi|21361953|ref|NM_030954.2|[21361953]; 2698: NM_030963 , "Homo sapiens ring finger protein 146 (RNF146), mRNA", gi|33636757|ref|NM_030963.2|[33636757]; 2699: NM_030968 , "Homo sapiens C1q and tumor necrosis factor related protein 1 (C1QTNF1),", "transcript variant 1, mRNA", gi|38372915|ref|NM_030968.2|[38372915]; 2700: NM_030974 , "Homo sapiens hypothetical protein DKFZp434N1923 (DKFZP434N1923), mRNA", gi|31542518|ref|NM_030974.2|[31542518]; 2701: NM_030978 , "Homo sapiens actin related protein 2/3 complex, subunit 5-like (ARPC5L), mRNA", gi|13569955|ref|NM_030978.1|[13569955]; 2702: NM_031210 , "Homo sapiens hypothetical protein DC50 (DC50), mRNA", gi|33667026|ref|NM_031210.3|[33667026]; 2703: NM_031213 , "Homo sapiens hypothetical protein MGC5244 (MGC5244), mRNA", gi|21361948|ref|NM_031213.2|[21361948]; 2704: NM_031217 , "Homo sapiens kinesin family member 18A (DKFZP434G2226), mRNA", gi|21314741|ref|NM_031217.2|[21314741]; 2705: NM_031219 , "Homo sapiens hypothetical protein MGC12904 (MGC12904), mRNA", gi|31377665|ref|NM_031219.2|[31377665]; 2706: NM_031231 , "Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2", "binding protein (APBA2BP), transcript variant 1, mRNA", gi|38569412|ref|NM_031231.2|[38569412]; 2707: NM_031275 , "Homo sapiens testis expressed sequence 12 (TEX12), mRNA", gi|14277686|ref|NM_031275.2|[14277686]; 2708: NM_031280 , "Homo sapiens mitochondrial ribosomal protein S15 (MRPS15), nuclear gene encoding", "mitochondrial protein, mRNA", gi|16554610|ref|NM_031280.2|[16554610]; 2709: NM_031284 , "Homo sapiens ATP-dependent glucokinase (ADP-GK), mRNA", gi|31542508|ref|NM_031284.3|[31542508]; 2710: NM_031287 , "Homo sapiens splicing factor 3b, subunit 5, 10kDa (SF3B5), mRNA", gi|42740890|ref|NM_031287.2|[42740890]; 2711: NM_031289 , "Homo sapiens germ cell associated 1 (GSG1), mRNA", gi|13775203|ref|NM_031289.1|[13775203]; 2712: NM_031296 , "Homo sapiens RAB33B, member RAS oncogene family (RAB33B), mRNA", gi|13786128|ref|NM_031296.1|[13786128]; 2713: NM_031298 , "Homo sapiens hypothetical protein MGC2963 (MGC2963), mRNA", gi|13775219|ref|NM_031298.1|[13775219]; 2714: NM_031299 , "Homo sapiens cell division cycle associated 3 (CDCA3), mRNA", gi|34147595|ref|NM_031299.3|[34147595]; 2715: NM_031307 , "Homo sapiens hypothetical protein FKSG32 (FKSG32), mRNA", gi|31542635|ref|NM_031307.2|[31542635]; 2716: NM_031310 , "Homo sapiens plasmalemma vesicle associated protein (PLVAP), mRNA", gi|13775237|ref|NM_031310.1|[13775237]; 2717: NM_031450 , "Homo sapiens hypothetical protein p5326 (P5326), mRNA", gi|31543378|ref|NM_031450.2|[31543378]; 2718: NM_031485 , "Homo sapiens glutamate-rich WD repeat containing 1 (GRWD1), mRNA", gi|31542861|ref|NM_031485.2|[31542861]; 2719: NM_031904 , "Homo sapiens hypothetical protein FKSG44 (FKSG44), mRNA", gi|31982912|ref|NM_031904.2|[31982912]; 2720: NM_031922 , "Homo sapiens RALBP1 associated Eps domain containing 1 (REPS1), mRNA", gi|39812393|ref|NM_031922.2|[39812393]; 2721: NM_031966 , "Homo sapiens cyclin B1

(CCNB1), mRNA", gi|34304372|ref|NM_031966.2|[34304372]; 2722: NM_032048 , "Homo sapiens elastin microfibril interfacer 2 (EMILIN2), mRNA", gi|14042987|ref|NM_032048.1|[14042987]; 2723: NM_032119 , "Homo sapiens monogenic, audiogenic seizure susceptibility 1 homolog (mouse)", "(MASS1), mRNA", gi|19882212|ref|NM_032119.1|[19882212]; 2724: NM_032144 , "Homo sapiens RAB6C, member RAS oncogene family (RAB6C), mRNA", gi|14149798|ref|NM_032144.1|[14149798]; 2725: NM_032153 , "Homo sapiens Zic family member 4 (ZIC4), mRNA", gi|22547200|ref|NM_032153.2|[22547200]; 2726: NM_032179 , "Homo sapiens hypothetical protein FLJ20542 (FLJ20542), mRNA", gi|14149862|ref|NM_032179.1|[14149862]; 2727: NM_032204 , "Homo sapiens ASC-1 complex subunit P100 (ASC1p100), mRNA", gi|34147616|ref|NM_032204.3|[34147616]; 2728: NM_032209 , "Homo sapiens hypothetical protein FLJ21777 (FLJ21777), mRNA", gi|14149905|ref|NM_032209.1|[14149905]; 2729: NM_032219 , "Homo sapiens hypothetical protein FLJ22269 (FLJ22269), mRNA", gi|31542730|ref|NM_032219.2|[31542730]; 2730: NM_032233 , "Homo sapiens hypothetical protein FLJ23027 (FLJ23027), transcript variant 1,", mRNA, gi|40068480|ref|NM_032233.2|[40068480]; 2731: NM_032338 , "Homo sapiens hypothetical protein MGC14817 (MGC14817), mRNA", gi|31543151|ref|NM_032338.2|[31543151]; 2732: NM_032348 , "Homo sapiens hypothetical protein MGC3047 (MGC3047), mRNA", gi|39725651|ref|NM_032348.2|[39725651]; 2733: NM_032389 , "Homo sapiens zinc finger protein 289, ID1 regulated (ZNF289), mRNA", gi|31543982|ref|NM_032389.2|[31543982]; 2734: NM_032477 , "Homo sapiens mitochondrial ribosomal protein L41 (MRPL41), nuclear gene encoding", "mitochondrial protein, mRNA", gi|21265092|ref|NM_032477.1|[21265092]; 2735: NM_032509 , "Homo sapiens RNA binding protein (LOC84549), mRNA", gi|31543090|ref|NM_032509.2|[31543090]; 2736: NM_032569 , "Homo sapiens cytokine-like nuclear factor n-pac (N-PAC), mRNA", gi|40556375|ref|NM_032569.2|[40556375]; 2737: NM_032668 , , ref|NM_032668.1|[14249231], This record was temporarily removed by RefSeq staff for additional review., , 2738: NM_032715 , , ref|NM_032715.1|[14249317], This record was replaced or removed. See revision history for details., , 2739: NM_032737 , "Homo sapiens lamin B2 (LMNB2), mRNA", gi|27436950|ref|NM_032737.2|[27436950]; 2740: NM_032765 , "Homo sapiens tripartite motif-containing 52 (TRIM52), mRNA", gi|34147443|ref|NM_032765.2|[34147443]; 2741: NM_032842 , "Homo sapiens hypothetical protein FLJ14803 (FLJ14803), mRNA", gi|14249557|ref|NM_032842.1|[14249557]; 2742: NM_032856 , "Homo sapiens hypothetical protein FLJ14888 (FLJ14888), mRNA", gi|14249585|ref|NM_032856.1|[14249585]; 2743: NM_032865 , "Homo sapiens C-terminal tensin-like (CTEN), mRNA", gi|23943811|ref|NM_032865.3|[23943811]; 2744: NM_032895 , "Homo sapiens hypothetical protein MGC14376 (MGC14376), mRNA", gi|14249657|ref|NM_032895.1|[14249657]; 2745: NM_033211 , "Homo sapiens hypothetical gene supported by AF038182; BC009203 (LOC90355), mRNA", gi|34147457|ref|NM_033211.2|[34147457]; 2746: NM_033284 , "Homo sapiens transducin (beta)-like 1Y-linked (TBL1Y), transcript variant 1,", mRNA, gi|15150804|ref|NM_033284.1|[15150804]; 2747: NM_033411 , "Homo sapiens RWD domain containing 2 (RWDD2), mRNA", gi|34222125|ref|NM_033411.2|[34222125]; 2748: NM_033415 , "Homo sapiens hypothetical gene MGC19595 (MGC19595), mRNA", gi|16445355|ref|NM_033415.2|[16445355]; 2749: NM_033416 , "Homo sapiens U3 snoRNP protein 4 homolog (IMP4), mRNA", gi|15529981|ref|NM_033416.1|[15529981]; 2750: NM_033418 , "Homo sapiens hypothetical protein MGC9084 (MGC9084), mRNA",

gi|15553096|ref|NM_033418.1|[15553096]; 2751: NM_033453 , Homo sapiens inosine triphosphatase (nucleoside triphosphate pyrophosphatase), "(ITPA), transcript variant 1, mRNA", gi|31657145|ref|NM_033453.2|[31657145]; 2752: NM_033546 , "Homo sapiens myosin regulatory light chain MRLC2 (MRLC2), mRNA", gi|29568092|ref|NM_033546.2|[29568092]; 2753: NM_052940 , "Homo sapiens hypothetical protein MGC8974 (MGC8974), mRNA", gi|31543202|ref|NM_052940.3|[31543202]; 2754: NM_079834 , "Homo sapiens secretory carrier membrane protein 4 (SCAMP4), mRNA", gi|17738286|ref|NM_079834.1|[17738286]; 2755: NM_080839 , "Homo sapiens gamma-glutamyltransferase-like 4 (GGTL4), transcript variant 2,", mRNA, gi|40353751|ref|NM_080839.4|[40353751]; 2756: NM_130463 , "Homo sapiens ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 2", "(ATP6V1G2), transcript variant 1, mRNA", gi|20357536|ref|NM_130463.2|[20357536]; 2757: NM_133455 , "Homo sapiens emilin and multimerin-domain containing protein 1 (EMU1), mRNA", gi|19263344|ref|NM_133455.1|[19263344]; 2758: NM_138288 , "Homo sapiens chromosome 14 open reading frame 147 (C14orf147), mRNA", gi|19923718|ref|NM_138288.1|[19923718]; 2759: NM_138402 , "Homo sapiens hypothetical protein BC004921 (LOC93349), mRNA", gi|20149710|ref|NM_138402.2|[20149710]; 2760: NM_138570 , "Homo sapiens hypothetical protein MGC15523 (MGC15523), mRNA", gi|20070375|ref|NM_138570.1|[20070375]; 2761: NM_139136 , "Homo sapiens potassium voltage-gated channel, Shaw-related subfamily, member 2", "(KCNC2), transcript variant 1, mRNA", gi|24497456|ref|NM_139136.2|[24497456]; 2762: NM_139170 , "Homo sapiens hypothetical protein AF447587 (LOC146562), mRNA", gi|21040258|ref|NM_139170.1|[21040258]; 2763: NM_139246 , "Homo sapiens PP4189 (LOC158427), mRNA", gi|31377600|ref|NM_139246.3|[31377600]; 2764: NM_139265 , "Homo sapiens EH-domain containing 4 (EHD4), mRNA", gi|34147619|ref|NM_139265.2|[34147619]; 2765: NM_144617 , "Homo sapiens hypothetical protein FLJ32389 (FLJ32389), mRNA", gi|21389432|ref|NM_144617.1|[21389432]; 2766: NM_144635 , "Homo sapiens hypothetical protein MGC21688 (MGC21688), mRNA", gi|40255250|ref|NM_144635.3|[40255250]; 2767: NM_144718 , "Homo sapiens hypothetical protein AY099107 (LOC152185), mRNA", gi|40255074|ref|NM_144718.2|[40255074]; 2768: NM_145060 , "Homo sapiens hypothetical protein MGC:10200 (MGC10200), mRNA", gi|21450831|ref|NM_145060.1|[21450831]; 2769: NM_145063 , "Homo sapiens chromosome 6 open reading frame 130 (C6orf130), mRNA", gi|34147711|ref|NM_145063.2|[34147711]; 2770: NM_145804 , "Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), mRNA", gi|21956638|ref|NM_145804.1|[21956638]; 2771: NM_147129 , "Homo sapiens hypothetical protein LOC259173 (FLJ36525), transcript variant 1,", mRNA, gi|33359214|ref|NM_147129.2|[33359214]; 2772: NM_152272 , "Homo sapiens hypothetical protein MGC29816 (MGC29816), mRNA", gi|22748640|ref|NM_152272.1|[22748640]; 2773: NM_152275 , "Homo sapiens hypothetical protein FLJ13946 (FLJ13946), mRNA", gi|38683852|ref|NM_152275.2|[38683852]; 2774: NM_152288 , "Homo sapiens hypothetical protein MGC13024 (MGC13024), mRNA", gi|22748650|ref|NM_152288.1|[22748650]; 2775: NM_152339 , "Homo sapiens hypothetical protein MGC26885 (MGC26885), mRNA", gi|31377584|ref|NM_152339.2|[31377584]; 2776: NM_152341 , "Homo sapiens hypothetical protein FLJ30002 (FLJ30002), mRNA", gi|31542755|ref|NM_152341.2|[31542755]; 2777: NM_152519 , "Homo sapiens hypothetical protein FLJ23861 (FLJ23861), mRNA", gi|40217793|ref|NM_152519.2|[40217793]; 2778: NM_152647 , "Homo sapiens hypothetical

protein FLJ32800 (FLJ32800), mRNA", gi|22749318|ref|NM_152647.1|[22749318]; 2779: NM_152660 , "Homo sapiens hypothetical protein MGC34648 (MGC34648), mRNA", gi|22749340|ref|NM_152660.1|[22749340]; 2780: NM_152688 , "Homo sapiens KH domain containing, RNA binding, signal transduction associated 2", "(KHDRBS2), mRNA", gi|22749380|ref|NM_152688.1|[22749380]; 2781: NM_152703 , , ref|NM_152703.1|[22749402], This record was temporarily removed by RefSeq staff for additional review., , 2782: NM_152726 , "Homo sapiens Smhs2 homolog (rat) (FLJ34588), mRNA", gi|22749442|ref|NM_152726.1|[22749442]; 2783: NM_152753 , "Homo sapiens CUB domain and EGF-like repeat containing 3 (CEGF3), mRNA", gi|31377567|ref|NM_152753.2|[31377567]; 2784: NM_152754 , "Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain,", "secreted, (semaphorin) 3D (SEMA3D), mRNA", gi|41406085|ref|NM_152754.2|[41406085]; 2785: NM_152758 , "Homo sapiens hypothetical protein FLJ31657 (FLJ31657), mRNA", gi|40255134|ref|NM_152758.2|[40255134]; 2786: NM_152769 , "Homo sapiens hypothetical protein MGC40084 (MGC40084), mRNA", gi|22749502|ref|NM_152769.1|[22749502]; 2787: NM_152902 , "Homo sapiens putative MAPK activating protein (MGC3794), mRNA", gi|33239373|ref|NM_152902.2|[33239373]; 2788: NM_153045 , "Homo sapiens DKFZp547P234 protein (DKFZp547P234), mRNA", gi|33356141|ref|NM_153045.2|[33356141]; 2789: NM_153354 , "Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA", gi|34222213|ref|NM_153354.2|[34222213]; 2790: NM_153603 , "Homo sapiens component of oligomeric golgi complex 7 (COG7), mRNA", gi|23957689|ref|NM_153603.1|[23957689]; 2791: NM_153811 , "Homo sapiens solute carrier family 38, member 6 (SLC38A6), mRNA", gi|24429573|ref|NM_153811.1|[24429573]; 2792: NM_172341 , "Homo sapiens presenilin enhancer 2 (PEN2), mRNA", gi|28144919|ref|NM_172341.1|[28144919]; 2793: NM_173481 , "Homo sapiens hypothetical protein LOC126353 (LOC126353), mRNA", gi|34222226|ref|NM_173481.2|[34222226]; 2794: NM_173500 , "Homo sapiens tau tubulin kinase 2 (TTBK2), mRNA", gi|28466990|ref|NM_173500.2|[28466990]; 2795: NM_173509 , "Homo sapiens hypothetical protein MGC16664 (MGC16664), mRNA", gi|34222229|ref|NM_173509.2|[34222229]; 2796: NM_173562 , "Homo sapiens chromosome 6 open reading frame 69 (C6orf69), mRNA", gi|40255181|ref|NM_173562.3|[40255181]; 2797: NM_175066 , "Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 51 (DDX51), mRNA", gi|37059776|ref|NM_175066.2|[37059776]; 2798: NM_175886 , "Homo sapiens phosphoribosyl pyrophosphate synthetase 1-like 1 (PRPS1L1), mRNA", gi|31343499|ref|NM_175886.2|[31343499]; 2799: NM_177966 , "Homo sapiens hypothetical protein DKFZp667B1218 (DKFZp667B1218), mRNA", gi|34222255|ref|NM_177966.3|[34222255], ,

Table 13. Genes having both an Errα binding motif and a Gabpa binding motif

1: NM_000164 , "Homo sapiens gastric inhibitory polypeptide receptor (GIPR), mRNA", gi|4503998|ref|NM_000164.1|[4503998]; 2: NM_000183 , Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A, "thiolase/enoyl-Coenzyme A hydratase (trifunctional protein); beta subunit", "(HADHB), mRNA", gi|4504326|ref|NM_000183.1|[4504326]; 3: NM_000249 , "Homo sapiens mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli) (MLH1),", mRNA, gi|28559089|ref|NM_000249.2|[28559089]; 4: NM_000274 , "Homo sapiens ornithine aminotransferase (gyrate atrophy) (OAT), nuclear gene", "encoding mitochondrial protein, mRNA", gi|4557808|ref|NM_000274.1|[4557808]; 5: NM_000297 , "Homo sapiens polycystic kidney disease 2 (autosomal dominant) (PKD2), mRNA", gi|33286447|ref|NM_000297.2|[33286447]; 6: NM_000347 , "Homo sapiens spectrin, beta, erythrocytic (includes spherocytosis, clinical type", "I) (SPTB), mRNA", gi|22507315|ref|NM_000347.3|[22507315]; 7: NM_000364 , "Homo sapiens troponin T2, cardiac (TNNT2), mRNA", gi|4507626|ref|NM_000364.1|[4507626]; 8: NM_000403 , "Homo sapiens galactose-4-epimerase, UDP (GALE), mRNA", gi|9945333|ref|NM_000403.2|[9945333]; 9: NM_000474 , Homo sapiens twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome), "(Drosophila) (TWIST1), mRNA", gi|17978464|ref|NM_000474.2|[17978464]; 10: NM_000483 , "Homo sapiens apolipoprotein C-II (APOC2), mRNA", gi|32130517|ref|NM_000483.3|[32130517]; 11: NM_000499 , "Homo sapiens cytochrome P450, family 1, subfamily A, polypeptide 1 (CYP1A1),", mRNA, gi|13325053|ref|NM_000499.2|[13325053]; 12: NM_000526 , "Homo sapiens keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)", "(KRT14), mRNA", gi|15431309|ref|NM_000526.3|[15431309]; 13: NM_000593 , "Homo sapiens transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) (TAP1),", mRNA, gi|24797159|ref|NM_000593.4|[24797159]; 14: NM_000603 , "Homo sapiens nitric oxide synthase 3 (endothelial cell) (NOS3), mRNA", gi|40254421|ref|NM_000603.2|[40254421]; 15: NM_000628 , "Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA", gi|24430214|ref|NM_000628.3|[24430214]; 16: NM_000688 , "Homo sapiens aminolevulinate, delta-, synthase 1 (ALAS1), transcript variant 1,", mRNA, gi|40316942|ref|NM_000688.4|[40316942]; 17: NM_000747 , "Homo sapiens cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)", "(CHRNB1), mRNA", gi|41327725|ref|NM_000747.2|[41327725]; 18: NM_000781 , "Homo sapiens cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1),", "nuclear gene encoding mitochondrial protein, mRNA", gi|4503188|ref|NM_000781.1|[4503188]; 19: NM_000806 , "Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 1 (GABRA1), mRNA", gi|38327553|ref|NM_000806.3|[38327553]; 20: NM_000813 , "Homo sapiens gamma-aminobutyric acid (GABA) A receptor, beta 2 (GABRB2),", "transcript variant 2, mRNA", gi|4503864|ref|NM_000813.1|[4503864]; 21: NM_000835 , "Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2C (GRIN2C),", mRNA, gi|6006004|ref|NM_000835.2|[6006004]; 22: NM_000915 , "Homo sapiens oxytocin, prepro-(neurophysin I) (OXT), mRNA", gi|12707574|ref|NM_000915.2|[12707574]; 23: NM_000932 , "Homo sapiens phospholipase C, beta 3 (phosphatidylinositol-specific) (PLCB3),", mRNA, gi|11386138|ref|NM_000932.1|[11386138]; 24: NM_001040 , "Homo sapiens sex hormone-binding globulin (SHBG), mRNA", gi|7382459|ref|NM_001040.2|[7382459]; 25: NM_001087 ,

"Homo sapiens angio-associated, migratory cell protein (AAMP), mRNA", gi|4557228|ref|NM_001087.1|[4557228]; 26: NM_001094 , "Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1),", "transcript variant 2, mRNA", gi|34452696|ref|NM_001094.4|[34452696]; 27: NM_001099 , "Homo sapiens acid phosphatase, prostate (ACPP), mRNA", gi|6382063|ref|NM_001099.2|[6382063]; 28: NM_001104 , "Homo sapiens actinin, alpha 3 (ACTN3), mRNA", gi|4557240|ref|NM_001104.1|[4557240]; 29: NM_001158 , "Homo sapiens amine oxidase, copper containing 2 (retina-specific) (AOC2),", "transcript variant 1, mRNA", gi|6806880|ref|NM_001158.2|[6806880]; 30: NM_001164 , "Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 1", "(Fe65) (APBB1), transcript variant 1, mRNA", gi|22035552|ref|NM_001164.2|[22035552]; 31: NM_001188 , "Homo sapiens BCL2-antagonist/killer 1 (BAK1), mRNA", gi|33457353|ref|NM_001188.2|[33457353]; 32: NM_001257 , "Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA", gi|16507956|ref|NM_001257.2|[16507956]; 33: NM_001261 , "Homo sapiens cyclin-dependent kinase 9 (CDC2-related kinase) (CDK9), mRNA", gi|17017983|ref|NM_001261.2|[17017983]; 34: NM_001425 , "Homo sapiens epithelial membrane protein 3 (EMP3), mRNA", gi|4503562|ref|NM_001425.1|[4503562]; 35: NM_001501 , "Homo sapiens gonadotropin-releasing hormone 2 (GNRH2), transcript variant 1,", mRNA, gi|4504056|ref|NM_001501.1|[4504056]; 36: NM_001542 , "Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA", gi|4504626|ref|NM_001542.1|[4504626]; 37: NM_001662 , "Homo sapiens ADP-ribosylation factor 5 (ARF5), mRNA", gi|6995999|ref|NM_001662.2|[6995999]; 38: NM_001666 , "Homo sapiens Rho GTPase activating protein 4 (ARHGAP4), mRNA", gi|41327157|ref|NM_001666.2|[41327157]; 39: NM_001702 , "Homo sapiens brain-specific angiogenesis inhibitor 1 (BAI1), mRNA", gi|4502354|ref|NM_001702.1|[4502354]; 40: NM_001722 , "Homo sapiens polymerase (RNA) III (DNA directed) polypeptide D, 44kDa (POLR3D),", mRNA, gi|4502436|ref|NM_001722.1|[4502436]; 41: NM_001823 , "Homo sapiens creatine kinase, brain (CKB), mRNA", gi|34335231|ref|NM_001823.3|[34335231]; 42: NM_001859 , "Homo sapiens solute carrier family 31 (copper transporters), member 1 (SLC31A1),", mRNA, gi|40254457|ref|NM_001859.2|[40254457]; 43: NM_001864 , "Homo sapiens cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1),", mRNA, gi|18105034|ref|NM_001864.2|[18105034]; 44: NM_001887 , "Homo sapiens crystallin, beta B1 (CRYBB1), mRNA", gi|21536279|ref|NM_001887.3|[21536279]; 45: NM_001893 , "Homo sapiens casein kinase 1, delta (CSNK1D), transcript variant 1, mRNA", gi|20544143|ref|NM_001893.3|[20544143]; 46: NM_001895 , "Homo sapiens casein kinase 2, alpha 1 polypeptide (CSNK2A1), transcript variant", "2, mRNA", gi|29570794|ref|NM_001895.2|[29570794]; 47: NM_001923 , "Homo sapiens damage-specific DNA binding protein 1, 127kDa (DDB1), mRNA", gi|13435358|ref|NM_001923.2|[13435358]; 48: NM_001958 , "Homo sapiens eukaryotic translation elongation factor 1 alpha 2 (EEF1A2), mRNA", gi|25453470|ref|NM_001958.2|[25453470]; 49: NM_002010 , "Homo sapiens fibroblast growth factor 9 (glia-activating factor) (FGF9), mRNA", gi|4503706|ref|NM_002010.1|[4503706]; 50: NM_002012 , "Homo sapiens fragile histidine triad gene (FHIT), mRNA", gi|4503718|ref|NM_002012.1|[4503718]; 51: NM_002083 , "Homo sapiens glutathione peroxidase 2 (gastrointestinal) (GPX2), mRNA", gi|32967606|ref|NM_002083.2|[32967606]; 52: NM_002151 , "Homo sapiens hepsin (transmembrane protease, serine 1) (HPN), transcript variant", "2, mRNA", gi|4504480|ref|NM_002151.1|[4504480]; 53: NM_002157 , "Homo sapiens heat shock 10kDa

protein 1 (chaperonin 10) (HSPE1), mRNA", gi|4504522|ref|NM_002157.1|[4504522]; 54: NM_002193 , "Homo sapiens inhibin, beta B (activin AB beta polypeptide) (INHBB), mRNA", gi|9257224|ref|NM_002193.1|[9257224]; 55: NM_002217 , "Homo sapiens pre-alpha (globulin) inhibitor, H3 polypeptide (ITIH3), mRNA", gi|10092578|ref|NM_002217.1|[10092578]; 56: NM_002238 , "Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member", "1 (KCNH1), transcript variant 2, mRNA", gi|27436999|ref|NM_002238.2|[27436999]; 57: NM_002257 , "Homo sapiens kallikrein 1, renal/pancreas/salivary (KLK1), mRNA", gi|22027643|ref|NM_002257.2|[22027643]; 58: NM_002280 , "Homo sapiens keratin, hair, acidic, 5 (KRTHA5), mRNA", gi|15431313|ref|NM_002280.3|[15431313]; 59: NM_002378 , "Homo sapiens megakaryocyte-associated tyrosine kinase (MATK), transcript variant", "2, mRNA", gi|21450841|ref|NM_002378.2|[21450841]; 60: NM_002419 , "Homo sapiens mitogen-activated protein kinase kinase kinase 11 (MAP3K11), mRNA", gi|21735553|ref|NM_002419.2|[21735553]; 61: NM_002437 , "Homo sapiens MpV17 transgene, murine homolog, glomerulosclerosis (MPV17), mRNA", gi|37059781|ref|NM_002437.3|[37059781]; 62: NM_002492 , "Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa", "(NDUFB5), nuclear gene encoding mitochondrial protein, mRNA", gi|33519467|ref|NM_002492.2|[33519467]; 63: NM_002506 , "Homo sapiens nerve growth factor, beta polypeptide (NGFB), mRNA", gi|4505390|ref|NM_002506.1|[4505390]; 64: NM_002590 , "Homo sapiens protocadherin 8 (PCDH8), transcript variant 1, mRNA", gi|6631101|ref|NM_002590.2|[6631101]; 65: NM_002599 , "Homo sapiens phosphodiesterase 2A, cGMP-stimulated (PDE2A), mRNA", gi|4505656|ref|NM_002599.1|[4505656]; 66: NM_002630 , "Homo sapiens progastricsin (pepsinogen C) (PGC), mRNA", gi|4505756|ref|NM_002630.1|[4505756]; 67: NM_002831 , "Homo sapiens protein tyrosine phosphatase, non-receptor type 6 (PTPN6),", "transcript variant 1, mRNA", gi|34328900|ref|NM_002831.3|[34328900]; 68: NM_002832 , "Homo sapiens protein tyrosine phosphatase, non-receptor type 7 (PTPN7),", "transcript variant 1, mRNA", gi|18375657|ref|NM_002832.2|[18375657]; 69: NM_002904 , "Homo sapiens RD RNA binding protein (RDBP), mRNA", gi|20631983|ref|NM_002904.4|[20631983]; 70: NM_002912 , "Homo sapiens REV3-like, catalytic subunit of DNA polymerase zeta (yeast)", "(REV3L), mRNA", gi|4506482|ref|NM_002912.1|[4506482]; 71: NM_002930 , "Homo sapiens Ras-like without CAAX 2 (RIT2), mRNA", gi|4506532|ref|NM_002930.1|[4506532]; 72: NM_002938 , "Homo sapiens ring finger protein 4 (RNF4), mRNA", gi|34305289|ref|NM_002938.2|[34305289]; 73: NM_002965 , "Homo sapiens S100 calcium binding protein A9 (calgranulin B) (S100A9), mRNA", gi|9845520|ref|NM_002965.2|[9845520]; 74: NM_003002 , "Homo sapiens succinate dehydrogenase complex, subunit D, integral membrane", "protein (SDHD), nuclear gene encoding mitochondrial protein, mRNA", gi|4506864|ref|NM_003002.1|[4506864]; 75: NM_003042 , "Homo sapiens solute carrier family 6 (neurotransmitter transporter, GABA),", "member 1 (SLC6A1), mRNA", gi|40254466|ref|NM_003042.2|[40254466]; 76: NM_003055 , "Homo sapiens solute carrier family 18 (vesicular acetylcholine), member 3", "(SLC18A3), mRNA", gi|4506990|ref|NM_003055.1|[4506990]; 77: NM_003115 , "Homo sapiens UDP-N-acteylglucosamine pyrophosphorylase 1 (UAP1), mRNA", gi|34147515|ref|NM_003115.3|[34147515]; 78: NM_003159 , "Homo sapiens cyclin-dependent kinase-like 5 (CDKL5), mRNA", gi|4507280|ref|NM_003159.1|[4507280]; 79: NM_003216 , "Homo sapiens thyrotrophic embryonic factor (TEF), mRNA", gi|34486096|ref|NM_003216.2|[34486096]; 80: NM_003239 , "Homo sapiens transforming

growth factor, beta 3 (TGFB3), mRNA", gi|4507464|ref|NM_003239.1|[4507464]; 81: NM_003259 , "Homo sapiens intercellular adhesion molecule 5, telencephalin (ICAM5), mRNA", gi|12545403|ref|NM_003259.2|[12545403]; 82: NM_003325 , Homo sapiens HIR histone cell cycle regulation defective homolog A (S., "cerevisiae) (HIRA), mRNA", gi|21536484|ref|NM_003325.3|[21536484]; 83: NM_003334 , Homo sapiens ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature, "sensitivity complementing) (UBE1), transcript variant 1, mRNA", gi|23510337|ref|NM_003334.2|[23510337]; 84: NM_003341 , "Homo sapiens ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)", "(UBE2E1), transcript variant 1, mRNA", gi|33359692|ref|NM_003341.3|[33359692]; 85: NM_003374 , "Homo sapiens voltage-dependent anion channel 1 (VDAC1), mRNA", gi|4507878|ref|NM_003374.1|[4507878]; 86: NM_003418 , Homo sapiens zinc finger protein 9 (a cellular retroviral nucleic acid binding, "protein) (ZNF9), mRNA", gi|4827070|ref|NM_003418.1|[4827070]; 87: NM_003492 , "Homo sapiens chromosome X open reading frame 12 (CXorf12), mRNA", gi|4504738|ref|NM_003492.1|[4504738]; 88: NM_003524 , "Homo sapiens histone 1, H2bh (HIST1H2BH), mRNA", gi|21166386|ref|NM_003524.2|[21166386]; 89: NM_003549 , "Homo sapiens hyaluronoglucosaminidase 3 (HYAL3), mRNA", gi|15208650|ref|NM_003549.2|[15208650]; 90: NM_003554 , "Homo sapiens olfactory receptor, family 1, subfamily E, member 2 (OR1E2), mRNA", gi|11386152|ref|NM_003554.1|[11386152]; 91: NM_003594 , "Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA", gi|40807470|ref|NM_003594.3|[40807470]; 92: NM_003627 , "Homo sapiens solute carrier family 43, member 1 (SLC43A1), mRNA", gi|42476323|ref|NM_003627.4|[42476323]; 93: NM_003632 , "Homo sapiens contactin associated protein 1 (CNTNAP1), mRNA", gi|4505462|ref|NM_003632.1|[4505462]; 94: NM_003691 , "Homo sapiens serine/threonine kinase 16 (STK16), mRNA", gi|4505836|ref|NM_003691.1|[4505836]; 95: NM_003860 , "Homo sapiens barrier to autointegration factor 1 (BANF1), mRNA", gi|11038645|ref|NM_003860.2|[11038645]; 96: NM_003957 , "Homo sapiens serine/threonine kinase 29 (STK29), mRNA", gi|27501463|ref|NM_003957.1|[27501463]; 97: NM_004074 , "Homo sapiens cytochrome c oxidase subunit VIII (COX8), mRNA", gi|4758043|ref|NM_004074.1|[4758043]; 98: NM_004078 , "Homo sapiens cysteine and glycine-rich protein 1 (CSRP1), mRNA", gi|4758085|ref|NM_004078.1|[4758085]; 99: NM_004100 , "Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), transcript variant 1,", mRNA, gi|26667248|ref|NM_004100.2|[26667248]; 100: NM_004106 , "Homo sapiens Fc fragment of IgE, high affinity I, receptor for; gamma", "polypeptide (FCER1G), mRNA", gi|4758343|ref|NM_004106.1|[4758343]; 101: NM_004178 , "Homo sapiens TAR (HIV) RNA binding protein 2 (TARBP2), transcript variant 3,", mRNA, gi|19743837|ref|NM_004178.3|[19743837]; 102: NM_004260 , "Homo sapiens RecQ protein-like 4 (RECQL4), mRNA", gi|4759029|ref|NM_004260.1|[4759029]; 103: NM_004267 , "Homo sapiens carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 (CHST2),", mRNA, gi|27369496|ref|NM_004267.2|[27369496]; 104: NM_004294 , "Homo sapiens mitochondrial translational release factor 1 (MTRF1), nuclear gene", "encoding mitochondrial protein, mRNA", gi|34577119|ref|NM_004294.2|[34577119]; 105: NM_004344 , "Homo sapiens centrin, EF-hand protein, 2 (CETN2), mRNA", gi|4757901|ref|NM_004344.1|[4757901]; 106: NM_004358 , "Homo sapiens cell division cycle 25B (CDC25B), transcript variant 1, mRNA", gi|11641416|ref|NM_004358.2|[11641416]; 107: NM_004374 , "Homo sapiens cytochrome c oxidase subunit VIc (COX6C), mRNA", gi|17999531|ref|NM_004374.2|[17999531]; 108:

NM_004427 , "Homo sapiens polyhomeotic-like 2 (Drosophila) (PHC2), transcript variant 2, mRNA", gi|37595529|ref|NM_004427.2|[37595529]; 109: NM_004470 , "Homo sapiens FK506 binding protein 2, 13kDa (FKBP2), transcript variant 1, mRNA", gi|17149841|ref|NM_004470.2|[17149841]; 110: NM_004528 , "Homo sapiens microsomal glutathione S-transferase 3 (MGST3), mRNA", gi|22035640|ref|NM_004528.2|[22035640]; 111: NM_004550 , "Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa", "(NADH-coenzyme Q reductase) (NDUFS2), mRNA", gi|34147556|ref|NM_004550.3|[34147556]; 112: NM_004604 , "Homo sapiens syntaxin 4A (placental) (STX4A), mRNA", gi|34147603|ref|NM_004604.3|[34147603]; 113: NM_004656 , Homo sapiens BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase), "(BAP1), mRNA", gi|19718752|ref|NM_004656.2|[19718752]; 114: NM_004672 , "Homo sapiens mitogen-activated protein kinase kinase kinase 6 (MAP3K6),", "transcript variant 1, mRNA", gi|24497521|ref|NM_004672.2|[24497521]; 115: NM_004704 , "Homo sapiens RNA, U3 small nucleolar interacting protein 2 (RNU3IP2), mRNA", gi|31543556|ref|NM_004704.2|[31543556]; 116: NM_004870 , "Homo sapiens mannose-P-dolichol utilization defect 1 (MPDU1), mRNA", gi|4759109|ref|NM_004870.1|[4759109]; 117: NM_004913 , "Homo sapiens chromosome 16 open reading frame 7 (C16orf7), mRNA", gi|4757805|ref|NM_004913.1|[4757805]; 118: NM_004927 , "Homo sapiens mitochondrial ribosomal protein L49 (MRPL49), nuclear gene encoding", "mitochondrial protein, mRNA", gi|27436906|ref|NM_004927.2|[27436906]; 119: NM_004941 , "Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 8 (DHX8), mRNA", gi|4826689|ref|NM_004941.1|[4826689]; 120: NM_004959 , "Homo sapiens nuclear receptor subfamily 5, group A, member 1 (NR5A1), mRNA", gi|24432033|ref|NM_004959.3|[24432033]; 121: NM_004987 , "Homo sapiens LIM and senescent cell antigen-like domains 1 (LIMS1), mRNA", gi|13518025|ref|NM_004987.2|[13518025]; 122: NM_004994 , "Homo sapiens matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa", "type IV collagenase) (MMP9), mRNA", gi|4826835|ref|NM_004994.1|[4826835]; 123: NM_005006 , "Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa", "(NADH-coenzyme Q reductase) (NDUFS1), nuclear gene encoding mitochondrial", "protein, mRNA", gi|33519474|ref|NM_005006.5|[33519474]; 124: NM_005023 , "Homo sapiens protein geranylgeranyltransferase type I, beta subunit (PGGT1B),", mRNA, gi|27597101|ref|NM_005023.2|[27597101]; 125: NM_005027 , "Homo sapiens phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85", "beta) (PIK3R2), mRNA", gi|4826907|ref|NM_005027.1|[4826907]; 126: NM_005124 , "Homo sapiens nucleoporin 153kDa (NUP153), mRNA", gi|24430145|ref|NM_005124.2|[24430145]; 127: NM_005125 , "Homo sapiens copper chaperone for superoxide dismutase (CCS), mRNA", gi|4826664|ref|NM_005125.1|[4826664]; 128: NM_005154 , "Homo sapiens ubiquitin specific protease 8 (USP8), mRNA", gi|41281375|ref|NM_005154.2|[41281375]; 129: NM_005161 , "Homo sapiens angiotensin II receptor-like 1 (AGTRL1), mRNA", gi|34577064|ref|NM_005161.2|[34577064]; 130: NM_005182 , "Homo sapiens carbonic anhydrase VII (CA7), mRNA", gi|4885100|ref|NM_005182.1|[4885100]; 131: NM_005186 , "Homo sapiens calpain 1, (mu/I) large subunit (CAPN1), mRNA", gi|12408655|ref|NM_005186.2|[12408655]; 132: NM_005223 , "Homo sapiens deoxyribonuclease I (DNASE1), mRNA", gi|21361253|ref|NM_005223.2|[21361253]; 133: NM_005260 , "Homo sapiens growth differentiation factor 9 (GDF9), mRNA", gi|6715598|ref|NM_005260.2|[6715598]; 134: NM_005286 , "Homo sapiens G protein-coupled receptor 8 (GPR8), mRNA", gi|30581163|ref|NM_005286.2|[30581163]; 135: NM_005288 ,

"Homo sapiens G protein-coupled receptor 12 (GPR12), mRNA", gi|4885294|ref|NM_005288.1|[4885294]; 136: NM_005302 , Homo sapiens G protein-coupled receptor 37 (endothelin receptor type B-like), "(GPR37), mRNA", gi|31377788|ref|NM_005302.2|[31377788]; 137: NM_005306 , "Homo sapiens G protein-coupled receptor 43 (GPR43), mRNA", gi|4885332|ref|NM_005306.1|[4885332]; 138: NM_005341 , "Homo sapiens GLI-Kruppel family member HKR3 (HKR3), mRNA", gi|4885418|ref|NM_005341.1|[4885418]; 139: NM_005393 , "Homo sapiens plexin B3 (PLXNB3), mRNA", gi|10864080|ref|NM_005393.1|[10864080]; 140: NM_005398 , "Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3C (PPP1R3C),", mRNA, gi|42476161|ref|NM_005398.3|[42476161]; 141: NM_005418 , "Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 1, mRNA", gi|21264611|ref|NM_005418.2|[21264611]; 142: NM_005453 , "Homo sapiens zinc finger protein 297 (ZNF297), mRNA", gi|20070223|ref|NM_005453.3|[20070223]; 143: NM_005475 , "Homo sapiens lymphocyte adaptor protein (LNK), mRNA", gi|4885454|ref|NM_005475.1|[4885454]; 144: NM_005485 , Homo sapiens ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)-like 3, "(ADPRTL3), mRNA", gi|11496992|ref|NM_005485.2|[11496992]; 145: NM_005550 , "Homo sapiens kinesin family member C3 (KIFC3), mRNA", gi|19923320|ref|NM_005550.2|[19923320]; 146: NM_005560 , "Homo sapiens laminin, alpha 5 (LAMA5), mRNA", gi|21264601|ref|NM_005560.3|[21264601]; 147: NM_005563 , "Homo sapiens stathmin 1/oncoprotein 18 (STMN1), mRNA", gi|13518023|ref|NM_005563.2|[13518023]; 148: NM_005626 , "Homo sapiens splicing factor, arginine/serine-rich 4 (SFRS4), mRNA", gi|34147660|ref|NM_005626.3|[34147660]; 149: NM_005634 , "Homo sapiens SRY (sex determining region Y)-box 3 (SOX3), mRNA", gi|30061555|ref|NM_005634.2|[30061555]; 150: NM_005698 , "Homo sapiens secretory carrier membrane protein 3 (SCAMP3), transcript variant", "1, mRNA", gi|16445418|ref|NM_005698.2|[16445418]; 151: NM_005716 , Homo sapiens regulator of G-protein signalling 19 interacting protein 1, "(RGS19IP1), transcript variant 1, mRNA", gi|42544147|ref|NM_005716.2|[42544147]; 152: NM_005726 , "Homo sapiens Ts translation elongation factor, mitochondrial (TSFM), mRNA", gi|21361279|ref|NM_005726.2|[21361279]; 153: NM_005727 , "Homo sapiens tetraspan 1 (TSPAN-1), mRNA", gi|21264577|ref|NM_005727.2|[21264577]; 154: NM_005845 , "Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4),", mRNA, gi|34452699|ref|NM_005845.2|[34452699]; 155: NM_005860 , "Homo sapiens follistatin-like 3 (secreted glycoprotein) (FSTL3), mRNA", gi|5031700|ref|NM_005860.1|[5031700]; 156: NM_005909 , "Homo sapiens microtubule-associated protein 1B (MAP1B), transcript variant 1,", mRNA, gi|14165457|ref|NM_005909.2|[14165457]; 157: NM_005965 , "Homo sapiens myosin, light polypeptide kinase (MYLK), transcript variant 6, mRNA", gi|16950600|ref|NM_005965.2|[16950600]; 158: NM_005984 , Homo sapiens solute carrier family 25 (mitochondrial carrier; citrate, "transporter), member 1 (SLC25A1), mRNA", gi|21389314|ref|NM_005984.1|[21389314]; 159: NM_006017 , "Homo sapiens prominin 1 (PROM1), mRNA", gi|5174386|ref|NM_006017.1|[5174386]; 160: NM_006067 , "Homo sapiens neighbor of COX4 (NOC4), mRNA", gi|34147520|ref|NM_006067.3|[34147520]; 161: NM_006090 , "Homo sapiens choline/ethanolaminephosphotransferase (CEPT1), mRNA", gi|21735567|ref|NM_006090.2|[21735567]; 162: NM_006091 , "Homo sapiens coronin, actin binding protein, 2B (CORO2B), mRNA", gi|24307902|ref|NM_006091.1|[24307902]; 163: NM_006114 , Homo sapiens translocase of outer mitochondrial membrane 40 homolog (yeast),

"(TOMM40), mRNA", gi|5174722|ref|NM_006114.1|[5174722]; 164: NM_006157 , "Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA", gi|5453763|ref|NM_006157.1|[5453763]; 165: NM_006172 , "Homo sapiens natriuretic peptide precursor A (NPPA), mRNA", gi|23510318|ref|NM_006172.1|[23510318]; 166: NM_006196 , "Homo sapiens poly(rC) binding protein 1 (PCBP1), mRNA", gi|14141164|ref|NM_006196.2|[14141164]; 167: NM_006205 , "Homo sapiens phosphodiesterase 6H, cGMP-specific, cone, gamma (PDE6H), mRNA", gi|5453867|ref|NM_006205.1|[5453867]; 168: NM_006228 , "Homo sapiens prepronociceptin (PNOC), mRNA", gi|11079650|ref|NM_006228.2|[11079650]; 169: NM_006261 , "Homo sapiens prophet of Pit1, paired-like homeodomain transcription factor", "(PROP1), mRNA", gi|40254838|ref|NM_006261.2|[40254838]; 170: NM_006289 , "Homo sapiens talin 1 (TLN1), mRNA", gi|16753232|ref|NM_006289.2|[16753232]; 171: NM_006365 , "Homo sapiens transcriptional activator of the c-fos promoter (CROC4), mRNA", gi|5453624|ref|NM_006365.1|[5453624]; 172: NM_006368 , "Homo sapiens cAMP responsive element binding protein 3 (CREB3), mRNA", gi|38327637|ref|NM_006368.4|[38327637]; 173: NM_006399 , "Homo sapiens basic leucine zipper transcription factor, ATF-like (BATF), mRNA", gi|18375640|ref|NM_006399.2|[18375640]; 174: NM_006477 , "Homo sapiens RAS-related on chromosome 22 (RRP22), mRNA", gi|42476128|ref|NM_006477.2|[42476128]; 175: NM_006698 , "Homo sapiens bladder cancer associated protein (BLCAP), mRNA", gi|5729737|ref|NM_006698.1|[5729737]; 176: NM_006747 , "Homo sapiens signal-induced proliferation-associated gene 1 (SIPA1), transcript", "variant 2, mRNA", gi|24497626|ref|NM_006747.2|[24497626]; 177: NM_006764 , "Homo sapiens interferon-related developmental regulator 2 (IFRD2), mRNA", gi|21361365|ref|NM_006764.2|[21361365]; 178: NM_006813 , "Homo sapiens proline-rich nuclear receptor coactivator 1 (PNRC1), mRNA", gi|5802981|ref|NM_006813.1|[5802981]; 179: NM_006841 , "Homo sapiens solute carrier family 38, member 3 (SLC38A3), mRNA", gi|40795668|ref|NM_006841.3|[40795668]; 180: NM_006876 , "Homo sapiens UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6", "(B3GNT6), mRNA", gi|5802983|ref|NM_006876.1|[5802983]; 181: NM_006917 , "Homo sapiens retinoid X receptor, gamma (RXRG), mRNA", gi|21361386|ref|NM_006917.2|[21361386]; 182: NM_006923 , "Homo sapiens stromal cell-derived factor 2 (SDF2), mRNA", gi|14141194|ref|NM_006923.2|[14141194]; 183: NM_006946 , "Homo sapiens spectrin, beta, non-erythrocytic 2 (SPTBN2), mRNA", gi|5902121|ref|NM_006946.1|[5902121]; 184: NM_006982 , "Homo sapiens cartilage paired-class homeoprotein 1 (CART1), mRNA", gi|5901917|ref|NM_006982.1|[5901917]; 185: NM_006998 , "Homo sapiens secretagogin, EF-hand calcium binding protein (SCGN), mRNA", gi|15055536|ref|NM_006998.2|[15055536]; 186: NM_007022 , "Homo sapiens putative tumor suppressor 101F6 (101F6), mRNA", gi|31541779|ref|NM_007022.3|[31541779]; 187: NM_007046 , "Homo sapiens elastin microfibril interfacer 1 (EMILIN1), mRNA", gi|5901943|ref|NM_007046.1|[5901943]; 188: NM_007076 , , ref|NM_007076.2|[42794619]; 189: NM_007149 , "Homo sapiens zinc finger protein 184 (Kruppel-like) (ZNF184), mRNA", gi|24307934|ref|NM_007149.1|[24307934]; 190: NM_007357 , "Homo sapiens component of oligomeric golgi complex 2 (COG2), mRNA", gi|6678675|ref|NM_007357.1|[6678675]; 191: NM_012105 , "Homo sapiens beta-site APP-cleaving enzyme 2 (BACE2), transcript variant a, mRNA", gi|21040358|ref|NM_012105.3|[21040358]; 192: NM_012164 , "Homo sapiens F-box and WD-40 domain protein 2 (FBXW2), mRNA", gi|7549806|ref|NM_012164.2|[7549806]; 193: NM_012168 , "Homo sapiens F-box only protein 2 (FBXO2), mRNA", gi|15812197|ref|NM_012168.2|[15812197]; 194: NM_012191 , "Homo sapiens putative tumor

suppressor (FUS2), mRNA", gi|6912379|ref|NM_012191.1|[6912379]; 195: NM_012204 , "Homo sapiens general transcription factor IIIC, polypeptide 4, 90kDa (GTF3C4),", mRNA, gi|6912399|ref|NM_012204.1|[6912399]; 196: NM_012285 , "Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member", "4 (KCNH4), mRNA", gi|6912445|ref|NM_012285.1|[6912445]; 197: NM_012311 , "Homo sapiens KIN, antigenic determinant of recA protein homolog (mouse) (KIN),", mRNA, gi|40068516|ref|NM_012311.2|[40068516]; 198: NM_012430 , "Homo sapiens SEC22 vesicle trafficking protein-like 2 (S. cerevisiae) (SEC22L2),", mRNA, gi|14591918|ref|NM_012430.2|[14591918]; 199: NM_012459 , Homo sapiens translocase of inner mitochondrial membrane 8 homolog B (yeast), "(TIMM8B), mRNA", gi|6912711|ref|NM_012459.1|[6912711]; 200: NM_012460 , Homo sapiens translocase of inner mitochondrial membrane 9 homolog (yeast), "(TIMM9), mRNA", gi|21359892|ref|NM_012460.2|[21359892]; 201: NM_012482 , "Homo sapiens zinc finger protein 281 (ZNF281), mRNA", gi|40255235|ref|NM_012482.3|[40255235]; 202: NM_013235 , "Homo sapiens nuclear RNase III Drosha (RNASE3L), mRNA", gi|21359821|ref|NM_013235.2|[21359821]; 203: NM_013333 , "Homo sapiens epsin 1 (EPN1), mRNA", gi|41350200|ref|NM_013333.2|[41350200]; 204: NM_013335 , "Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA), mRNA", gi|31881778|ref|NM_013335.2|[31881778]; 205: NM_013343 , "Homo sapiens loss of heterozygosity, 3, chromosomal region 2, gene A (LOH3CR2A),", mRNA, gi|7106370|ref|NM_013343.1|[7106370]; 206: NM_013387 , "Homo sapiens ubiquinol-cytochrome c reductase complex (7.2 kD) (HSPC051), mRNA", gi|41281884|ref|NM_013387.2|[41281884]; 207: NM_013403 , "Homo sapiens striatin, calmodulin binding protein 4 (STRN4), mRNA", gi|7019572|ref|NM_013403.1|[7019572]; 208: NM_013441 , "Homo sapiens Down syndrome critical region gene 1-like 2 (DSCR1L2), mRNA", gi|38455419|ref|NM_013441.2|[38455419]; 209: NM_014099 , , ref|NM_014099.1|[7662610], This record was temporarily removed by RefSeq staff for additional review., , 210: NM_014124 , , ref|NM_014124.1|[7662541], This record was temporarily removed by RefSeq staff for additional review., , 211: NM_014165 , "Homo sapiens chromosome 6 open reading frame 66 (C6orf66), mRNA", gi|7661785|ref|NM_014165.1|[7661785]; 212: NM_014236 , "Homo sapiens glyceronephosphate O-acyltransferase (GNPAT), mRNA", gi|7657133|ref|NM_014236.1|[7657133]; 213: NM_014301 , "Homo sapiens nitrogen fixation cluster-like (NIFU), mRNA", gi|24307952|ref|NM_014301.1|[24307952]; 214: NM_014342 , "Homo sapiens mitochondrial carrier homolog 2 (C. elegans) (MTCH2), nuclear gene", "encoding mitochondrial protein, mRNA", gi|40254847|ref|NM_014342.2|[40254847]; 215: NM_014348 , "Homo sapiens POM121 membrane glycoprotein-like 1 (rat) (POM121L1), mRNA", gi|7657468|ref|NM_014348.1|[7657468]; 216: NM_014453 , "Homo sapiens putative breast adenocarcinoma marker (32kD) (BC-2), transcript", "variant 1, mRNA", gi|38372936|ref|NM_014453.2|[38372936]; 217: NM_014548 , "Homo sapiens tropomodulin 2 (neuronal) (TMOD2), mRNA", gi|40789262|ref|NM_014548.2|[40789262]; 218: NM_014606 , , ref|NM_014606.1|[7657151], This record was temporarily removed by RefSeq staff for additional review., , 219: NM_014662 , , ref|NM_014662.1|[7662221], This record was temporarily removed by RefSeq staff for additional review., , 220: NM_014674 , , ref|NM_014674.1|[7662001], This record was temporarily removed by RefSeq staff for additional review., , 221: NM_014748 , "Homo sapiens sorting nexin 17 (SNX17), mRNA", gi|23238249|ref|NM_014748.2|[23238249]; 222: NM_014786 , "Homo sapiens Rho guanine

nucleotide exchange factor (GEF) 17 (ARHGEF17), mRNA", gi|21361457|ref|NM_014786.2|[21361457]; 223: NM_014813 , , ref|NM_014813.1|[7662319], This record was temporarily removed by RefSeq staff for additional review., , 224: NM_014814 , "Homo sapiens proteasome regulatory particle subunit p44S10 (p44S10), mRNA", gi|7661913|ref|NM_014814.1|[7661913]; 225: NM_014901 , "Homo sapiens ring finger protein 44 (RNF44), mRNA", gi|42718018|ref|NM_014901.4|[42718018]; 226: NM_014907 , "Homo sapiens FERM and PDZ domain containing 1 (FRMPD1), mRNA", gi|7662415|ref|NM_014907.1|[7662415]; 227: NM_015089 , "Homo sapiens p53-associated parkin-like cytoplasmic protein (PARC), mRNA", gi|24307990|ref|NM_015089.1|[24307990]; 228: NM_015163 , "Homo sapiens tripartite motif-containing 9 (TRIM9), transcript variant 1, mRNA", gi|29543553|ref|NM_015163.3|[29543553]; 229: NM_015343 , "Homo sapiens dullard homolog (Xenopus laevis) (DULLARD), mRNA", gi|34222318|ref|NM_015343.3|[34222318]; 230: NM_015362 , , ref|NM_015362.3|[44662829]; 231: NM_015372 , "Homo sapiens hypothetical protein HSN44A4A (HSN44A4A), mRNA", gi|7661723|ref|NM_015372.1|[7661723]; 232: NM_015480 , "Homo sapiens poliovirus receptor-related 3 (PVRL3), mRNA", gi|11386198|ref|NM_015480.1|[11386198]; 233: NM_015623 , , ref|NM_015623.2|[32306520], This record was temporarily removed by RefSeq staff for additional review., , 234: NM_015710 , "Homo sapiens glioma tumor suppressor candidate region gene 2 (GLTSCR2), mRNA", gi|21359905|ref|NM_015710.2|[21359905]; 235: NM_015926 , "Homo sapiens putative secreted protein ZSIG11 (ZSIG11), mRNA", gi|34147580|ref|NM_015926.3|[34147580]; 236: NM_015964 , "Homo sapiens brain specific protein (CGI-38), mRNA", gi|7706275|ref|NM_015964.1|[7706275]; 237: NM_016004 , "Homo sapiens chromosome 20 open reading frame 9 (C20orf9), mRNA", gi|7705768|ref|NM_016004.1|[7705768]; 238: NM_016067 , "Homo sapiens mitochondrial ribosomal protein S18C (MRPS18C), nuclear gene", "encoding mitochondrial protein, mRNA", gi|7705629|ref|NM_016067.1|[7705629]; 239: NM_016082 , "Homo sapiens CDK5 regulatory subunit associated protein 1 (CDK5RAP1), transcript", "variant 2, mRNA", gi|28872783|ref|NM_016082.3|[28872783]; 240: NM_016090 , "Homo sapiens RNA binding motif protein 7 (RBM7), mRNA", gi|31543547|ref|NM_016090.2|[31543547]; 241: NM_016187 , "Homo sapiens bridging integrator 2 (BIN2), mRNA", gi|7705295|ref|NM_016187.1|[7705295]; 242: NM_016210 , "Homo sapiens g20 protein (LOC51161), mRNA", gi|31543080|ref|NM_016210.2|[31543080]; 243: NM_016231 , "Homo sapiens nemo like kinase (NLK), mRNA", gi|42734431|ref|NM_016231.2|[42734431]; 244: NM_016324 , "Homo sapiens zinc finger protein 274 (ZNF274), transcript variant ZNF274b, mRNA", gi|19743797|ref|NM_016324.2|[19743797]; 245: NM_016368 , "Homo sapiens myo-inositol 1-phosphate synthase A1 (ISYNA1), mRNA", gi|21902536|ref|NM_016368.3|[21902536]; 246: NM_017582 , "Homo sapiens ubiquitin-conjugating enzyme E2Q (putative) (UBE2Q), mRNA", gi|38045949|ref|NM_017582.5|[38045949]; 247: NM_017704 , "Homo sapiens fetal globin-inducing factor (FGIF), mRNA", gi|41350197|ref|NM_017704.2|[41350197]; 248: NM_017740 , "Homo sapiens zinc finger, DHHC domain containing 7 (ZDHHC7), mRNA", gi|8923254|ref|NM_017740.1|[8923254]; 249: NM_017745 , "Homo sapiens BCL6 co-repressor (BCOR), transcript variant 1, mRNA", gi|21071036|ref|NM_017745.4|[21071036]; 250: NM_017746 , "Homo sapiens testis expressed gene 10 (TEX10), mRNA", gi|8923268|ref|NM_017746.1|[8923268]; 251: NM_017806 , "Homo sapiens hypothetical protein FLJ20406 (FLJ20406), mRNA", gi|8923377|ref|NM_017806.1|[8923377]; 252:

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protein 4 (PCBP4), transcript variant 1, mRNA", gi|14670367|ref|NM_020418.2|[14670367]; 282: NM_020465 , "Homo sapiens NDRG family member 4 (NDRG4), mRNA", gi|14165263|ref|NM_020465.1|[14165263]; 283: NM_020999 , "Homo sapiens neurogenin 3 (NEUROG3), mRNA", gi|10337610|ref|NM_020999.1|[10337610]; 284: NM_021018 , "Homo sapiens histone 1, H3f (HIST1H3F), mRNA", gi|21396497|ref|NM_021018.2|[21396497]; 285: NM_021025 , "Homo sapiens T-cell leukemia, homeobox 3 (TLX3), mRNA", gi|10440563|ref|NM_021025.1|[10440563]; 286: NM_021062 , "Homo sapiens histone 1, H2bb (HIST1H2BB), mRNA", gi|19924303|ref|NM_021062.2|[19924303]; 287: NM_021161 , "Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), transcript", "variant 1, mRNA", gi|20143942|ref|NM_021161.3|[20143942]; 288: NM_021174 , "Homo sapiens p30 DBC protein (DBC-1), transcript variant 1, mRNA", gi|40548406|ref|NM_021174.4|[40548406]; 289: NM_021184 , "Homo sapiens chromosome 6 open reading frame 47 (C6orf47), mRNA", gi|10863984|ref|NM_021184.1|[10863984]; 290: NM_021249 , "Homo sapiens sorting nexin 6 (SNX6), transcript variant 1, mRNA", gi|23111048|ref|NM_021249.2|[23111048]; 291: NM_021259 , "Homo sapiens transmembrane protein 8 (five membrane-spanning domains) (TMEM8),", mRNA, gi|10864068|ref|NM_021259.1|[10864068]; 292: NM_021812 , "Homo sapiens blepharophimosis, epicanthus inversus and ptosis, candidate 1", "(BPESC1), mRNA", gi|11141882|ref|NM_021812.1|[11141882]; 293: NM_021830 , "Homo sapiens progressive external ophthalmoplegia 1 (PEO1), mRNA", gi|39725941|ref|NM_021830.3|[39725941]; 294: NM_021833 , "Homo sapiens uncoupling protein 1 (mitochondrial, proton carrier) (UCP1),", "nuclear gene encoding mitochondrial protein, mRNA", gi|21614550|ref|NM_021833.3|[21614550]; 295: NM_021926 , "Homo sapiens aristaless-like homeobox 4 (ALX4), mRNA", gi|11496266|ref|NM_021926.1|[11496266]; 296: NM_021934 , "Homo sapiens hypothetical protein FLJ11773 (FLJ11773), mRNA", gi|34222337|ref|NM_021934.3|[34222337]; 297: NM_022039 , "Homo sapiens split hand/foot malformation (ectrodactyly) type 3 (SHFM3), mRNA", gi|24475655|ref|NM_022039.2|[24475655]; 298: NM_022054 , "Homo sapiens potassium channel, subfamily K, member 13 (KCNK13), mRNA", gi|16306554|ref|NM_022054.2|[16306554]; 299: NM_022064 , "Homo sapiens ring finger protein 123 (RNF123), mRNA", gi|37588868|ref|NM_022064.2|[37588868]; 300: NM_022082 , "Homo sapiens chromosome 20 open reading frame 59 (C20orf59), mRNA", gi|31542262|ref|NM_022082.2|[31542262]; 301: NM_022114 , "Homo sapiens PR domain containing 16 (PRDM16), transcript variant 1, mRNA", gi|41349469|ref|NM_022114.2|[41349469]; 302: NM_022120 , "Homo sapiens 3-oxoacid CoA transferase 2 (OXCT2), mRNA", gi|11545840|ref|NM_022120.1|[11545840]; 303: NM_022135 , "Homo sapiens popeye domain containing 2 (POPDC2), mRNA", gi|22209003|ref|NM_022135.2|[22209003]; 304: NM_022354 , "Homo sapiens spermatogenesis associated 1 (SPATA1), mRNA", gi|11641266|ref|NM_022354.1|[11641266]; 305: NM_022452 , "Homo sapiens fibrosin 1 (FBS1), mRNA", gi|11967986|ref|NM_022452.1|[11967986]; 306: NM_022494 , "Homo sapiens zinc finger, DHHC domain containing 6 (ZDHHC6), mRNA", gi|11968052|ref|NM_022494.1|[11968052]; 307: NM_022727 , "Homo sapiens HpaII tiny fragments locus 9C (HTF9C), transcript variant 2, mRNA", gi|21361611|ref|NM_022727.3|[21361611]; 308: NM_022754 , "Homo sapiens sideroflexin 1 (SFXN1), mRNA", gi|40255158|ref|NM_022754.4|[40255158]; 309: NM_022765 , Homo sapiens NEDD9 interacting protein with calponin homology and LIM domains, "(NICAL), mRNA", gi|20127615|ref|NM_022765.2|[20127615]; 310: NM_022766 , "Homo sapiens

ceramide kinase (CERK), transcript variant 1, mRNA", gi|32967301|ref|NM_022766.4|[32967301]; 311: NM_023933 , "Homo sapiens hypothetical protein MGC2494 (MGC2494), mRNA", gi|13027599|ref|NM_023933.1|[13027599]; 312: NM_024034 , Homo sapiens ganglioside-induced differentiation-associated protein 1-like 1, "(GDAP1L1), mRNA", gi|30581159|ref|NM_024034.3|[30581159]; 313: NM_024057 , "Homo sapiens nucleoporin Nup37 (Nup37), mRNA", gi|34222120|ref|NM_024057.2|[34222120]; 314: NM_024294 , "Homo sapiens hypothetical protein MGC4614 (MGC4614), mRNA", gi|13236513|ref|NM_024294.1|[13236513]; 315: NM_024323 , "Homo sapiens hypothetical protein MGC11271 (MGC11271), mRNA", gi|31543147|ref|NM_024323.3|[31543147]; 316: NM_024506 , "Homo sapiens galactosidase, beta 1-like (GLB1L), mRNA", gi|40255042|ref|NM_024506.3|[40255042]; 317: NM_024523 , "Homo sapiens GRIP and coiled-coil domain-containing 1 (GCC1), mRNA", gi|34305454|ref|NM_024523.5|[34305454]; 318: NM_024546 , "Homo sapiens chromosome 13 open reading frame 7 (C13orf7), mRNA", gi|21362045|ref|NM_024546.2|[21362045]; 319: NM_024589 , "Homo sapiens leucine zipper domain protein (FLJ22386), mRNA", gi|13375778|ref|NM_024589.1|[13375778]; 320: NM_024604 , "Homo sapiens hypothetical protein FLJ21908 (FLJ21908), mRNA", gi|13375808|ref|NM_024604.1|[13375808]; 321: NM_024624 , Homo sapiens SMC6 structural maintenance of chromosomes 6-like 1 (yeast), "(SMC6L1), mRNA", gi|31543646|ref|NM_024624.2|[31543646]; 322: NM_024630 , "Homo sapiens zinc finger, DHHC domain containing 14 (ZDHHC14), mRNA", gi|24371240|ref|NM_024630.2|[24371240]; 323: NM_024643 , "Homo sapiens chromosome 14 open reading frame 140 (C14orf140), mRNA", gi|13375882|ref|NM_024643.1|[13375882]; 324: NM_024696 , "Homo sapiens hypothetical protein FLJ23058 (FLJ23058), mRNA", gi|13375978|ref|NM_024696.1|[13375978]; 325: NM_024728 , "Homo sapiens chromosome 7 open reading frame 10 (C7orf10), mRNA", gi|13376041|ref|NM_024728.1|[13376041]; 326: NM_024731 , "Homo sapiens chromosome 16 open reading frame 44 (C16orf44), mRNA", gi|31542245|ref|NM_024731.2|[31542245]; 327: NM_024778 , "Homo sapiens ring finger protein 127 (RNF127), mRNA", gi|37622895|ref|NM_024778.3|[37622895]; 328: NM_024783 , "Homo sapiens hypothetical protein FLJ23598 (FLJ23598), mRNA", gi|31657118|ref|NM_024783.2|[31657118]; 329: NM_024799 , "Homo sapiens hypothetical protein FLJ13224 (FLJ13224), mRNA", gi|13376172|ref|NM_024799.1|[13376172]; 330: NM_024827 , "Homo sapiens histone deacetylase 11 (HDAC11), mRNA", gi|13376227|ref|NM_024827.1|[13376227]; 331: NM_024958 , "Homo sapiens chromosome 20 open reading frame 98 (C20orf98), mRNA", gi|13376446|ref|NM_024958.1|[13376446]; 332: NM_025079 , "Homo sapiens hypothetical protein FLJ23231 (FLJ23231), mRNA", gi|13376631|ref|NM_025079.1|[13376631]; 333: NM_025137 , "Homo sapiens hypothetical protein FLJ21439 (FLJ21439), mRNA", gi|33636747|ref|NM_025137.2|[33636747]; 334: NM_025140 , "Homo sapiens limkain beta 2 (FLJ22471), mRNA", gi|13376724|ref|NM_025140.1|[13376724]; 335: NM_025212 , "Homo sapiens CXXC finger 4 (CXXC4), mRNA", gi|13376815|ref|NM_025212.1|[13376815]; 336: NM_025236 , "Homo sapiens ring finger protein 39 (RNF39), transcript variant 1, mRNA", gi|25777714|ref|NM_025236.2|[25777714]; 337: NM_030804 , , ref|NM_030804.1|[13540591], This record was temporarily removed by RefSeq staff for additional review., ; 338: NM_030818 , "Homo sapiens hypothetical protein MGC10471 (MGC10471), mRNA", gi|34147391|ref|NM_030818.2|[34147391]; 339: NM_031219 , "Homo sapiens hypothetical protein MGC12904 (MGC12904), mRNA", gi|31377665|ref|NM_031219.2|[31377665]; 340:

NM_031284 , "Homo sapiens ATP-dependent glucokinase (ADP-GK), mRNA", gi|31542508|ref|NM_031284.3|[31542508]; 341: NM_031298 , "Homo sapiens hypothetical protein MGC2963 (MGC2963), mRNA", gi|13775219|ref|NM_031298.1|[13775219]; 342: NM_031450 , "Homo sapiens hypothetical protein p5326 (P5326), mRNA", gi|31543378|ref|NM_031450.2|[31543378]; 343: NM_032179 , "Homo sapiens hypothetical protein FLJ20542 (FLJ20542), mRNA", gi|14149862|ref|NM_032179.1|[14149862]; 344: NM_032204 , "Homo sapiens ASC-1 complex subunit P100 (ASC1p100), mRNA", gi|34147616|ref|NM_032204.3|[34147616]; 345: NM_032209 , "Homo sapiens hypothetical protein FLJ21777 (FLJ21777), mRNA", gi|14149905|ref|NM_032209.1|[14149905]; 346: NM_032338 , "Homo sapiens hypothetical protein MGC14817 (MGC14817), mRNA", gi|31543151|ref|NM_032338.2|[31543151]; 347: NM_032348 , "Homo sapiens hypothetical protein MGC3047 (MGC3047), mRNA", gi|39725651|ref|NM_032348.2|[39725651]; 348: NM_032389 , "Homo sapiens zinc finger protein 289, ID1 regulated (ZNF289), mRNA", gi|31543982|ref|NM_032389.2|[31543982]; 349: NM_032842 , "Homo sapiens hypothetical protein FLJ14803 (FLJ14803), mRNA", gi|14249557|ref|NM_032842.1|[14249557]; 350: NM_130463 , "Homo sapiens ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 2", "(ATP6V1G2), transcript variant 1, mRNA", gi|20357536|ref|NM_130463.2|[20357536]; 351: NM_144718 , "Homo sapiens hypothetical protein AY099107 (LOC152185), mRNA", gi|40255074|ref|NM_144718.2|[40255074]; 352: NM_145804 , "Homo sapiens ankyrin repeat and BTB (POZ) domain containing 2 (ABTB2), mRNA", gi|21956638|ref|NM_145804.1|[21956638]; 353: NM_153045 , "Homo sapiens DKFZp547P234 protein (DKFZp547P234), mRNA", gi|33356141|ref|NM_153045.2|[33356141]; 354: NM_153354 , "Homo sapiens hypothetical protein MGC33214 (MGC33214), mRNA", gi|34222213|ref|NM_153354.2|[34222213], ,